



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:45 PM UTC

PDB ID : 5D2L / pdb_00005d2l
Title : Crystal structure of TCR C7 in complex with HCMV NLV epitope presented by HLA-A2
Authors : Gao, M.; Mariuzza, R.A.
Deposited on : 2015-08-05
Resolution : 3.51 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

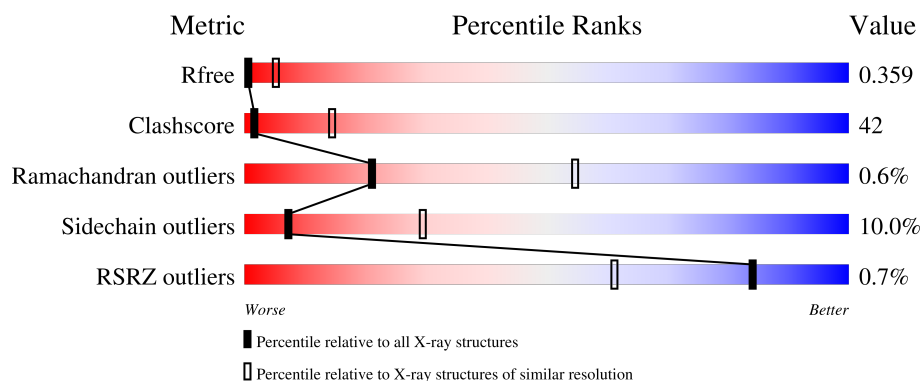
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.51 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



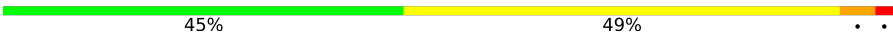
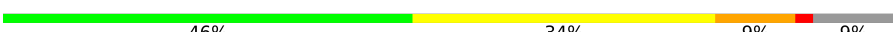
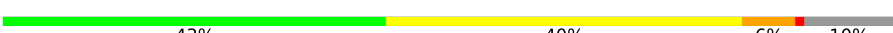
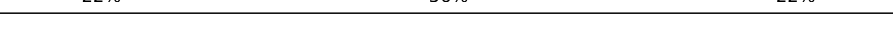
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1025 (3.56-3.48)
Clashscore	190562	1079 (3.56-3.48)
Ramachandran outliers	187476	1052 (3.56-3.48)
Sidechain outliers	187428	1053 (3.56-3.48)
RSRZ outliers	180081	1024 (3.56-3.48)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	276	
1	C	276	
1	G	276	
1	M	276	
2	B	100	

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Mol	Chain	Length	Quality of chain
2	D	100	
2	H	100	
2	N	100	
3	E	205	
3	I	205	
3	K	205	
3	O	205	
4	F	245	
4	J	245	
4	L	245	
4	P	245	
5	Q	9	
5	R	9	
5	T	9	
5	U	9	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 25272 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called HLA class I histocompatibility antigen, A-2 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	0	0
			2242	1401	408	424	9			
1	G	270	Total	C	N	O	S	0	0	0
			2199	1379	395	416	9			
1	M	273	Total	C	N	O	S	0	0	0
			2210	1379	401	421	9			
1	C	274	Total	C	N	O	S	0	0	0
			2242	1401	408	424	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P01892
G	0	MET	-	initiating methionine	UNP P01892
M	0	MET	-	initiating methionine	UNP P01892
C	0	MET	-	initiating methionine	UNP P01892

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	0	0
			823	522	140	158	3			
2	H	96	Total	C	N	O	S	0	0	0
			777	494	128	152	3			
2	N	100	Total	C	N	O	S	0	0	0
			825	524	138	159	4			
2	D	100	Total	C	N	O	S	0	0	0
			827	527	137	159	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
H	0	MET	-	initiating methionine	UNP P61769
N	0	MET	-	initiating methionine	UNP P61769
D	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called C7 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	185	Total	C	N	O	S	0	0	0
			1404	878	227	293	6			
3	K	192	Total	C	N	O	S	0	0	0
			1452	912	237	296	7			
3	O	187	Total	C	N	O	S	0	0	0
			1435	900	234	294	7			
3	E	187	Total	C	N	O	S	0	0	0
			1432	897	234	294	7			

- Molecule 4 is a protein called C7 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	J	226	Total	C	N	O	S	0	0	0
			1759	1108	303	343	5			
4	L	226	Total	C	N	O	S	0	0	0
			1699	1064	299	331	5			
4	P	235	Total	C	N	O	S	0	0	0
			1784	1122	306	351	5			
4	F	238	Total	C	N	O	S	0	0	0
			1852	1163	323	361	5			

- Molecule 5 is a protein called ASN-LEU-VAL-PRO-MET-VAL-ALA-THR-VAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	Q	9	Total	C	N	O	S	0	0	0
			64	42	10	11	1			
5	U	9	Total	C	N	O	S	0	0	0
			64	42	10	11	1			
5	T	9	Total	C	N	O	S	0	0	0
			64	42	10	11	1			
5	R	9	Total	C	N	O	S	0	0	0
			64	42	10	11	1			

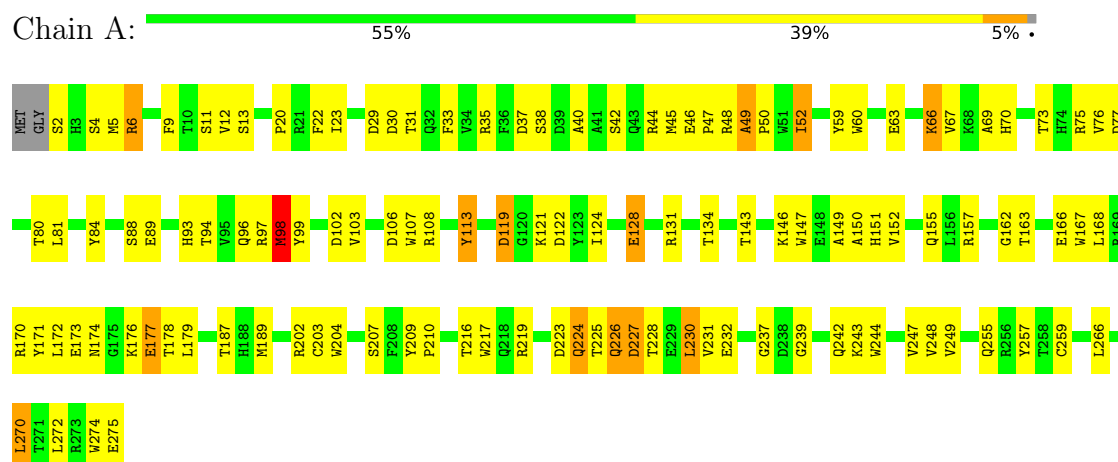
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	9	Total O 9 9	0	0
6	B	1	Total O 1 1	0	0
6	I	3	Total O 3 3	0	0
6	J	2	Total O 2 2	0	0
6	G	7	Total O 7 7	0	0
6	K	2	Total O 2 2	0	0
6	M	3	Total O 3 3	0	0
6	N	5	Total O 5 5	0	0
6	O	5	Total O 5 5	0	0
6	P	5	Total O 5 5	0	0
6	C	8	Total O 8 8	0	0
6	D	2	Total O 2 2	0	0
6	E	2	Total O 2 2	0	0

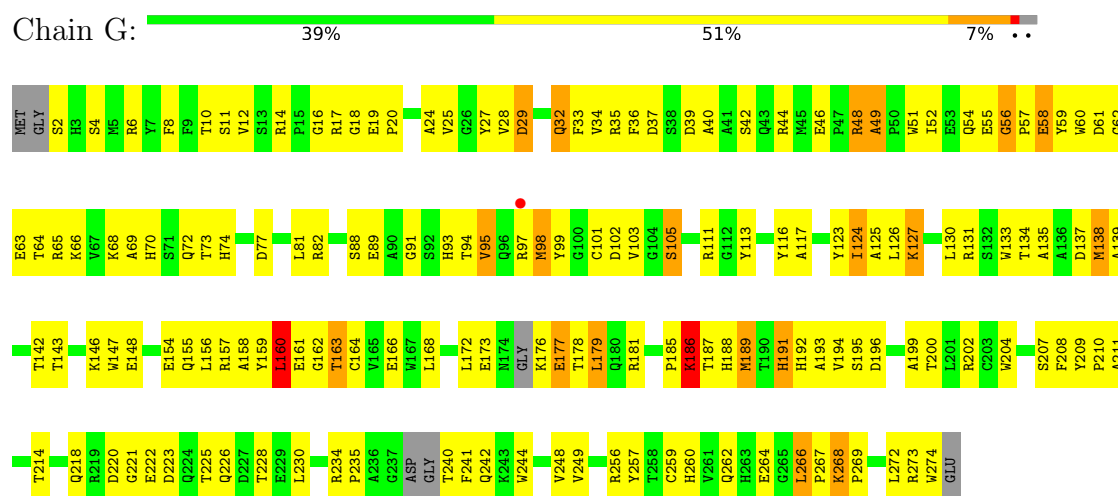
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain

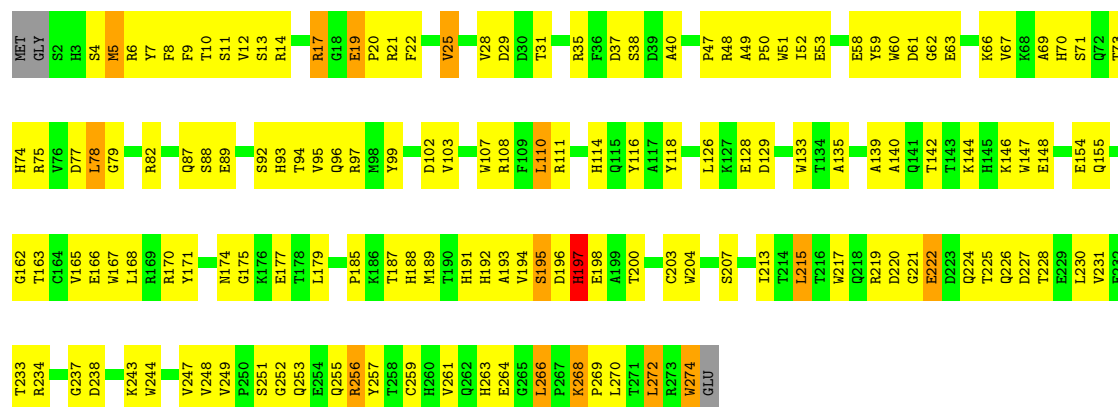


- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain



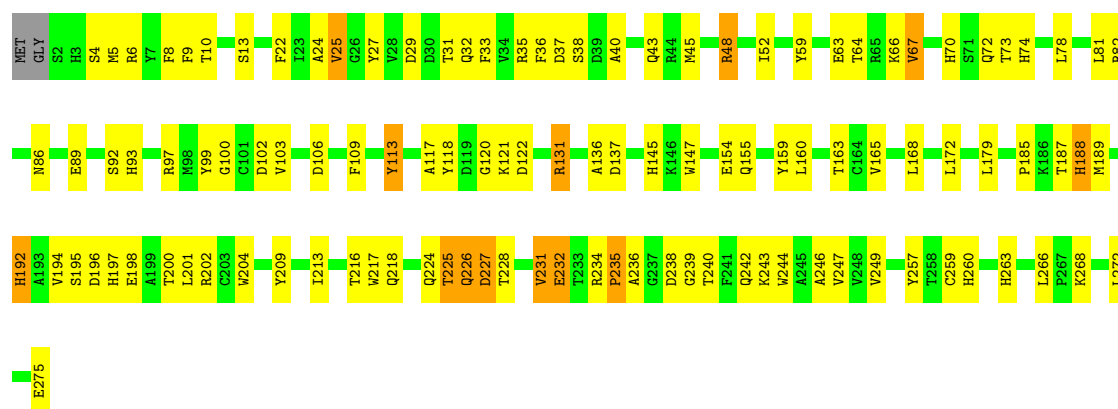
- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain





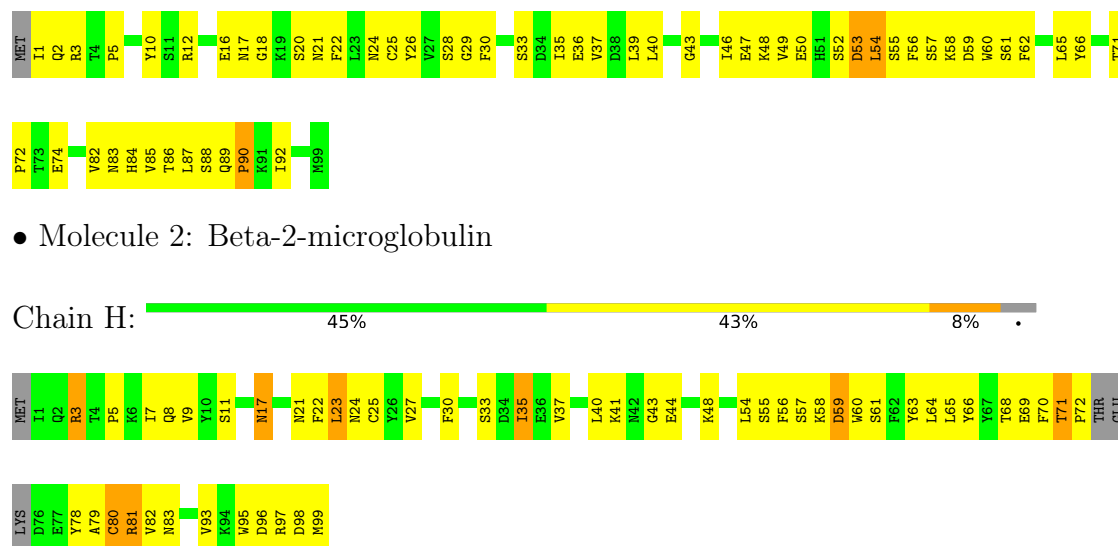
- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain

Chain C: 58% 36% 5% •

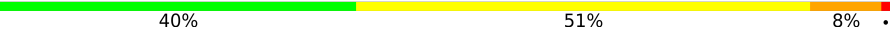


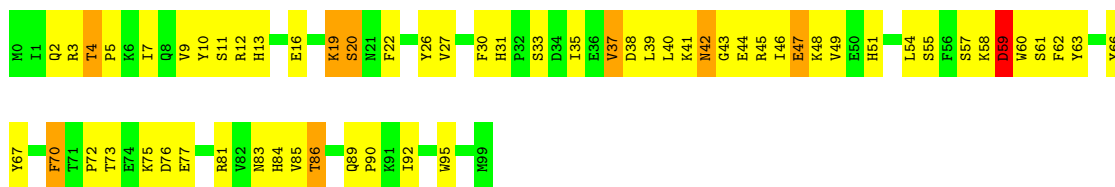
- Molecule 2: Beta-2-microglobulin

Chain B: 43% 53% • •



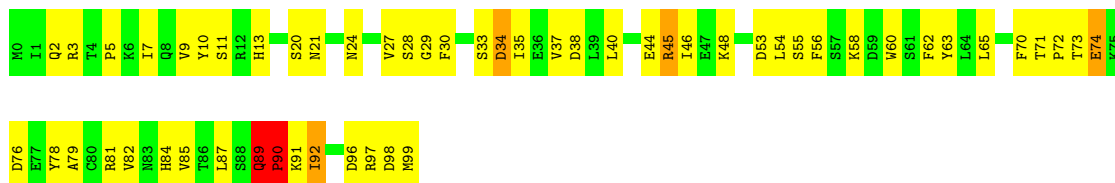
- Molecule 2: Beta-2-microglobulin

Chain N: 

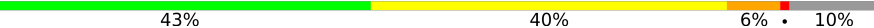


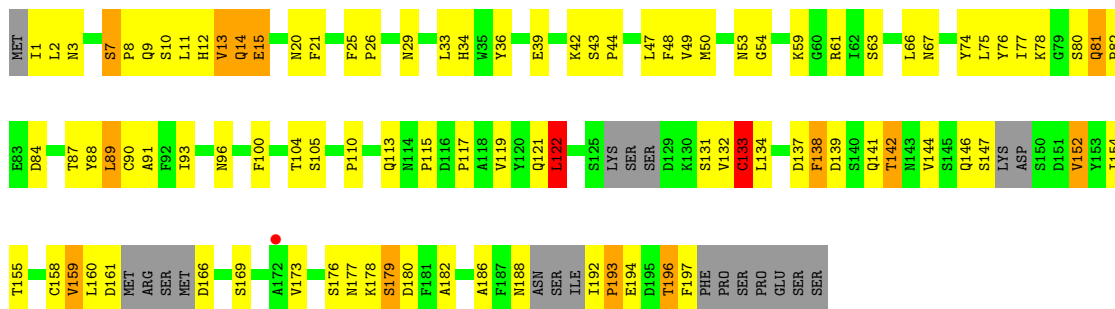
• Molecule 2: Beta-2-microglobulin

Chain D: 

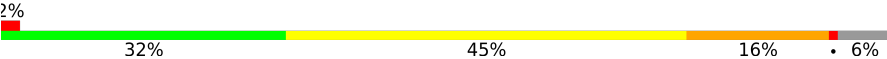


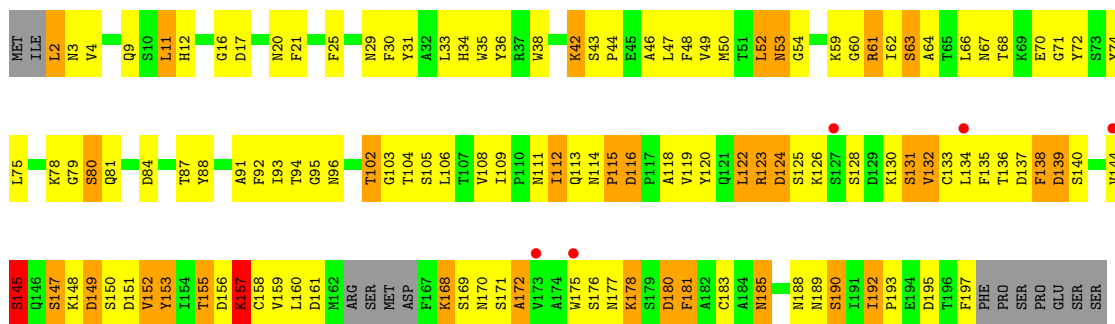
• Molecule 3: C7 TCR alpha chain

Chain I: 



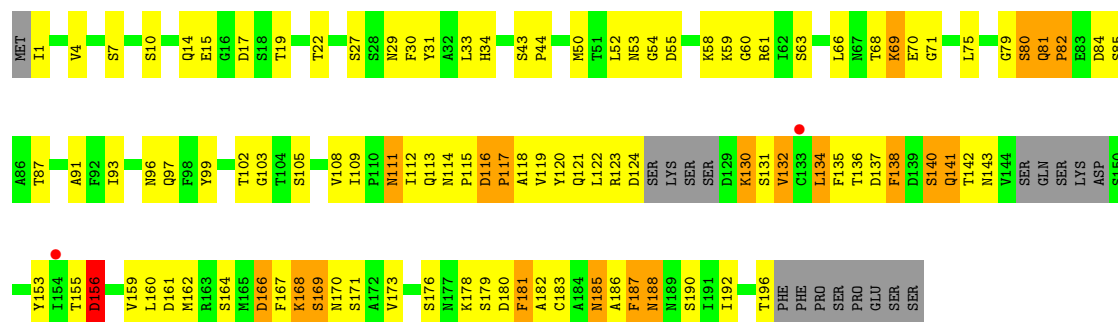
• Molecule 3: C7 TCR alpha chain

Chain K: 



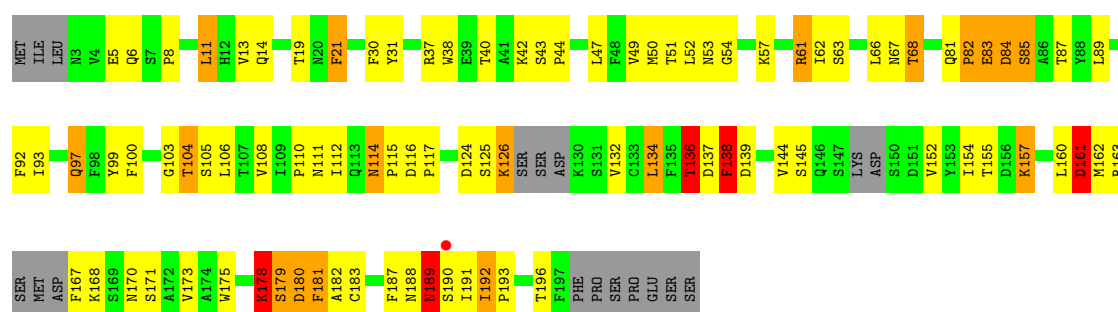
• Molecule 3: C7 TCR alpha chain

Chain O: 



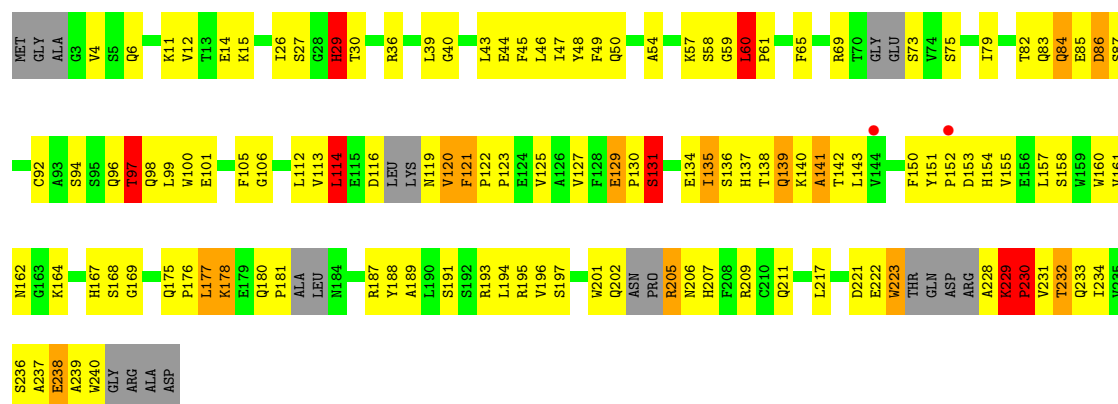
• Molecule 3: C7 TCR alpha chain

Chain E: 46% 34% 9% 9%



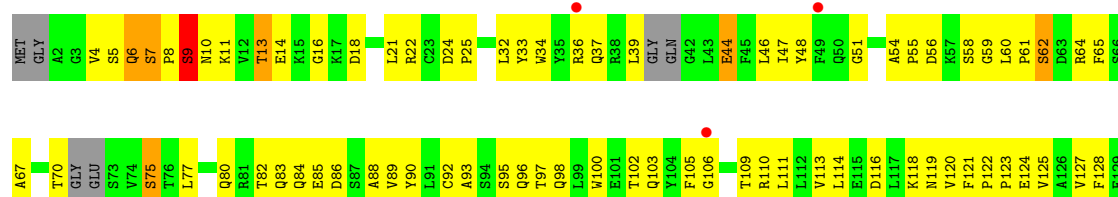
• Molecule 4: C7 TCR beta chain

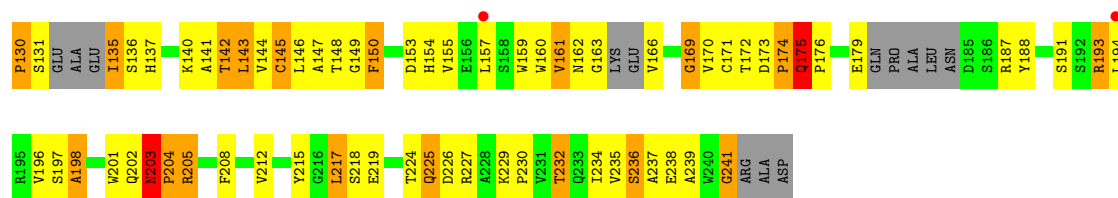
Chain J: 41% 42% 6% 8%



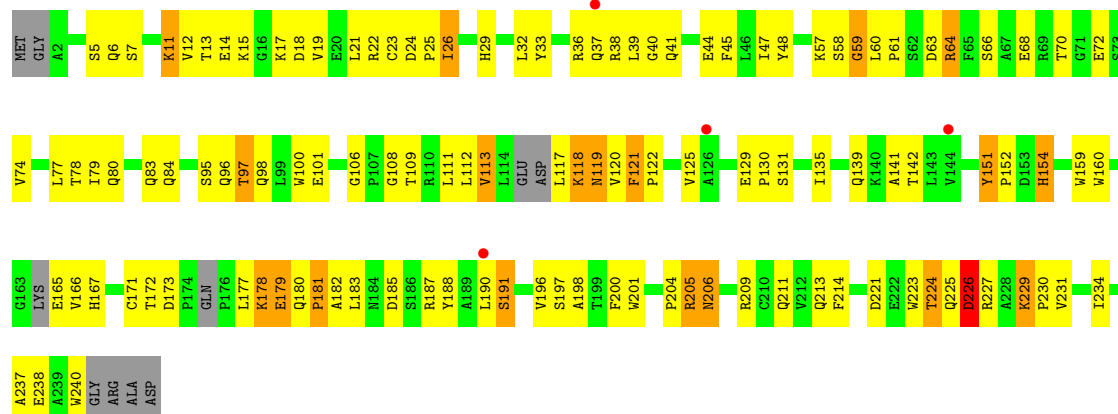
• Molecule 4: C7 TCR beta chain

Chain L: 33% 48% 10% 8%

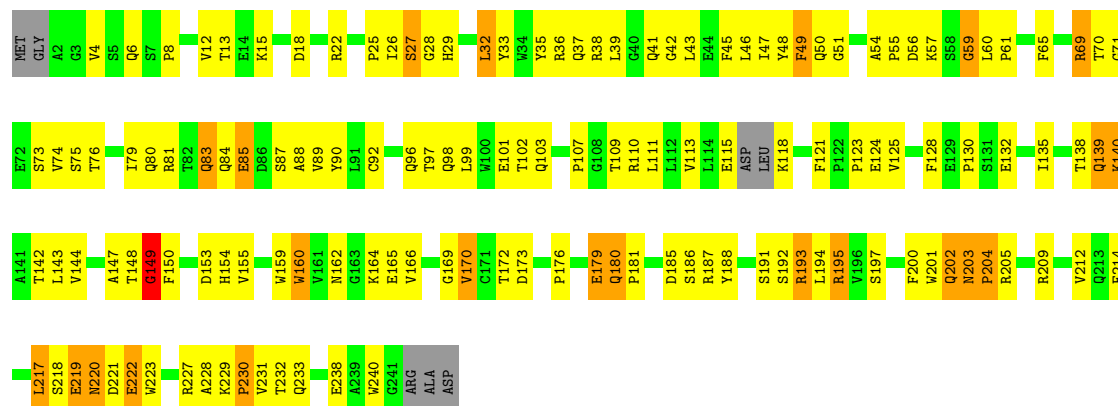




• Molecule 4: C7 TCR beta chain



• Molecule 4: C7 TCR beta chain



• Molecule 5: ASN-LEU-VAL-PRO-MET-VAL-ALA-THR-VAL

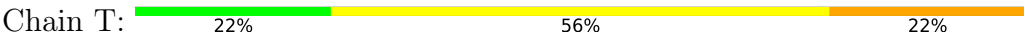


• Molecule 5: ASN-LEU-VAL-PRO-MET-VAL-ALA-THR-VAL

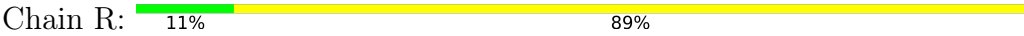




• Molecule 5: ASN-LEU-VAL-PRO-MET-VAL-ALA-THR-VAL



• Molecule 5: ASN-LEU-VAL-PRO-MET-VAL-ALA-THR-VAL



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	151.76Å 366.64Å 151.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.51 – 3.51 49.51 – 3.51	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.51-3.51) 91.3 (49.51-3.51)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 3.48Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.270 , 0.355 0.276 , 0.359	Depositor DCC
R_{free} test set	2702 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	79.4	Xtrriage
Anisotropy	0.599	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 63.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	25272	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 26.44 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.6340e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.62	3/2307 (0.1%)	0.96	8/3132 (0.3%)
1	C	0.58	1/2307 (0.0%)	0.92	6/3132 (0.2%)
1	G	0.69	1/2262 (0.0%)	1.13	12/3072 (0.4%)
1	M	0.55	1/2272 (0.0%)	1.03	9/3085 (0.3%)
2	B	0.60	0/845	1.02	3/1143 (0.3%)
2	D	0.64	1/850 (0.1%)	1.01	7/1151 (0.6%)
2	H	0.57	0/798	0.97	1/1083 (0.1%)
2	N	0.65	0/848	1.17	8/1150 (0.7%)
3	E	0.56	0/1463	1.10	13/1987 (0.7%)
3	I	0.74	2/1433 (0.1%)	1.14	9/1946 (0.5%)
3	K	0.73	1/1486 (0.1%)	1.32	28/2018 (1.4%)
3	O	0.75	5/1466 (0.3%)	1.24	21/1992 (1.1%)
4	F	0.71	2/1900 (0.1%)	1.12	11/2586 (0.4%)
4	J	0.65	2/1801 (0.1%)	1.18	12/2448 (0.5%)
4	L	0.72	3/1737 (0.2%)	1.43	35/2362 (1.5%)
4	P	0.59	2/1829 (0.1%)	1.15	16/2494 (0.6%)
5	Q	0.63	0/64	1.07	0/88
5	R	0.50	0/64	1.03	0/88
5	T	0.90	0/64	1.34	2/88 (2.3%)
5	U	0.44	0/64	0.76	0/88
All	All	0.65	24/25860 (0.1%)	1.12	201/35133 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	G	0	4
2	H	0	1
2	N	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	E	0	3
3	K	0	5
3	O	0	3
4	F	0	3
4	J	0	2
4	L	0	5
4	P	0	3
All	All	0	32

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	O	43	SER	C-N	8.17	1.41	1.33
3	K	172	ALA	CA-CB	-7.55	1.41	1.53
4	L	203	ASN	C-N	5.75	1.41	1.33
3	O	116	ASP	C-N	5.75	1.40	1.33
4	L	54	ALA	C-N	5.65	1.40	1.33
4	F	229	LYS	C-N	5.52	1.40	1.33
1	A	98	MET	C-O	-5.50	1.17	1.24
3	O	81	GLN	C-N	5.49	1.41	1.34
4	P	180	GLN	C-N	5.41	1.40	1.33
1	A	226	GLN	N-CA	-5.39	1.38	1.45
1	M	19	GLU	C-N	5.34	1.40	1.33
1	G	267	PRO	N-CD	5.32	1.55	1.47
4	J	230	PRO	N-CD	5.28	1.55	1.47
3	I	119	VAL	CA-CB	5.27	1.59	1.53
3	O	82	PRO	N-CD	5.20	1.55	1.47
3	O	117	PRO	N-CD	5.20	1.55	1.47
3	I	133	CYS	CA-C	5.19	1.58	1.52
4	F	230	PRO	N-CD	5.15	1.54	1.47
4	J	61	PRO	N-CD	5.07	1.54	1.47
1	A	20	PRO	N-CD	5.07	1.54	1.47
4	L	55	PRO	N-CD	5.06	1.54	1.47
1	C	232	GLU	CA-C	-5.03	1.46	1.52
2	D	90	PRO	N-CD	5.03	1.54	1.47
4	P	181	PRO	N-CD	5.01	1.54	1.47

All (201) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	179	LEU	N-CA-C	17.75	132.81	111.33
4	L	149	GLY	N-CA-C	16.17	139.73	115.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	138	THR	N-CA-C	14.73	127.05	111.14
4	L	4	VAL	N-CA-C	12.04	125.99	108.53
3	I	7	SER	C-N-CD	-11.91	94.40	120.60
3	E	114	ASN	CA-C-N	10.76	131.45	119.83
3	E	114	ASN	C-N-CA	10.76	131.45	119.83
4	L	241	GLY	N-CA-C	10.66	144.23	113.30
3	K	157	LYS	N-CA-C	10.04	124.66	110.50
4	P	151	TYR	N-CA-C	-9.88	99.33	108.22
4	F	204	PRO	N-CA-C	9.03	126.08	113.53
4	P	178	LYS	N-CA-C	-8.79	98.93	110.53
3	O	130	LYS	N-CA-C	8.76	121.21	108.86
4	J	60	LEU	N-CA-C	-8.75	99.08	109.93
1	A	227	ASP	N-CA-C	-8.74	102.32	113.16
4	L	9	SER	N-CA-C	8.71	120.39	111.07
1	M	197	HIS	N-CA-C	-8.71	102.83	113.97
4	P	118	LYS	N-CA-C	8.58	120.63	111.28
1	M	110	LEU	N-CA-C	8.46	120.51	111.28
2	N	59	ASP	N-CA-C	-8.42	102.79	113.23
3	K	185	ASN	N-CA-C	-8.32	102.44	112.59
3	O	185	ASN	N-CA-C	-8.09	102.42	111.07
4	L	86	ASP	N-CA-C	-8.08	97.50	109.62
1	G	193	ALA	CA-C-N	8.08	133.75	122.28
1	G	193	ALA	C-N-CA	8.08	133.75	122.28
2	B	53	ASP	N-CA-C	-8.03	99.18	110.50
4	J	229	LYS	C-N-CD	8.02	138.24	120.60
4	L	169	GLY	N-CA-C	-7.95	104.59	114.92
3	E	189	ASN	N-CA-C	-7.89	104.81	114.75
3	K	190	SER	N-CA-C	-7.88	94.22	108.02
3	K	176	SER	N-CA-C	7.54	120.71	108.41
4	P	179	GLU	N-CA-C	-7.54	99.87	110.50
1	C	236	ALA	N-CA-C	-7.52	100.82	110.53
4	L	225	GLN	N-CA-C	7.50	121.36	109.65
3	I	122	LEU	N-CA-C	-7.47	94.88	110.80
4	L	56	ASP	N-CA-C	-7.43	94.97	110.80
4	F	229	LYS	CA-C-N	-7.30	112.48	119.85
4	F	229	LYS	C-N-CA	-7.30	112.48	119.85
1	G	194	VAL	N-CA-C	-7.25	105.47	112.29
4	L	54	ALA	CA-C-N	-7.21	112.89	120.03
4	L	54	ALA	C-N-CA	-7.21	112.89	120.03
3	O	113	GLN	CA-C-N	7.18	130.16	122.26
3	O	113	GLN	C-N-CA	7.18	130.16	122.26
4	J	232	THR	N-CA-C	-7.15	99.31	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	GLY	N-CA-C	7.11	116.68	110.21
3	O	116	ASP	CA-C-N	-7.09	113.40	120.21
3	O	116	ASP	C-N-CA	-7.09	113.40	120.21
2	B	48	LYS	N-CA-C	-7.06	104.59	112.57
1	A	224	GLN	CA-C-N	6.97	129.61	120.28
1	A	224	GLN	C-N-CA	6.97	129.61	120.28
4	L	174	PRO	N-CA-CB	6.96	110.55	103.25
4	L	60	LEU	CA-C-N	6.89	126.36	118.85
4	L	60	LEU	C-N-CA	6.89	126.36	118.85
3	K	122	LEU	CA-C-N	-6.82	113.04	122.93
3	K	122	LEU	C-N-CA	-6.82	113.04	122.93
3	K	46	ALA	N-CA-C	-6.81	101.54	110.53
3	O	141	GLN	N-CA-C	-6.80	104.71	112.87
4	L	106	GLY	CA-C-N	6.76	126.27	119.24
4	L	106	GLY	C-N-CA	6.76	126.27	119.24
4	P	63	ASP	N-CA-C	6.74	118.62	111.28
4	F	202	GLN	N-CA-C	6.73	118.27	111.07
1	A	49	ALA	CA-C-N	6.71	128.23	119.84
1	A	49	ALA	C-N-CA	6.71	128.23	119.84
3	I	139	ASP	N-CA-C	6.68	118.93	110.24
1	M	252	GLY	N-CA-C	-6.67	105.99	113.79
4	J	168	SER	N-CA-C	6.66	118.33	111.14
4	L	203	ASN	CA-C-N	-6.63	112.95	119.78
4	L	203	ASN	C-N-CA	-6.63	112.95	119.78
4	F	83	GLN	N-CA-C	6.58	116.93	108.24
2	N	48	LYS	N-CA-C	-6.56	104.42	112.88
4	P	180	GLN	CA-C-N	-6.53	113.04	119.76
4	P	180	GLN	C-N-CA	-6.53	113.04	119.76
4	J	141	ALA	N-CA-C	-6.50	99.53	109.41
4	L	62	SER	N-CA-C	6.49	118.01	111.07
4	L	137	HIS	N-CA-C	-6.42	105.61	113.50
3	K	145	SER	N-CA-C	6.41	119.06	108.49
1	G	160	LEU	N-CA-C	-6.38	104.25	111.14
4	J	121	PHE	N-CA-C	6.38	113.96	108.22
4	L	198	ALA	CB-CA-C	-6.37	109.24	116.63
4	P	185	ASP	N-CA-C	6.36	116.97	108.38
4	P	226	ASP	N-CA-C	6.35	118.20	111.28
2	D	2	GLN	CA-CB-CG	6.32	126.74	114.10
3	I	196	THR	N-CA-C	6.30	120.73	111.34
3	K	140	SER	N-CA-C	6.29	118.53	108.41
3	E	188	ASN	N-CA-C	6.28	119.04	107.99
1	M	50	PRO	N-CA-CB	6.26	110.15	103.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	193	PRO	CA-N-CD	-6.24	103.27	112.00
1	G	163	THR	N-CA-C	6.23	117.73	111.07
1	C	232	GLU	N-CA-C	-6.22	101.07	110.28
3	O	169	SER	CA-C-N	-6.19	113.46	122.19
3	O	169	SER	C-N-CA	-6.19	113.46	122.19
2	N	42	ASN	N-CA-C	6.17	123.94	110.80
3	K	63	SER	N-CA-C	6.14	119.25	108.75
4	J	129	GLU	CA-C-N	6.09	127.45	119.84
4	J	129	GLU	C-N-CA	6.09	127.45	119.84
3	K	181	PHE	N-CA-C	6.00	120.18	112.26
3	E	136	THR	N-CA-C	6.00	118.30	109.24
1	M	256	ARG	N-CA-C	-6.00	106.00	113.38
1	A	6	ARG	N-CA-C	5.99	119.24	109.06
4	L	130	PRO	N-CA-C	5.96	120.02	111.13
3	K	132	VAL	N-CA-C	5.94	118.31	109.17
1	G	177	GLU	N-CA-C	5.93	117.82	111.36
4	F	149	GLY	N-CA-C	-5.92	99.14	113.18
1	G	49	ALA	CA-C-N	5.88	125.58	119.82
1	G	49	ALA	C-N-CA	5.88	125.58	119.82
3	K	116	ASP	CA-C-N	5.86	127.16	119.84
3	K	116	ASP	C-N-CA	5.86	127.16	119.84
3	O	132	VAL	N-CA-C	5.84	116.41	110.05
2	N	19	LYS	N-CA-C	5.82	117.25	108.46
4	L	75	SER	N-CA-C	5.81	117.08	108.60
3	K	125	SER	N-CA-C	-5.80	100.33	109.50
5	T	8	THR	N-CA-C	5.80	117.58	107.49
4	J	29	HIS	N-CA-C	-5.78	102.90	110.53
2	N	47	GLU	N-CA-C	5.78	117.46	109.54
1	M	78	LEU	N-CA-C	-5.77	104.19	111.11
4	F	219	GLU	N-CA-C	-5.77	101.75	110.28
3	E	138	PHE	N-CA-C	5.74	118.25	108.90
4	L	205	ARG	N-CA-C	5.71	118.26	109.07
4	F	59	GLY	N-CA-C	-5.69	105.90	112.73
3	K	152	VAL	N-CA-C	5.67	115.86	110.42
4	P	121	PHE	CA-C-N	5.66	126.21	120.38
4	P	121	PHE	C-N-CA	5.66	126.21	120.38
3	K	192	ILE	N-CA-CB	-5.66	107.93	111.83
1	M	19	GLU	CA-C-N	-5.64	113.97	119.78
1	M	19	GLU	C-N-CA	-5.64	113.97	119.78
3	K	138	PHE	CA-C-N	-5.63	113.00	122.29
3	K	138	PHE	C-N-CA	-5.63	113.00	122.29
3	O	156	ASP	N-CA-C	5.62	117.81	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	106	GLY	CA-C-N	5.61	126.85	119.84
4	P	106	GLY	C-N-CA	5.61	126.85	119.84
3	K	172	ALA	N-CA-C	5.58	117.60	108.55
1	G	32	GLN	N-CA-C	5.57	119.17	110.32
3	E	82	PRO	CA-C-N	-5.56	114.91	123.14
3	E	82	PRO	C-N-CA	-5.56	114.91	123.14
1	C	268	LYS	CA-C-N	-5.55	113.98	119.92
1	C	268	LYS	C-N-CA	-5.55	113.98	119.92
2	D	89	GLN	N-CA-C	-5.55	101.81	108.25
4	L	236	SER	N-CA-C	5.54	118.28	109.24
4	L	225	GLN	CA-CB-CG	5.54	125.17	114.10
4	L	13	THR	N-CA-C	5.54	116.38	108.74
4	L	7	SER	N-CA-C	-5.53	102.50	110.40
1	M	195	SER	N-CA-C	5.52	119.05	111.54
4	P	188	TYR	N-CA-C	5.52	117.81	109.41
1	G	266	LEU	CA-C-N	-5.50	112.95	119.05
1	G	266	LEU	C-N-CA	-5.50	112.95	119.05
3	O	181	PHE	N-CA-C	-5.50	105.29	111.28
2	N	4	THR	N-CA-C	5.45	116.27	109.57
2	D	89	GLN	CA-C-N	-5.43	113.05	119.84
2	D	89	GLN	C-N-CA	-5.43	113.05	119.84
2	D	71	THR	CA-C-N	5.42	125.88	120.14
2	D	71	THR	C-N-CA	5.42	125.88	120.14
3	E	192	ILE	CA-C-N	-5.41	114.77	120.66
3	E	192	ILE	C-N-CA	-5.41	114.77	120.66
4	J	131	SER	N-CA-C	5.40	118.35	109.76
2	N	20	SER	N-CA-C	5.36	122.22	110.80
3	K	147	SER	N-CA-C	5.35	122.19	110.80
4	P	224	THR	N-CA-C	5.34	116.91	111.14
4	P	26	ILE	N-CA-C	-5.33	102.17	109.37
3	O	43	SER	CA-C-N	-5.33	112.63	120.46
3	O	43	SER	C-N-CA	-5.33	112.63	120.46
4	L	229	LYS	CA-C-N	5.32	126.49	119.84
4	L	229	LYS	C-N-CA	5.32	126.49	119.84
1	C	29	ASP	CB-CA-C	-5.31	110.01	117.23
3	K	124	ASP	N-CA-C	5.31	117.40	108.96
3	E	116	ASP	CA-C-N	5.30	126.46	119.84
3	E	116	ASP	C-N-CA	5.30	126.46	119.84
4	L	175	GLN	CA-C-N	5.28	126.45	119.84
4	L	175	GLN	C-N-CA	5.28	126.45	119.84
2	H	59	ASP	N-CA-C	-5.28	106.23	113.30
4	F	233	GLN	N-CA-C	5.27	116.82	108.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	O	81	GLN	CA-C-N	-5.25	113.51	118.97
3	O	81	GLN	C-N-CA	-5.25	113.51	118.97
1	C	239	GLY	N-CA-C	-5.24	107.82	115.63
3	I	119	VAL	CA-C-N	-5.22	116.06	122.84
3	I	119	VAL	C-N-CA	-5.22	116.06	122.84
4	L	161	VAL	N-CA-C	5.16	116.44	108.44
4	L	51	GLY	N-CA-C	-5.16	102.53	111.50
3	O	159	VAL	N-CA-C	5.15	116.72	108.89
1	A	177	GLU	N-CA-C	5.14	117.28	111.11
3	K	178	LYS	N-CA-C	5.13	119.16	108.53
3	O	82	PRO	CA-C-N	-5.12	112.54	122.06
3	O	82	PRO	C-N-CA	-5.12	112.54	122.06
2	N	86	THR	N-CA-C	-5.11	105.71	111.28
2	D	34	ASP	N-CA-C	-5.11	99.46	108.20
3	K	192	ILE	CA-C-N	-5.10	113.46	119.84
3	K	192	ILE	C-N-CA	-5.10	113.46	119.84
3	E	178	LYS	N-CA-C	5.09	116.95	107.99
3	O	190	SER	N-CA-C	-5.09	105.85	113.89
4	F	28	GLY	N-CA-C	-5.07	101.16	113.18
5	T	3	VAL	N-CA-C	-5.07	104.31	109.02
3	I	142	THR	CA-C-N	-5.04	116.00	123.05
3	I	142	THR	C-N-CA	-5.04	116.00	123.05
2	B	90	PRO	N-CA-C	-5.03	103.29	111.14
4	F	179	GLU	N-CA-C	5.03	116.61	111.03
4	L	229	LYS	N-CA-C	5.02	115.38	109.60
3	K	123	ARG	N-CA-C	5.02	117.67	109.59
4	L	198	ALA	N-CA-C	5.02	116.56	108.08
4	J	230	PRO	CA-N-CD	-5.01	104.48	111.50
3	K	109	ILE	CA-C-N	5.01	125.00	119.89
3	K	109	ILE	C-N-CA	5.01	125.00	119.89
3	O	188	ASN	N-CA-C	-5.00	105.72	111.07

There are no chirality outliers.

All (32) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	224	GLN	Mainchain
1	C	225	THR	Peptide
3	E	161	ASP	Peptide
3	E	181	PHE	Peptide
3	E	84	ASP	Peptide
4	F	149	GLY	Peptide

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Mol	Chain	Res	Type	Group
4	F	27	SER	Peptide
4	F	69	ARG	Peptide
1	G	105	SER	Peptide
1	G	160	LEU	Mainchain
1	G	186	LYS	Peptide
1	G	56	GLY	Peptide
2	H	17	ASN	Peptide
4	J	229	LYS	Peptide
4	J	97	THR	Peptide
3	K	130	LYS	Peptide
3	K	131	SER	Peptide
3	K	139	ASP	Peptide
3	K	145	SER	Peptide
3	K	54	GLY	Peptide
4	L	136	SER	Peptide
4	L	204	PRO	Peptide
4	L	232	THR	Peptide
4	L	58	SER	Peptide
4	L	9	SER	Peptide
2	N	19	LYS	Peptide
3	O	111	ASN	Peptide
3	O	136	THR	Peptide
3	O	156	ASP	Peptide
4	P	206	ASN	Peptide
4	P	224	THR	Peptide
4	P	59	GLY	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2242	0	2090	137	0
1	C	2242	0	2090	126	0
1	G	2199	0	2039	230	0
1	M	2210	0	2042	167	0
2	B	823	0	787	48	0
2	D	827	0	781	51	0
2	H	777	0	715	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	N	825	0	770	80	0
3	E	1432	0	1307	109	0
3	I	1404	0	1269	128	1
3	K	1452	0	1320	214	4
3	O	1435	0	1323	110	2
4	F	1852	0	1726	186	0
4	J	1759	0	1634	161	0
4	L	1699	0	1542	208	0
4	P	1784	0	1638	138	2
5	Q	64	0	74	15	0
5	R	64	0	74	12	0
5	T	64	0	74	14	0
5	U	64	0	74	27	0
6	A	9	0	0	4	0
6	B	1	0	0	0	0
6	C	8	0	0	1	0
6	D	2	0	0	0	0
6	E	2	0	0	0	0
6	G	7	0	0	3	0
6	I	3	0	0	1	0
6	J	2	0	0	1	0
6	K	2	0	0	0	0
6	M	3	0	0	3	0
6	N	5	0	0	2	0
6	O	5	0	0	0	0
6	P	5	0	0	1	0
All	All	25272	0	23369	2036	5

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 42.

All (2036) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:192:ILE:HG23	3:I:193:PRO:CD	1.42	1.46
1:A:230:LEU:HD21	1:A:243:LYS:NZ	1.27	1.43
3:K:175:TRP:CZ2	4:L:146:LEU:HD22	1.53	1.42
4:L:88:ALA:CB	4:L:110:ARG:HG3	1.46	1.41
1:G:98:MET:HE1	1:G:113:TYR:CE1	1.56	1.41
3:K:112:ILE:CG2	3:K:139:ASP:HB3	1.48	1.41
3:K:175:TRP:CZ2	4:L:146:LEU:HD13	1.57	1.38

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:170:VAL:HA	4:L:194:LEU:CD2	1.51	1.38
3:K:38:TRP:CE3	3:K:44:PRO:HG3	1.59	1.38
4:P:112:LEU:CD1	4:P:154:HIS:CE1	2.05	1.38
1:C:202:ARG:CD	1:C:244:TRP:HE1	1.37	1.35
3:I:192:ILE:CG2	3:I:193:PRO:HD3	1.57	1.35
4:J:29:HIS:HD2	4:J:94:SER:CB	1.40	1.34
3:K:61:ARG:HD2	3:K:78:LYS:O	1.25	1.32
4:P:14:GLU:OE2	4:P:117:LEU:CD2	1.76	1.31
1:A:102:ASP:CG	1:A:113:TYR:OH	1.73	1.31
1:G:98:MET:HE2	1:G:113:TYR:CD1	1.66	1.31
1:G:98:MET:CE	1:G:113:TYR:CE1	2.15	1.30
2:N:13:HIS:CE1	4:F:81:ARG:NH2	1.99	1.29
2:D:44:GLU:OE2	2:D:46:ILE:HD11	1.28	1.28
3:K:138:PHE:HE1	3:K:157:LYS:CE	1.45	1.27
3:I:8:PRO:O	3:I:104:THR:HG23	1.23	1.27
1:G:192:HIS:CD2	1:G:202:ARG:HH21	1.51	1.26
1:G:98:MET:CE	1:G:113:TYR:CD1	2.19	1.26
4:F:170:VAL:CG1	4:F:194:LEU:HD13	1.64	1.26
1:A:4:SER:HB2	1:A:102:ASP:OD1	1.36	1.25
3:K:175:TRP:CZ2	4:L:146:LEU:CD2	2.19	1.25
4:P:7:SER:OG	4:P:22:ARG:HB3	1.35	1.25
1:A:230:LEU:CD2	1:A:243:LYS:NZ	1.98	1.24
4:J:47:ILE:HD11	4:J:60:LEU:CD2	1.66	1.24
3:K:175:TRP:HZ2	4:L:146:LEU:CG	1.52	1.21
1:G:97:ARG:NH1	5:U:6:VAL:CG1	2.01	1.21
4:L:88:ALA:HB3	4:L:110:ARG:CG	1.70	1.20
3:K:175:TRP:CZ2	4:L:146:LEU:CD1	2.23	1.20
3:E:167:PHE:HD2	3:E:168:LYS:N	1.39	1.20
1:G:97:ARG:HH11	5:U:6:VAL:CG1	1.52	1.19
3:K:161:ASP:CG	3:K:168:LYS:HD3	1.65	1.19
3:O:138:PHE:CE1	3:O:142:THR:HG21	1.75	1.19
1:G:97:ARG:HH11	5:U:6:VAL:HG11	1.08	1.19
3:K:136:THR:HG22	3:K:171:SER:HA	1.23	1.19
3:K:112:ILE:CG2	3:K:139:ASP:CB	2.21	1.17
4:J:29:HIS:CD2	4:J:94:SER:CB	2.27	1.17
3:K:138:PHE:CE1	3:K:157:LYS:CE	2.27	1.17
4:P:112:LEU:HD11	4:P:154:HIS:CE1	1.74	1.16
1:G:97:ARG:NE	1:G:116:TYR:HE1	1.41	1.16
3:I:122:LEU:CA	3:I:132:VAL:O	1.93	1.15
1:A:230:LEU:HD21	1:A:243:LYS:CE	1.77	1.14
3:O:182:ALA:HB1	3:O:185:ASN:HB3	1.24	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:89:VAL:HG12	4:L:110:ARG:CB	1.75	1.14
3:K:148:LYS:HB3	3:K:149:ASP:O	1.46	1.14
4:L:89:VAL:HG12	4:L:110:ARG:HB2	1.27	1.14
3:K:138:PHE:CE1	3:K:157:LYS:HE2	1.84	1.13
1:G:16:GLY:HA3	1:G:17:ARG:HB2	1.29	1.12
1:C:202:ARG:HD3	1:C:244:TRP:HE1	1.01	1.12
4:L:83:GLN:HG3	4:L:84:GLN:H	0.98	1.12
2:N:40:LEU:HD23	2:N:43:GLY:HA3	1.13	1.12
3:K:175:TRP:CE2	4:L:146:LEU:HD22	1.82	1.12
1:A:230:LEU:CD2	1:A:243:LYS:CE	2.28	1.12
1:A:4:SER:HB3	1:A:102:ASP:CG	1.75	1.11
4:F:170:VAL:HG13	4:F:194:LEU:CD1	1.78	1.11
3:I:146:GLN:CD	3:I:154:ILE:HG12	1.75	1.11
3:K:175:TRP:HZ2	4:L:146:LEU:CD2	1.58	1.11
4:J:29:HIS:HD2	4:J:94:SER:HB2	1.07	1.10
4:L:88:ALA:HB1	4:L:89:VAL:HA	1.31	1.09
4:P:112:LEU:HD12	4:P:154:HIS:CE1	1.83	1.09
3:O:53:ASN:HB2	3:O:68:THR:HG23	1.33	1.09
4:F:54:ALA:HB1	4:F:57:LYS:HE3	1.27	1.09
3:K:175:TRP:HZ2	4:L:146:LEU:CD1	1.64	1.09
3:K:138:PHE:HE1	3:K:157:LYS:HE2	0.97	1.08
1:G:192:HIS:CD2	1:G:202:ARG:NH2	2.22	1.08
3:K:138:PHE:CE1	3:K:157:LYS:HE3	1.89	1.08
3:O:138:PHE:CE1	3:O:142:THR:CG2	2.35	1.07
4:P:14:GLU:CD	4:P:117:LEU:HD21	1.77	1.07
4:J:47:ILE:HD11	4:J:60:LEU:HD21	1.12	1.07
2:N:73:THR:CG2	2:N:76:ASP:OD1	2.01	1.07
4:F:218:SER:OG	4:F:221:ASP:HB2	1.55	1.07
3:E:136:THR:HG23	3:E:171:SER:HB2	1.14	1.07
1:G:2:SER:N	1:G:105:SER:HG	1.52	1.07
3:O:138:PHE:HE1	3:O:142:THR:CG2	1.68	1.07
4:P:97:THR:HG22	4:P:98:GLN:HG2	1.37	1.07
1:A:102:ASP:CG	1:A:113:TYR:HH	1.55	1.06
4:J:141:ALA:HB3	4:J:196:VAL:O	1.55	1.06
1:M:78:LEU:HD23	1:M:95:VAL:CG2	1.86	1.06
3:K:148:LYS:HB3	3:K:149:ASP:C	1.79	1.06
4:P:223:TRP:CH2	4:P:229:LYS:O	2.09	1.06
1:G:97:ARG:NE	1:G:116:TYR:CE1	2.15	1.06
3:K:112:ILE:HG23	3:K:139:ASP:HB3	1.10	1.05
1:C:202:ARG:HD3	1:C:244:TRP:NE1	1.69	1.05
1:C:202:ARG:CG	1:C:244:TRP:HE1	1.68	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:88:ALA:CB	4:L:110:ARG:CG	2.27	1.05
4:J:29:HIS:CD2	4:J:94:SER:HB2	1.87	1.05
4:P:14:GLU:HG2	4:P:117:LEU:HG	1.06	1.05
3:K:61:ARG:CD	3:K:78:LYS:O	2.04	1.05
2:B:37:VAL:HG12	2:B:82:VAL:HG22	1.10	1.05
1:M:19:GLU:OE1	1:M:19:GLU:N	1.88	1.04
1:M:66:LYS:HZ1	3:O:29:ASN:CG	1.65	1.04
4:J:29:HIS:CD2	4:J:94:SER:OG	2.09	1.04
2:N:73:THR:HG22	2:N:76:ASP:OD1	1.56	1.04
4:P:14:GLU:HG2	4:P:117:LEU:CG	1.87	1.04
3:I:33:LEU:HD12	3:I:91:ALA:O	1.58	1.04
4:P:112:LEU:HD11	4:P:154:HIS:HE1	1.10	1.04
4:J:113:VAL:O	4:J:114:LEU:HG	1.57	1.03
4:L:170:VAL:CA	4:L:194:LEU:CD2	2.35	1.03
4:P:14:GLU:OE2	4:P:117:LEU:HD21	0.87	1.03
4:P:14:GLU:CG	4:P:117:LEU:HG	1.89	1.03
3:K:185:ASN:O	3:K:188:ASN:ND2	1.91	1.03
1:M:20:PRO:HD2	1:M:75:ARG:CD	1.89	1.03
4:J:136:SER:HA	4:J:139:GLN:OE1	1.58	1.03
4:L:170:VAL:CA	4:L:194:LEU:HD23	1.89	1.02
1:C:226:GLN:NE2	1:C:227:ASP:OD1	1.92	1.02
1:A:4:SER:CB	1:A:102:ASP:CG	2.32	1.02
4:J:47:ILE:CD1	4:J:60:LEU:CD2	2.37	1.02
4:L:204:PRO:HG3	4:L:241:GLY:HA3	1.42	1.01
1:C:202:ARG:CD	1:C:244:TRP:NE1	2.21	1.01
4:J:194:LEU:HD23	4:J:195:ARG:N	1.75	1.01
4:F:218:SER:OG	4:F:221:ASP:CB	2.07	1.01
4:P:223:TRP:CZ2	4:P:229:LYS:O	2.13	1.01
1:M:82:ARG:NH1	1:M:93:HIS:HD2	1.56	1.01
3:E:136:THR:HG23	3:E:171:SER:CB	1.89	1.01
3:E:136:THR:CG2	3:E:171:SER:CB	2.40	1.00
1:A:4:SER:CB	1:A:102:ASP:OD1	2.08	1.00
1:M:78:LEU:HD23	1:M:95:VAL:HG23	1.41	1.00
4:P:196:VAL:HG22	4:P:197:SER:H	1.23	1.00
3:O:53:ASN:HB2	3:O:68:THR:CG2	1.89	1.00
3:K:185:ASN:CG	3:K:188:ASN:ND2	2.20	1.00
4:J:47:ILE:CD1	4:J:60:LEU:HD23	1.91	0.99
3:E:181:PHE:HB2	3:E:182:ALA:HA	1.44	0.99
1:G:35:ARG:HH21	1:G:48:ARG:CG	1.76	0.99
1:G:116:TYR:HD2	1:G:117:ALA:N	1.61	0.98
3:K:175:TRP:HE1	4:L:146:LEU:HD21	1.25	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:112:LEU:HD12	4:P:154:HIS:NE2	1.78	0.97
2:D:44:GLU:OE2	2:D:46:ILE:CD1	2.10	0.97
3:E:167:PHE:CD2	3:E:168:LYS:N	2.18	0.97
3:E:192:ILE:HG22	3:E:193:PRO:CD	1.94	0.97
1:G:82:ARG:HH21	1:G:89:GLU:N	1.61	0.97
4:L:170:VAL:HG22	4:L:194:LEU:HD21	1.44	0.97
4:L:89:VAL:CG1	4:L:110:ARG:HB2	1.93	0.97
1:M:82:ARG:HH11	1:M:93:HIS:HD2	1.03	0.97
3:E:83:GLU:HA	3:E:84:ASP:OD1	1.64	0.96
1:G:98:MET:CE	1:G:113:TYR:HE1	1.67	0.96
3:K:175:TRP:CH2	4:L:146:LEU:HD13	2.00	0.96
4:F:149:GLY:H	4:F:150:PHE:HD2	1.14	0.96
1:G:125:ALA:O	1:G:134:THR:HG22	1.64	0.95
1:A:227:ASP:OD2	1:A:248:VAL:HG22	1.65	0.95
3:E:136:THR:CG2	3:E:171:SER:HB2	1.93	0.95
1:M:73:THR:HG21	5:T:6:VAL:HG23	1.44	0.95
4:F:54:ALA:HB1	4:F:57:LYS:CE	1.96	0.95
1:A:230:LEU:CD2	1:A:243:LYS:HZ3	1.72	0.95
3:K:49:VAL:HG21	4:L:102:THR:HG22	1.47	0.95
1:G:97:ARG:HG2	1:G:116:TYR:CD1	2.02	0.95
1:G:98:MET:HE2	1:G:113:TYR:HD1	1.22	0.95
4:L:83:GLN:HG3	4:L:84:GLN:N	1.82	0.95
2:H:22:PHE:CD2	2:H:68:THR:O	2.20	0.95
4:L:97:THR:CB	4:L:98:GLN:OE1	2.15	0.95
4:P:97:THR:CG2	4:P:98:GLN:HG2	1.96	0.94
1:C:102:ASP:CG	1:C:113:TYR:OH	2.10	0.94
3:K:161:ASP:CG	3:K:168:LYS:CD	2.39	0.94
1:G:2:SER:N	1:G:105:SER:OG	1.98	0.94
1:G:97:ARG:NH1	5:U:6:VAL:HG13	1.81	0.94
2:N:42:ASN:H	2:N:43:GLY:HA2	1.32	0.94
1:G:187:THR:HB	1:G:272:LEU:HD21	1.49	0.94
4:P:223:TRP:CZ2	4:P:225:GLN:NE2	2.34	0.94
3:I:14:GLN:OE1	3:I:14:GLN:N	2.00	0.94
3:K:112:ILE:HG21	3:K:139:ASP:HB3	1.47	0.94
3:K:148:LYS:HB2	3:K:149:ASP:HA	1.48	0.93
2:N:13:HIS:HE1	4:F:81:ARG:NH2	1.60	0.93
3:O:81:GLN:HB3	3:O:82:PRO:HD2	1.48	0.93
1:A:35:ARG:HD3	1:A:48:ARG:HE	1.32	0.93
4:F:160:TRP:NE1	4:F:165:GLU:HA	1.81	0.93
2:N:13:HIS:CE1	4:F:81:ARG:HH22	1.75	0.93
4:P:223:TRP:CH2	4:P:225:GLN:NE2	2.35	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:83:GLN:CG	4:L:84:GLN:H	1.80	0.93
3:K:192:ILE:HG13	3:K:193:PRO:HD2	1.50	0.93
4:L:191:SER:OG	4:L:193:ARG:NH2	2.02	0.93
2:N:13:HIS:CE1	4:F:81:ARG:HH21	1.74	0.93
1:C:231:VAL:HG11	1:C:244:TRP:HE3	1.33	0.92
1:G:16:GLY:CA	1:G:17:ARG:HB2	1.99	0.92
1:M:20:PRO:HD2	1:M:75:ARG:HD3	1.47	0.92
3:I:8:PRO:O	3:I:104:THR:CG2	2.15	0.92
1:A:98:MET:HE3	1:A:98:MET:C	1.95	0.92
3:K:136:THR:HB	3:K:170:ASN:O	1.69	0.92
1:M:219:ARG:HD3	1:M:224:GLN:NE2	1.86	0.91
4:P:160:TRP:HE3	4:P:209:ARG:HD2	1.34	0.91
1:C:4:SER:HB3	1:C:102:ASP:OD1	1.71	0.91
4:L:170:VAL:HA	4:L:194:LEU:HD23	0.93	0.91
4:F:223:TRP:HH2	4:F:228:ALA:O	1.54	0.91
1:G:98:MET:HE1	1:G:113:TYR:HE1	0.90	0.91
3:K:112:ILE:HG23	3:K:139:ASP:CB	1.95	0.91
4:J:135:ILE:HA	4:J:140:LYS:O	1.71	0.91
3:K:53:ASN:HA	3:K:66:LEU:HD22	1.53	0.91
4:F:170:VAL:HG13	4:F:194:LEU:HD13	0.94	0.91
3:K:136:THR:HG22	3:K:171:SER:CA	2.00	0.91
1:C:131:ARG:HH11	1:C:131:ARG:HG3	1.35	0.90
1:G:35:ARG:HH21	1:G:48:ARG:HG2	1.36	0.90
2:N:4:THR:HG23	2:N:86:THR:HG21	1.51	0.90
3:K:175:TRP:CE2	4:L:146:LEU:CD2	2.49	0.90
4:L:202:GLN:CA	4:L:204:PRO:HD2	2.01	0.90
4:F:149:GLY:HA3	4:F:150:PHE:HB3	1.53	0.90
3:O:138:PHE:CD1	3:O:142:THR:HG21	2.06	0.90
3:I:178:LYS:CG	3:I:179:SER:OG	2.19	0.90
1:G:162:GLY:O	1:G:166:GLU:HG2	1.72	0.90
4:L:89:VAL:HG12	4:L:110:ARG:CG	1.99	0.89
4:P:112:LEU:CD1	4:P:154:HIS:NE2	2.33	0.89
1:G:17:ARG:HG3	1:G:17:ARG:HH11	1.37	0.89
3:E:178:LYS:C	3:E:179:SER:OG	2.11	0.89
3:K:38:TRP:HE3	3:K:44:PRO:HG3	1.35	0.89
1:M:10:THR:HG21	2:N:54:LEU:HD22	1.53	0.89
1:C:100:GLY:O	1:C:113:TYR:HD2	1.56	0.89
4:F:160:TRP:O	4:F:209:ARG:HG2	1.73	0.89
4:F:201:TRP:C	4:F:204:PRO:HD3	1.97	0.89
2:H:24:ASN:HD21	2:H:65:LEU:HG	1.38	0.89
1:M:188:HIS:HB2	1:M:204:TRP:HB2	1.55	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:193:ARG:HH11	4:F:193:ARG:HG3	1.38	0.89
3:I:138:PHE:HE1	3:I:142:THR:HG1	1.18	0.89
3:K:156:ASP:OD1	3:K:157:LYS:N	2.06	0.88
1:A:230:LEU:HD21	1:A:243:LYS:HZ3	0.84	0.88
3:K:175:TRP:CZ2	4:L:146:LEU:CG	2.45	0.88
1:M:82:ARG:NH1	1:M:93:HIS:CD2	2.41	0.88
2:N:40:LEU:CD2	2:N:43:GLY:HA3	2.02	0.88
3:K:161:ASP:OD1	3:K:168:LYS:CD	2.20	0.88
3:K:144:VAL:HG23	3:K:157:LYS:NZ	1.89	0.88
4:L:88:ALA:HB3	4:L:110:ARG:HG3	0.88	0.87
2:N:54:LEU:HD21	2:N:62:PHE:CD1	2.09	0.87
1:G:98:MET:CE	1:G:113:TYR:HD1	1.75	0.87
1:C:202:ARG:CG	1:C:244:TRP:NE1	2.37	0.87
4:L:88:ALA:HB1	4:L:110:ARG:HG3	1.57	0.87
1:M:66:LYS:NZ	3:O:29:ASN:CG	2.32	0.87
3:O:138:PHE:CE1	3:O:142:THR:CB	2.56	0.87
1:A:102:ASP:OD2	1:A:113:TYR:OH	1.93	0.86
3:K:112:ILE:HG22	3:K:139:ASP:OD2	1.75	0.86
4:P:151:TYR:O	4:P:214:PHE:CE1	2.27	0.86
3:K:135:PHE:HZ	3:K:192:ILE:CD1	1.88	0.86
2:N:13:HIS:HE1	4:F:81:ARG:HH22	1.12	0.86
1:G:116:TYR:CD2	1:G:117:ALA:N	2.43	0.86
3:I:146:GLN:OE1	3:I:154:ILE:CD1	2.24	0.86
1:G:16:GLY:HA3	1:G:17:ARG:CB	2.05	0.86
3:K:148:LYS:CB	3:K:149:ASP:C	2.49	0.86
3:K:175:TRP:NE1	4:L:146:LEU:HD21	1.90	0.86
1:M:215:LEU:HD21	1:M:261:VAL:HG22	1.55	0.86
1:M:82:ARG:HH11	1:M:93:HIS:CD2	1.93	0.85
1:A:230:LEU:HD23	1:A:243:LYS:CE	2.03	0.85
4:P:7:SER:OG	4:P:22:ARG:CB	2.22	0.85
3:O:61:ARG:NH1	3:O:84:ASP:OD2	2.09	0.85
3:O:80:SER:O	3:O:81:GLN:NE2	2.09	0.85
4:F:121:PHE:CE2	4:F:187:ARG:NH2	2.44	0.85
3:E:178:LYS:O	3:E:179:SER:OG	1.95	0.85
3:I:146:GLN:OE1	3:I:154:ILE:HD11	1.75	0.85
3:E:38:TRP:HD1	3:E:44:PRO:HG3	1.41	0.85
4:F:110:ARG:NH2	4:F:154:HIS:CD2	2.45	0.85
2:N:2:GLN:NE2	2:N:85:VAL:HB	1.91	0.85
4:L:127:VAL:HG11	4:L:239:ALA:HB2	1.57	0.84
1:C:226:GLN:OE1	1:C:227:ASP:N	2.09	0.84
3:E:136:THR:CG2	3:E:171:SER:HB3	2.06	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:225:THR:O	6:G:301:HOH:O	1.95	0.84
1:A:42:SER:OG	1:A:44:ARG:HG2	1.77	0.84
4:F:96:GLN:O	4:F:97:THR:OG1	1.94	0.84
3:E:138:PHE:O	3:E:139:ASP:C	2.16	0.84
3:I:15:GLU:OE2	6:I:301:HOH:O	1.94	0.84
3:O:119:VAL:HA	3:O:134:LEU:O	1.77	0.84
1:M:9:PHE:HB2	1:M:97:ARG:HB3	1.60	0.84
3:K:175:TRP:NE1	4:L:146:LEU:CD2	2.40	0.84
4:J:223:TRP:HA	4:J:223:TRP:CE3	2.13	0.83
4:L:161:VAL:HG23	4:L:166:VAL:HG11	1.59	0.83
4:F:54:ALA:CB	4:F:57:LYS:HE3	2.07	0.83
3:O:53:ASN:CB	3:O:68:THR:HG23	2.06	0.83
4:F:160:TRP:HE1	4:F:165:GLU:HA	1.37	0.83
4:P:39:LEU:HD12	4:P:39:LEU:O	1.77	0.83
1:C:45:MET:H	1:C:64:THR:HG22	1.41	0.83
3:I:178:LYS:C	3:I:179:SER:OG	2.16	0.83
2:D:79:ALA:HB1	2:D:92:ILE:HD11	1.59	0.83
4:F:26:ILE:O	4:F:27:SER:OG	1.96	0.83
1:G:125:ALA:HB3	1:G:134:THR:CG2	2.08	0.83
3:I:146:GLN:CD	3:I:154:ILE:CG1	2.52	0.83
1:G:218:GLN:HB3	1:G:223:ASP:HA	1.59	0.83
4:F:197:SER:HB3	4:F:200:PHE:HB2	1.60	0.83
4:J:84:GLN:NE2	1:G:177:GLU:OE1	2.11	0.83
4:J:129:GLU:HG3	4:J:130:PRO:HD2	1.59	0.83
3:E:192:ILE:HG22	3:E:193:PRO:HD2	1.60	0.83
4:J:194:LEU:CD2	4:J:196:VAL:HG23	2.08	0.82
1:G:58:GLU:O	1:G:62:GLY:N	2.13	0.82
1:G:98:MET:HE3	1:G:99:TYR:HA	1.59	0.82
4:L:150:PHE:CE1	4:L:188:TYR:O	2.33	0.82
3:I:178:LYS:HG2	3:I:179:SER:HG	1.44	0.82
2:N:12:ARG:O	2:N:13:HIS:CG	2.32	0.82
3:O:138:PHE:CE1	3:O:142:THR:HB	2.14	0.82
3:K:112:ILE:HG22	3:K:139:ASP:CG	2.05	0.82
3:E:30:PHE:HD2	3:E:92:PHE:CE2	1.98	0.82
4:F:46:LEU:O	4:F:59:GLY:HA3	1.80	0.82
3:K:38:TRP:CE3	3:K:44:PRO:CG	2.55	0.82
1:C:100:GLY:O	1:C:113:TYR:CD2	2.32	0.82
2:D:54:LEU:HD21	2:D:62:PHE:CD1	2.13	0.82
3:E:136:THR:HA	3:E:138:PHE:HE1	1.45	0.82
4:P:160:TRP:HD1	4:P:165:GLU:HG3	1.44	0.82
1:A:230:LEU:CD2	1:A:243:LYS:HZ1	1.90	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:123:PRO:HG3	4:L:150:PHE:HD2	1.43	0.81
3:I:194:GLU:O	3:I:196:THR:CG2	2.28	0.81
3:K:161:ASP:OD1	3:K:168:LYS:HD2	1.81	0.81
1:C:192:HIS:CE1	1:C:202:ARG:HH12	1.98	0.81
1:C:225:THR:O	1:C:228:THR:HG22	1.79	0.81
2:B:17:ASN:ND2	2:B:74:GLU:OE1	2.14	0.81
2:B:37:VAL:CG1	2:B:82:VAL:HG22	2.04	0.81
3:I:178:LYS:HG2	3:I:179:SER:OG	1.79	0.80
4:J:160:TRP:CZ3	4:J:211:GLN:CB	2.64	0.80
4:P:112:LEU:CG	4:P:154:HIS:CE1	2.63	0.80
4:P:19:VAL:HG22	4:P:79:ILE:HG12	1.63	0.80
3:E:136:THR:HG22	3:E:171:SER:HB3	1.63	0.80
1:G:14:ARG:O	1:G:18:GLY:HA3	1.80	0.80
3:O:122:LEU:HD22	4:P:130:PRO:HA	1.64	0.80
1:C:4:SER:CB	1:C:102:ASP:OD1	2.29	0.80
3:K:93:ILE:HG22	5:U:5:MET:HE1	1.64	0.79
1:G:192:HIS:HD2	1:G:202:ARG:NH2	1.69	0.79
3:K:185:ASN:C	3:K:188:ASN:HD22	1.90	0.79
1:A:223:ASP:O	1:A:225:THR:HG23	1.82	0.79
4:J:29:HIS:CD2	4:J:94:SER:C	2.59	0.79
3:I:138:PHE:CD1	3:I:142:THR:OG1	2.35	0.79
2:H:70:PHE:HE1	2:H:78:TYR:CD1	2.00	0.79
1:M:220:ASP:OD1	6:M:301:HOH:O	2.01	0.79
1:C:234:ARG:NH2	1:C:242:GLN:OE1	2.12	0.79
4:F:223:TRP:CZ3	4:F:230:PRO:HD2	2.18	0.79
3:K:49:VAL:HG21	4:L:102:THR:CG2	2.13	0.79
3:K:131:SER:HG	4:L:128:PHE:HD1	1.30	0.78
3:O:81:GLN:HB3	3:O:82:PRO:CD	2.12	0.78
4:F:110:ARG:NH2	4:F:154:HIS:HD2	1.80	0.78
1:G:125:ALA:HB3	1:G:134:THR:HG21	1.64	0.78
4:J:27:SER:OG	6:J:301:HOH:O	2.00	0.78
4:P:178:LYS:HA	4:P:187:ARG:O	1.81	0.78
3:I:192:ILE:HG23	3:I:193:PRO:HD3	0.78	0.78
3:K:38:TRP:CZ3	3:K:42:LYS:O	2.35	0.78
4:L:25:PRO:HG3	4:L:32:LEU:HD13	1.65	0.78
4:L:64:ARG:O	4:L:80:GLN:NE2	2.17	0.78
1:C:35:ARG:HD2	2:D:53:ASP:CG	2.08	0.78
4:F:149:GLY:N	4:F:150:PHE:HD2	1.81	0.78
3:K:175:TRP:HE1	4:L:146:LEU:CD2	1.96	0.78
3:K:185:ASN:CG	3:K:188:ASN:HD22	1.89	0.78
1:G:133:TRP:CZ3	1:G:147:TRP:CZ3	2.72	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:144:VAL:HG23	3:K:157:LYS:HZ1	1.46	0.78
2:N:73:THR:HG21	2:N:76:ASP:OD1	1.81	0.78
3:E:49:VAL:CG2	4:F:102:THR:HG22	2.13	0.78
3:I:115:PRO:CB	3:I:137:ASP:OD2	2.32	0.77
3:K:148:LYS:CB	3:K:149:ASP:CA	2.61	0.77
3:K:49:VAL:CG2	4:L:102:THR:HG22	2.15	0.77
1:C:93:HIS:ND1	1:C:118:TYR:OH	2.14	0.77
2:B:37:VAL:HG21	2:B:66:TYR:CE1	2.19	0.77
3:I:178:LYS:HG3	3:I:179:SER:OG	1.83	0.77
4:J:60:LEU:HD12	4:J:60:LEU:O	1.83	0.77
1:C:72:GLN:HG3	4:F:55:PRO:HB2	1.66	0.77
1:M:192:HIS:O	1:M:200:THR:OG1	2.02	0.77
1:C:66:LYS:NZ	5:R:1:ASN:OD1	2.18	0.77
4:L:202:GLN:C	4:L:204:PRO:HD2	2.09	0.77
1:M:87:GLN:OE1	1:M:93:HIS:NE2	2.17	0.77
2:N:42:ASN:O	6:N:101:HOH:O	2.01	0.77
3:O:138:PHE:HD1	3:O:142:THR:OG1	1.67	0.77
2:N:42:ASN:N	2:N:43:GLY:HA2	1.96	0.77
4:F:97:THR:OG1	4:F:98:GLN:HG2	1.85	0.77
4:J:217:LEU:HD13	4:J:221:ASP:HB3	1.67	0.77
4:L:170:VAL:CG2	4:L:194:LEU:HD21	2.15	0.77
1:A:187:THR:HB	1:A:272:LEU:HD11	1.67	0.77
1:G:188:HIS:HB3	1:G:204:TRP:HB2	1.66	0.77
1:G:220:ASP:OD2	1:G:256:ARG:CZ	2.32	0.77
3:K:138:PHE:CZ	3:K:157:LYS:HE3	2.19	0.77
1:M:78:LEU:CD2	1:M:95:VAL:HG23	2.13	0.77
2:D:87:LEU:HD13	2:D:90:PRO:HA	1.66	0.77
4:F:217:LEU:CD1	4:F:218:SER:H	1.97	0.77
4:J:84:GLN:HA	4:J:113:VAL:HG21	1.67	0.77
3:I:138:PHE:CE1	3:I:142:THR:OG1	2.38	0.76
4:P:14:GLU:H	4:P:17:LYS:HZ1	1.33	0.76
1:G:218:GLN:HB2	1:G:222:GLU:O	1.86	0.76
1:A:4:SER:HB3	1:A:102:ASP:OD2	1.84	0.76
4:F:132:GLU:HG3	4:F:135:ILE:HG21	1.68	0.76
2:N:30:PHE:CE1	2:N:62:PHE:HB2	2.20	0.76
4:F:159:TRP:O	4:F:166:VAL:HB	1.84	0.76
1:G:133:TRP:CZ3	1:G:147:TRP:CE3	2.72	0.76
4:L:143:LEU:HD12	4:L:144:VAL:N	2.00	0.76
1:C:235:PRO:O	2:D:10:TYR:OH	2.01	0.76
3:K:161:ASP:OD1	3:K:168:LYS:HD3	1.83	0.76
1:A:230:LEU:HD21	1:A:243:LYS:HE2	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:143:LEU:HD12	4:L:144:VAL:H	1.50	0.76
2:N:54:LEU:HD21	2:N:62:PHE:HD1	1.51	0.76
2:D:76:ASP:HB3	2:D:78:TYR:HE1	1.50	0.76
3:O:53:ASN:CB	3:O:68:THR:CG2	2.62	0.75
2:B:89:GLN:HB2	2:B:90:PRO:HD2	1.68	0.75
4:J:100:TRP:HE3	5:Q:5:MET:HE3	1.50	0.75
2:H:24:ASN:OD1	2:H:65:LEU:HD23	1.86	0.75
3:K:17:ASP:O	3:K:80:SER:OG	2.04	0.75
4:P:7:SER:HG	4:P:22:ARG:HB3	1.51	0.75
4:P:223:TRP:HZ2	4:P:225:GLN:HE21	1.30	0.75
1:G:97:ARG:NH1	5:U:6:VAL:HG11	1.84	0.75
3:K:135:PHE:CZ	3:K:192:ILE:CD1	2.70	0.75
2:D:44:GLU:HG2	2:D:46:ILE:HG12	1.67	0.75
1:A:122:ASP:OD1	2:B:60:TRP:NE1	2.20	0.75
4:J:223:TRP:HA	4:J:223:TRP:HE3	1.47	0.75
3:K:59:LYS:HD2	3:K:60:GLY:H	1.50	0.75
4:F:84:GLN:CD	4:F:85:GLU:H	1.93	0.75
4:J:113:VAL:O	4:J:114:LEU:CG	2.35	0.75
1:G:17:ARG:HG3	1:G:17:ARG:NH1	1.99	0.75
4:P:151:TYR:O	4:P:214:PHE:CZ	2.40	0.75
4:J:57:LYS:O	4:J:59:GLY:N	2.17	0.75
1:M:20:PRO:HD2	1:M:75:ARG:HD2	1.67	0.75
4:P:122:PRO:HD3	4:P:230:PRO:HG3	1.69	0.75
1:G:97:ARG:HH12	5:U:6:VAL:CG1	1.99	0.75
3:K:31:TYR:HD1	5:U:4:PRO:HB2	1.52	0.75
4:P:14:GLU:HB2	4:P:17:LYS:HE3	1.69	0.75
3:E:84:ASP:HB3	3:E:85:SER:HB2	1.69	0.75
4:F:142:THR:HA	4:F:195:ARG:HB2	1.66	0.75
1:A:96:GLN:OE1	2:B:60:TRP:CE3	2.39	0.75
1:G:192:HIS:CD2	1:G:202:ARG:HD2	2.21	0.75
3:K:112:ILE:CG2	3:K:139:ASP:CG	2.59	0.75
3:E:49:VAL:HG21	4:F:102:THR:HG22	1.67	0.75
1:A:230:LEU:CD2	1:A:243:LYS:HE2	2.13	0.74
4:P:112:LEU:CG	4:P:154:HIS:NE2	2.50	0.74
4:L:153:ASP:HB2	4:L:188:TYR:CD2	2.22	0.74
3:K:148:LYS:HB2	3:K:149:ASP:CA	2.17	0.74
1:C:192:HIS:ND1	1:C:202:ARG:NH1	2.30	0.74
4:P:112:LEU:HG	4:P:154:HIS:NE2	2.02	0.74
1:C:131:ARG:HG3	1:C:131:ARG:NH1	1.98	0.74
3:E:136:THR:CA	3:E:138:PHE:HE1	2.00	0.74
3:O:53:ASN:HB2	3:O:68:THR:CB	2.17	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:135:PHE:CZ	3:K:192:ILE:HG12	2.23	0.74
4:P:112:LEU:CD1	4:P:154:HIS:HE1	1.71	0.74
3:E:97:GLN:NE2	3:E:99:TYR:OH	2.20	0.74
4:F:218:SER:OG	4:F:221:ASP:HB3	1.86	0.74
4:F:223:TRP:CH2	4:F:228:ALA:O	2.39	0.74
1:A:93:HIS:ND1	1:A:119:ASP:OD1	2.20	0.74
4:J:47:ILE:CG1	4:J:60:LEU:HD23	2.18	0.74
4:L:88:ALA:CB	4:L:89:VAL:HA	2.03	0.74
1:C:66:LYS:HD2	5:R:4:PRO:HA	1.67	0.74
3:K:25:PHE:CZ	3:K:71:GLY:HA2	2.22	0.74
3:K:192:ILE:HG13	3:K:193:PRO:CD	2.17	0.74
1:A:33:PHE:HD1	1:A:52:ILE:HD12	1.52	0.73
3:O:138:PHE:CD1	3:O:142:THR:CB	2.71	0.73
3:I:48:PHE:HE1	3:I:59:LYS:HG3	1.52	0.73
4:F:205:ARG:HA	4:F:240:TRP:CH2	2.23	0.73
4:J:178:LYS:HD2	4:J:188:TYR:CE1	2.23	0.73
3:O:138:PHE:HE1	3:O:142:THR:CB	1.96	0.73
3:E:192:ILE:CG2	3:E:193:PRO:HD3	2.17	0.73
1:A:202:ARG:HG3	1:A:244:TRP:HE1	1.53	0.73
4:F:201:TRP:O	4:F:204:PRO:CD	2.36	0.73
1:G:186:LYS:HG3	1:G:186:LYS:O	1.87	0.73
1:G:192:HIS:HD2	1:G:202:ARG:HH21	0.87	0.73
1:M:259:CYS:HB3	1:M:272:LEU:HB2	1.70	0.73
3:I:194:GLU:O	3:I:196:THR:HG23	1.89	0.73
1:G:214:THR:HG23	1:G:214:THR:O	1.89	0.73
2:H:21:ASN:OD1	2:H:22:PHE:N	2.22	0.73
2:B:36:GLU:HB2	2:B:83:ASN:HB3	1.71	0.73
3:I:192:ILE:CG2	3:I:193:PRO:CD	2.36	0.73
4:J:129:GLU:CG	4:J:130:PRO:HD2	2.18	0.73
4:P:159:TRP:CD1	4:P:209:ARG:O	2.41	0.73
3:E:192:ILE:CG2	3:E:193:PRO:CD	2.66	0.73
1:G:191:HIS:ND1	1:G:191:HIS:O	2.20	0.72
4:L:10:ASN:HB2	4:L:154:HIS:NE2	2.04	0.72
1:C:202:ARG:HE	1:C:244:TRP:HZ2	1.33	0.72
3:I:146:GLN:NE2	3:I:154:ILE:HG12	2.04	0.72
4:J:116:ASP:HB3	4:J:119:ASN:N	2.05	0.72
2:H:37:VAL:HG23	2:H:81:ARG:O	1.88	0.72
3:K:138:PHE:O	3:K:139:ASP:OD1	2.07	0.72
4:L:173:ASP:OD2	4:L:191:SER:OG	2.07	0.72
1:C:225:THR:O	1:C:228:THR:N	2.16	0.72
1:A:99:TYR:OH	5:Q:3:VAL:HG12	1.90	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:120:TYR:HH	4:L:135:ILE:N	1.87	0.72
4:P:18:ASP:OD2	2:D:20:SER:OG	2.08	0.72
3:E:42:LYS:HD2	3:E:43:SER:H	1.55	0.72
4:J:100:TRP:CE3	5:Q:5:MET:HE3	2.24	0.72
4:J:194:LEU:HD22	4:J:196:VAL:HG23	1.70	0.72
3:K:34:HIS:HB2	3:K:91:ALA:HB3	1.71	0.72
4:F:160:TRP:O	4:F:209:ARG:CG	2.37	0.72
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.70	0.72
1:G:98:MET:HE3	1:G:99:TYR:CA	2.19	0.72
4:F:150:PHE:CE1	4:F:155:VAL:HG11	2.23	0.72
3:K:2:LEU:HB3	3:K:3:ASN:HA	1.70	0.72
4:L:88:ALA:HB1	4:L:89:VAL:CA	2.15	0.72
1:C:235:PRO:HD2	2:D:10:TYR:OH	1.89	0.72
3:I:117:PRO:HB2	3:I:196:THR:HB	1.71	0.72
3:K:9:GLN:HA	3:K:104:THR:HA	1.70	0.72
4:L:202:GLN:HA	4:L:204:PRO:HD2	1.70	0.72
4:J:98:GLN:HB2	4:J:101:GLU:OE1	1.90	0.72
4:J:113:VAL:C	4:J:114:LEU:HG	2.14	0.72
1:M:96:GLN:NE2	2:N:31:HIS:HE1	1.87	0.72
2:D:89:GLN:HG3	2:D:90:PRO:HD2	1.72	0.72
1:M:59:TYR:OH	1:M:171:TYR:OH	2.06	0.71
4:J:114:LEU:N	4:J:114:LEU:HD12	2.03	0.71
1:M:197:HIS:O	1:M:198:GLU:HG2	1.90	0.71
1:M:224:GLN:OE1	1:M:227:ASP:HB3	1.90	0.71
3:O:70:GLU:N	3:O:71:GLY:HA2	2.05	0.71
4:P:160:TRP:CE3	4:P:209:ARG:HD2	2.22	0.71
4:J:29:HIS:NE2	4:J:94:SER:O	2.22	0.71
3:E:30:PHE:HD2	3:E:92:PHE:HE2	1.39	0.71
4:J:178:LYS:HD2	4:J:188:TYR:HE1	1.55	0.71
1:M:89:GLU:HG2	1:M:89:GLU:O	1.90	0.71
1:M:87:GLN:OE1	1:M:93:HIS:CE1	2.44	0.71
4:F:170:VAL:HA	4:F:194:LEU:HD12	1.72	0.71
1:A:223:ASP:O	1:A:225:THR:CG2	2.38	0.71
2:N:12:ARG:O	2:N:13:HIS:ND1	2.23	0.71
2:H:24:ASN:HD21	2:H:65:LEU:CG	2.03	0.70
2:H:24:ASN:OD1	2:H:65:LEU:CD2	2.39	0.70
3:K:102:THR:OG1	3:K:103:GLY:N	2.23	0.70
3:K:151:ASP:CG	3:K:177:ASN:H	1.99	0.70
3:E:112:ILE:HG22	3:E:115:PRO:HD3	1.73	0.70
3:I:178:LYS:C	3:I:179:SER:HG	1.98	0.70
3:I:194:GLU:O	3:I:196:THR:HG22	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:112:LEU:HG	4:P:154:HIS:CE1	2.26	0.70
3:E:178:LYS:O	3:E:180:ASP:N	2.21	0.70
1:A:230:LEU:HD23	1:A:243:LYS:HE3	1.71	0.70
3:I:13:VAL:C	3:I:14:GLN:OE1	2.33	0.70
4:P:151:TYR:O	4:P:214:PHE:HE1	1.75	0.70
4:L:160:TRP:NE1	4:L:163:GLY:O	2.23	0.70
2:D:33:SER:HB3	2:D:62:PHE:CD2	2.25	0.70
4:F:217:LEU:HD13	4:F:218:SER:H	1.54	0.70
1:G:192:HIS:CG	1:G:202:ARG:NH2	2.60	0.70
4:F:121:PHE:HE2	4:F:187:ARG:HH21	1.37	0.70
1:M:66:LYS:CE	3:O:29:ASN:ND2	2.54	0.70
1:M:95:VAL:CG1	1:M:116:TYR:CE1	2.74	0.70
4:L:89:VAL:HG12	4:L:110:ARG:HG3	1.73	0.70
3:O:155:THR:HG23	4:P:173:ASP:OD2	1.91	0.70
1:C:218:GLN:HG2	1:C:260:HIS:CD2	2.27	0.70
4:P:119:ASN:HB3	4:P:151:TYR:CD2	2.27	0.70
4:L:204:PRO:CG	4:L:241:GLY:HA3	2.19	0.69
2:N:4:THR:CG2	2:N:86:THR:HG21	2.22	0.69
1:C:231:VAL:HG11	1:C:244:TRP:CE3	2.24	0.69
3:K:50:MET:HB3	3:K:66:LEU:HD12	1.73	0.69
2:N:57:SER:O	2:N:59:ASP:N	2.24	0.69
4:P:25:PRO:HD3	4:P:32:LEU:HD21	1.74	0.69
3:E:136:THR:HA	3:E:138:PHE:CE1	2.27	0.69
1:A:102:ASP:OD1	1:A:113:TYR:OH	1.93	0.69
4:J:160:TRP:HB2	4:J:209:ARG:CB	2.23	0.69
3:K:35:TRP:HE1	3:K:75:LEU:HD22	1.56	0.69
3:K:59:LYS:HD2	3:K:60:GLY:N	2.07	0.69
4:L:202:GLN:HA	4:L:202:GLN:OE1	1.90	0.69
3:O:34:HIS:HB2	3:O:91:ALA:HB3	1.72	0.69
4:L:9:SER:O	4:L:10:ASN:OD1	2.09	0.69
4:L:127:VAL:CG1	4:L:239:ALA:HB2	2.22	0.69
2:D:24:ASN:HB3	2:D:65:LEU:HD11	1.73	0.69
3:I:122:LEU:CA	3:I:132:VAL:H	2.05	0.69
1:G:24:ALA:HB3	1:G:36:PHE:HB3	1.74	0.69
3:K:148:LYS:CB	3:K:149:ASP:HA	2.20	0.69
4:L:33:TYR:HB2	4:L:93:ALA:HB3	1.73	0.69
4:L:88:ALA:HB1	4:L:110:ARG:HA	1.75	0.69
4:L:170:VAL:HA	4:L:194:LEU:HD21	1.69	0.69
1:C:187:THR:C	1:C:188:HIS:ND1	2.50	0.69
4:F:201:TRP:O	4:F:204:PRO:HD3	1.93	0.69
2:B:24:ASN:HB3	2:B:65:LEU:HD11	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:146:GLN:CD	3:I:154:ILE:CD1	2.66	0.69
4:L:125:VAL:HB	4:L:237:ALA:HB2	1.73	0.69
4:F:159:TRP:NE1	4:F:192:SER:OG	2.19	0.69
1:A:99:TYR:CZ	5:Q:3:VAL:HG12	2.26	0.69
3:I:161:ASP:OD2	3:I:166:ASP:N	2.25	0.69
3:I:194:GLU:C	3:I:196:THR:HG23	2.18	0.69
3:O:138:PHE:HD1	3:O:142:THR:HG1	1.37	0.69
4:P:160:TRP:CD1	4:P:165:GLU:HG3	2.27	0.69
2:H:71:THR:OG1	2:H:72:PRO:HD3	1.92	0.68
4:L:97:THR:CB	4:L:98:GLN:CD	2.66	0.68
4:J:47:ILE:HG13	4:J:60:LEU:HD23	1.74	0.68
1:M:219:ARG:NH2	1:M:222:GLU:OE1	2.26	0.68
3:I:146:GLN:NE2	3:I:154:ILE:CG1	2.57	0.68
4:J:85:GLU:O	4:J:87:SER:N	2.27	0.68
1:G:35:ARG:HE	1:G:48:ARG:HG3	1.56	0.68
1:G:159:TYR:CD1	1:G:163:THR:OG1	2.46	0.68
4:F:98:GLN:NE2	4:F:98:GLN:HA	2.08	0.68
1:G:192:HIS:HB2	1:G:202:ARG:HH22	1.57	0.68
1:M:22:PHE:H	1:M:38:SER:HB2	1.56	0.68
3:I:117:PRO:O	3:I:196:THR:O	2.12	0.68
2:H:22:PHE:HD2	2:H:68:THR:O	1.75	0.68
3:I:34:HIS:HB2	3:I:91:ALA:HB3	1.73	0.68
1:G:162:GLY:O	1:G:166:GLU:CG	2.41	0.68
1:M:5:MET:HB3	1:M:168:LEU:HD13	1.75	0.68
4:J:129:GLU:CD	4:J:130:PRO:CD	2.66	0.68
3:O:140:SER:C	3:O:142:THR:H	2.02	0.68
3:K:112:ILE:HG22	3:K:139:ASP:CB	2.21	0.68
4:L:10:ASN:HB2	4:L:154:HIS:CE1	2.28	0.68
4:L:36:ARG:HB3	4:L:89:VAL:O	1.94	0.68
4:L:114:LEU:HD23	4:L:116:ASP:H	1.59	0.68
4:L:150:PHE:CE1	4:L:188:TYR:C	2.72	0.68
4:L:90:TYR:N	4:L:109:THR:O	2.22	0.68
1:M:200:THR:HG22	1:M:248:VAL:HA	1.75	0.68
1:C:27:TYR:CE2	1:C:32:GLN:HB2	2.28	0.68
4:J:153:ASP:O	4:J:155:VAL:N	2.26	0.67
4:L:201:TRP:C	4:L:204:PRO:CD	2.67	0.67
3:O:53:ASN:CB	3:O:68:THR:OG1	2.43	0.67
3:I:146:GLN:HE22	3:I:154:ILE:HD13	1.57	0.67
4:L:123:PRO:HG3	4:L:150:PHE:CD2	2.27	0.67
1:M:21:ARG:HG3	1:M:38:SER:HB3	1.76	0.67
1:G:6:ARG:HB3	1:G:8:PHE:HE2	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:62:SER:CA	4:L:65:PHE:CE2	2.78	0.67
1:C:10:THR:HG21	2:D:54:LEU:HD22	1.75	0.67
3:E:50:MET:HB3	3:E:66:LEU:HD12	1.75	0.67
3:K:148:LYS:CB	3:K:149:ASP:O	2.34	0.67
4:L:47:ILE:HD11	4:L:67:ALA:HB3	1.77	0.67
3:O:117:PRO:HB2	3:O:196:THR:HA	1.77	0.67
1:A:121:LYS:HE3	2:B:1:ILE:HD13	1.77	0.67
1:G:55:GLU:O	1:G:59:TYR:HB3	1.95	0.67
3:K:123:ARG:HA	3:K:131:SER:OG	1.94	0.67
3:O:134:LEU:HD13	3:O:173:VAL:HG12	1.75	0.67
3:E:93:ILE:HG22	5:R:5:MET:HE1	1.77	0.67
4:F:98:GLN:HB2	4:F:101:GLU:OE1	1.95	0.67
3:K:11:LEU:HB3	3:K:106:LEU:HD13	1.76	0.67
3:O:160:LEU:O	3:O:168:LYS:HA	1.95	0.67
3:E:132:VAL:HG22	3:E:175:TRP:HB3	1.75	0.67
1:A:42:SER:OG	1:A:44:ARG:CG	2.42	0.67
4:P:14:GLU:OE2	4:P:117:LEU:CG	2.40	0.67
1:G:143:THR:HB	5:U:9:VAL:HG23	1.76	0.66
2:H:24:ASN:CG	2:H:65:LEU:HD21	2.20	0.66
3:K:112:ILE:HG21	3:K:139:ASP:CB	2.13	0.66
2:N:47:GLU:HG3	2:N:47:GLU:O	1.94	0.66
1:G:66:LYS:HD2	5:U:4:PRO:HA	1.76	0.66
4:P:204:PRO:HB2	4:P:205:ARG:HA	1.78	0.66
1:M:78:LEU:HD23	1:M:95:VAL:HG21	1.74	0.66
4:F:170:VAL:CG1	4:F:194:LEU:CD1	2.53	0.66
3:K:135:PHE:HZ	3:K:192:ILE:CG1	2.08	0.66
3:K:144:VAL:CG2	3:K:157:LYS:NZ	2.57	0.66
1:M:133:TRP:HB2	1:M:144:LYS:HG3	1.77	0.66
3:O:138:PHE:CD1	3:O:142:THR:OG1	2.48	0.66
4:P:26:ILE:HB	4:P:29:HIS:CD2	2.30	0.66
4:J:206:ASN:OD1	4:J:207:HIS:N	2.28	0.66
3:E:181:PHE:CB	3:E:182:ALA:HA	2.20	0.66
3:O:53:ASN:HB2	3:O:68:THR:OG1	1.96	0.66
3:E:84:ASP:HA	3:E:85:SER:OG	1.95	0.66
4:F:79:ILE:O	4:F:79:ILE:HG13	1.96	0.66
4:J:223:TRP:CZ2	4:J:228:ALA:O	2.49	0.66
3:E:84:ASP:HB3	3:E:85:SER:O	1.95	0.66
1:G:35:ARG:CG	1:G:46:GLU:HB3	2.26	0.65
4:P:14:GLU:CD	4:P:117:LEU:CD2	2.53	0.65
4:F:165:GLU:O	4:F:166:VAL:HG23	1.95	0.65
1:A:255:GLN:NE2	6:A:301:HOH:O	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:135:PHE:HZ	3:K:192:ILE:HD11	1.62	0.65
4:L:170:VAL:HG22	4:L:194:LEU:CD2	2.21	0.65
3:E:124:ASP:HB3	4:F:128:PHE:HA	1.75	0.65
4:F:98:GLN:HA	4:F:98:GLN:HE21	1.61	0.65
3:I:160:LEU:HD12	3:I:169:SER:HB2	1.77	0.65
4:J:65:PHE:HA	4:J:79:ILE:HG22	1.78	0.65
1:M:77:ASP:OD2	5:T:8:THR:HB	1.97	0.65
3:O:15:GLU:OE1	3:O:168:LYS:NZ	2.29	0.65
4:P:100:TRP:HH2	5:T:7:ALA:HB2	1.61	0.65
4:F:6:GLN:HB3	4:F:107:PRO:HD2	1.77	0.65
2:B:29:GLY:HA2	2:B:61:SER:HB2	1.79	0.65
3:K:185:ASN:O	3:K:188:ASN:CB	2.44	0.65
1:M:66:LYS:HZ2	3:O:29:ASN:HB2	1.61	0.65
1:M:237:GLY:O	1:M:238:ASP:HB2	1.94	0.65
3:O:17:ASP:O	3:O:80:SER:OG	2.15	0.65
3:E:82:PRO:O	3:E:85:SER:OG	2.08	0.65
1:G:97:ARG:CG	1:G:116:TYR:CD1	2.80	0.65
1:M:87:GLN:OE1	1:M:93:HIS:CD2	2.50	0.65
2:N:81:ARG:HG3	2:N:92:ILE:HG13	1.76	0.65
3:O:138:PHE:CD1	3:O:142:THR:CG2	2.75	0.65
4:L:159:TRP:CZ2	4:L:194:LEU:HG	2.32	0.65
4:F:195:ARG:HG2	4:F:195:ARG:HH11	1.61	0.65
4:F:160:TRP:CD1	4:F:165:GLU:HA	2.31	0.65
1:C:202:ARG:NE	1:C:244:TRP:HZ2	1.94	0.65
1:A:98:MET:HE3	1:A:98:MET:O	1.96	0.65
4:L:5:SER:HB2	4:L:24:ASP:HB3	1.79	0.65
2:N:2:GLN:NE2	2:N:85:VAL:CG2	2.60	0.65
1:G:137:ASP:OD1	1:G:138:MET:N	2.25	0.64
2:H:17:ASN:OD1	2:H:97:ARG:NH1	2.30	0.64
3:I:192:ILE:HG23	3:I:193:PRO:N	2.13	0.64
3:I:178:LYS:O	3:I:180:ASP:N	2.25	0.64
4:J:26:ILE:HG22	4:J:27:SER:H	1.63	0.64
1:M:35:ARG:HD3	1:M:48:ARG:HH11	1.61	0.64
1:M:95:VAL:CG1	1:M:116:TYR:HE1	2.10	0.64
3:O:118:ALA:HB1	3:O:120:TYR:CE1	2.32	0.64
4:P:11:LYS:NZ	4:P:19:VAL:HB	2.12	0.64
4:J:129:GLU:CD	4:J:130:PRO:HD2	2.22	0.64
1:M:37:ASP:HB3	1:M:40:ALA:HB2	1.80	0.64
2:B:37:VAL:HG21	2:B:66:TYR:CZ	2.32	0.64
3:I:132:VAL:CG1	3:I:173:VAL:HG13	2.28	0.64
3:I:160:LEU:CD2	4:J:169:GLY:O	2.46	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:194:LEU:HD23	4:J:195:ARG:H	1.61	0.64
2:H:72:PRO:HB2	2:H:78:TYR:OH	1.98	0.64
4:L:90:TYR:HB2	4:L:109:THR:HG23	1.79	0.64
1:M:58:GLU:HA	1:M:61:ASP:HB3	1.79	0.64
1:M:219:ARG:HG3	1:M:257:TYR:CE2	2.32	0.64
4:P:196:VAL:HG22	4:P:197:SER:N	2.02	0.64
3:E:82:PRO:HA	3:E:108:VAL:HG21	1.78	0.64
1:G:27:TYR:OH	2:H:63:TYR:OH	2.12	0.64
4:L:103:GLN:HG2	4:L:105:PHE:HE1	1.63	0.64
3:I:7:SER:CB	3:I:8:PRO:HD3	2.28	0.64
4:J:129:GLU:CD	4:J:130:PRO:HD3	2.23	0.64
1:C:35:ARG:HH11	2:D:53:ASP:CG	2.06	0.64
1:A:81:LEU:HG	5:Q:9:VAL:HG21	1.80	0.64
4:J:127:VAL:HG11	4:J:239:ALA:HB2	1.79	0.64
4:L:161:VAL:HG23	4:L:166:VAL:CG1	2.27	0.64
4:F:170:VAL:HG12	4:F:194:LEU:HD13	1.76	0.64
3:I:138:PHE:HE1	3:I:142:THR:O	1.81	0.64
3:K:16:GLY:N	3:K:80:SER:O	2.31	0.64
4:L:161:VAL:CG2	4:L:166:VAL:HG11	2.27	0.64
3:E:53:ASN:HB2	3:E:68:THR:HB	1.79	0.64
1:A:35:ARG:HD2	2:B:53:ASP:OD1	1.98	0.63
1:G:155:GLN:HE22	4:L:100:TRP:CG	2.16	0.63
3:K:135:PHE:CE1	3:K:138:PHE:HB3	2.33	0.63
4:F:121:PHE:CD2	4:F:187:ARG:NH2	2.66	0.63
3:I:141:GLN:HG3	3:I:141:GLN:O	1.98	0.63
4:J:113:VAL:C	4:J:114:LEU:CG	2.69	0.63
1:G:234:ARG:HG3	1:G:242:GLN:HB2	1.79	0.63
2:H:70:PHE:CE1	2:H:78:TYR:CE1	2.86	0.63
4:L:201:TRP:C	4:L:204:PRO:HD3	2.23	0.63
1:C:120:GLY:O	2:D:3:ARG:NH2	2.32	0.63
1:C:202:ARG:NE	1:C:244:TRP:CZ2	2.66	0.63
1:A:59:TYR:HH	1:A:171:TYR:HH	1.43	0.63
1:A:80:THR:HG23	5:Q:9:VAL:HG23	1.79	0.63
4:J:97:THR:HB	4:J:98:GLN:HG2	1.80	0.63
1:G:97:ARG:NH1	5:U:6:VAL:HG12	2.10	0.63
4:L:191:SER:CB	4:L:193:ARG:HH21	2.12	0.63
3:O:138:PHE:HE1	3:O:142:THR:HB	1.58	0.63
4:F:173:ASP:OD2	4:F:191:SER:OG	2.17	0.63
4:F:200:PHE:O	4:F:204:PRO:HB3	1.99	0.63
4:J:83:GLN:HG2	4:J:84:GLN:H	1.63	0.63
2:H:5:PRO:HB3	2:H:30:PHE:HB3	1.78	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:218:SER:O	4:L:218:SER:OG	2.12	0.63
2:N:2:GLN:NE2	2:N:85:VAL:CB	2.60	0.63
3:I:196:THR:OG1	3:I:197:PHE:N	2.32	0.63
4:J:238:GLU:HG3	4:J:239:ALA:N	2.14	0.63
1:G:77:ASP:OD1	1:G:97:ARG:NH2	2.32	0.63
1:G:192:HIS:HB2	1:G:202:ARG:NH2	2.12	0.62
2:H:11:SER:HB2	2:H:95:TRP:HZ2	1.63	0.62
1:M:12:VAL:HG22	1:M:94:THR:HG23	1.81	0.62
3:O:123:ARG:HG2	3:O:124:ASP:H	1.64	0.62
3:O:180:ASP:OD1	3:O:182:ALA:HB2	1.98	0.62
4:F:230:PRO:O	4:F:231:VAL:CG2	2.47	0.62
3:I:10:SER:O	3:I:11:LEU:HD23	1.99	0.62
3:K:38:TRP:HZ3	3:K:42:LYS:O	1.81	0.62
3:I:33:LEU:CD1	3:I:91:ALA:O	2.42	0.62
2:H:70:PHE:CE1	2:H:78:TYR:CD1	2.87	0.62
3:O:33:LEU:HB3	3:O:50:MET:HB2	1.81	0.62
4:F:165:GLU:O	4:F:166:VAL:CG2	2.46	0.62
4:F:193:ARG:HH11	4:F:193:ARG:CG	2.09	0.62
4:F:195:ARG:HH11	4:F:195:ARG:CG	2.13	0.62
1:G:126:LEU:HD11	1:G:130:LEU:HA	1.82	0.62
4:P:21:LEU:HB2	4:P:77:LEU:HB3	1.82	0.62
1:M:20:PRO:CD	1:M:75:ARG:HD2	2.29	0.62
4:F:47:ILE:HG22	4:F:48:TYR:N	2.13	0.62
1:A:59:TYR:OH	1:A:171:TYR:OH	2.16	0.62
1:A:96:GLN:OE1	2:B:60:TRP:HE3	1.83	0.62
3:K:115:PRO:HB3	3:K:139:ASP:OD2	2.00	0.62
3:E:38:TRP:CD1	3:E:44:PRO:HG3	2.29	0.62
1:G:98:MET:HE2	1:G:113:TYR:CE1	2.00	0.62
3:I:146:GLN:NE2	3:I:154:ILE:HD13	2.15	0.62
1:G:73:THR:HG21	5:U:6:VAL:HG12	1.82	0.62
4:L:119:ASN:OD1	4:L:187:ARG:NH2	2.33	0.62
4:L:161:VAL:HG13	4:L:208:PHE:HA	1.81	0.61
1:G:133:TRP:CE3	1:G:147:TRP:HE3	2.18	0.61
4:L:153:ASP:HB2	4:L:188:TYR:HD2	1.64	0.61
3:O:183:CYS:O	3:O:186:ALA:HB2	2.00	0.61
4:P:64:ARG:HH11	4:P:64:ARG:CG	2.13	0.61
1:C:213:ILE:HG13	1:C:263:HIS:HB2	1.82	0.61
1:A:22:PHE:H	1:A:38:SER:HB3	1.65	0.61
4:J:234:ILE:HD12	4:J:234:ILE:O	1.99	0.61
3:K:161:ASP:CB	3:K:168:LYS:HD3	2.29	0.61
3:K:185:ASN:ND2	3:K:188:ASN:ND2	2.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:73:THR:HG23	2:N:75:LYS:H	1.64	0.61
1:C:102:ASP:OD1	1:C:113:TYR:OH	2.10	0.61
4:F:132:GLU:CG	4:F:135:ILE:HG21	2.31	0.61
3:K:185:ASN:O	3:K:188:ASN:N	2.30	0.61
1:M:103:VAL:HA	1:M:108:ARG:O	2.01	0.61
1:M:146:LYS:NZ	4:P:97:THR:OG1	2.31	0.61
3:E:181:PHE:HB2	3:E:182:ALA:CA	2.25	0.61
3:K:185:ASN:O	3:K:188:ASN:HB3	2.01	0.61
1:C:197:HIS:ND1	1:C:198:GLU:HG3	2.16	0.61
2:N:59:ASP:HB3	2:N:61:SER:OG	2.01	0.61
2:B:36:GLU:CB	2:B:83:ASN:HB3	2.29	0.61
1:G:82:ARG:HH21	1:G:88:SER:C	2.08	0.61
2:N:81:ARG:HD3	2:N:92:ILE:HG12	1.83	0.61
1:M:47:PRO:HB3	1:M:60:TRP:CH2	2.36	0.61
2:D:89:GLN:HG3	2:D:90:PRO:CD	2.31	0.61
3:E:126:LYS:HD2	3:E:126:LYS:N	2.16	0.61
3:O:140:SER:C	3:O:142:THR:N	2.56	0.60
4:F:25:PRO:HG2	4:F:73:SER:HB2	1.81	0.60
1:A:66:LYS:HE2	3:I:29:ASN:CG	2.25	0.60
4:L:161:VAL:HG12	4:L:162:ASN:N	2.16	0.60
1:G:27:TYR:CD1	1:G:32:GLN:NE2	2.66	0.60
2:H:44:GLU:OE1	4:F:71:GLY:HA2	2.00	0.60
2:N:81:ARG:HD3	2:N:92:ILE:CG1	2.30	0.60
1:A:73:THR:HG23	3:I:96:ASN:HD21	1.67	0.60
1:G:218:GLN:OE1	1:G:221:GLY:HA2	2.01	0.60
2:D:87:LEU:HD13	2:D:89:GLN:O	2.01	0.60
3:I:13:VAL:HG23	3:I:15:GLU:H	1.66	0.60
3:I:87:THR:HA	3:I:105:SER:HA	1.83	0.60
1:G:99:TYR:CZ	5:U:3:VAL:HG12	2.37	0.60
1:G:207:SER:HA	1:G:240:THR:HB	1.83	0.60
4:L:150:PHE:O	4:L:150:PHE:HD1	1.84	0.60
2:D:82:VAL:O	2:D:90:PRO:HB2	2.02	0.60
1:A:231:VAL:HG23	1:A:231:VAL:O	2.00	0.60
1:M:195:SER:O	1:M:197:HIS:ND1	2.34	0.60
1:C:187:THR:HB	1:C:272:LEU:HD11	1.81	0.60
3:I:15:GLU:HG3	3:I:15:GLU:O	1.99	0.60
1:G:6:ARG:HB2	1:G:27:TYR:HB2	1.83	0.60
1:G:56:GLY:HA2	1:G:60:TRP:CE2	2.36	0.60
1:M:95:VAL:HG13	1:M:116:TYR:CE1	2.37	0.60
2:D:30:PHE:HE1	2:D:62:PHE:HB2	1.66	0.60
1:A:93:HIS:HB3	1:A:119:ASP:OD1	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:129:GLU:CG	4:J:130:PRO:CD	2.79	0.60
1:G:35:ARG:NH2	1:G:48:ARG:CG	2.58	0.60
1:G:159:TYR:HD1	1:G:163:THR:OG1	1.84	0.60
3:K:68:THR:O	3:K:68:THR:HG22	2.02	0.60
1:G:123:TYR:CE2	1:G:143:THR:HG21	2.37	0.60
4:F:222:GLU:HG2	4:F:223:TRP:N	2.15	0.60
4:J:12:VAL:HG22	4:J:154:HIS:CE1	2.37	0.59
1:G:195:SER:CB	1:G:196:ASP:HA	2.32	0.59
2:H:70:PHE:CZ	2:H:78:TYR:CE2	2.90	0.59
2:N:2:GLN:HE21	2:N:85:VAL:HB	1.65	0.59
4:F:88:ALA:HB3	4:F:90:TYR:CE1	2.37	0.59
4:F:125:VAL:HG22	4:F:147:ALA:HA	1.84	0.59
4:F:170:VAL:CA	4:F:194:LEU:HD12	2.32	0.59
4:F:197:SER:CB	4:F:200:PHE:HB2	2.30	0.59
1:G:97:ARG:CG	1:G:116:TYR:CE1	2.85	0.59
1:C:81:LEU:HG	5:R:9:VAL:HG21	1.83	0.59
2:D:45:ARG:O	2:D:45:ARG:HG2	2.00	0.59
3:I:74:TYR:HB3	3:I:76:TYR:HE1	1.66	0.59
4:J:223:TRP:HZ2	4:J:228:ALA:O	1.86	0.59
3:K:135:PHE:CZ	3:K:192:ILE:CG1	2.85	0.59
2:N:41:LYS:O	2:N:42:ASN:OD1	2.20	0.59
1:A:37:ASP:HB3	1:A:40:ALA:HB2	1.84	0.59
1:G:209:TYR:CD1	1:G:210:PRO:HA	2.37	0.59
1:G:220:ASP:OD2	1:G:256:ARG:NH1	2.35	0.59
3:K:135:PHE:HE1	3:K:138:PHE:HB3	1.66	0.59
1:A:203:CYS:HB2	1:A:217:TRP:CZ3	2.38	0.59
1:G:192:HIS:CE1	2:H:98:ASP:HB3	2.37	0.59
1:G:259:CYS:HB3	1:G:272:LEU:HB2	1.84	0.59
1:M:103:VAL:HB	1:M:107:TRP:HA	1.83	0.59
4:J:194:LEU:HD21	4:J:196:VAL:CG2	2.33	0.59
3:K:136:THR:CG2	3:K:171:SER:CB	2.80	0.59
3:K:192:ILE:CG1	3:K:193:PRO:HD2	2.29	0.59
4:L:201:TRP:C	4:L:204:PRO:HD2	2.28	0.59
4:F:223:TRP:CE3	4:F:230:PRO:HD2	2.37	0.59
1:A:170:ARG:O	1:A:174:ASN:ND2	2.32	0.59
3:I:115:PRO:HB3	3:I:137:ASP:OD2	2.01	0.59
3:K:21:PHE:HB2	3:K:75:LEU:HB3	1.85	0.59
1:M:197:HIS:N	1:M:197:HIS:HD1	2.01	0.59
1:M:213:ILE:HG13	1:M:263:HIS:HB2	1.85	0.59
1:A:103:VAL:HG12	1:A:108:ARG:C	2.28	0.59
4:J:69:ARG:HA	4:J:75:SER:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:218:GLN:CD	1:G:221:GLY:HA2	2.27	0.59
3:K:20:ASN:HA	3:K:75:LEU:O	2.03	0.59
3:K:144:VAL:HG23	3:K:157:LYS:HZ2	1.67	0.59
1:M:255:GLN:NE2	1:M:255:GLN:O	2.35	0.59
4:P:23:CYS:SG	4:P:24:ASP:N	2.76	0.59
2:B:92:ILE:HG23	2:B:92:ILE:O	2.03	0.58
1:G:133:TRP:CE3	1:G:147:TRP:CE3	2.90	0.58
1:M:270:LEU:HD13	1:M:272:LEU:CD2	2.32	0.58
4:F:110:ARG:HH21	4:F:154:HIS:CD2	2.20	0.58
4:J:26:ILE:HG22	4:J:27:SER:N	2.18	0.58
3:K:136:THR:HG21	3:K:171:SER:CB	2.33	0.58
1:M:197:HIS:O	1:M:198:GLU:CG	2.50	0.58
2:H:35:ILE:HG13	2:H:83:ASN:O	2.03	0.58
1:M:198:GLU:HA	1:M:251:SER:H	1.67	0.58
1:M:203:CYS:HB2	1:M:217:TRP:HE1	1.68	0.58
3:K:138:PHE:HZ	3:K:157:LYS:HG2	1.68	0.58
3:O:118:ALA:HB1	3:O:120:TYR:CZ	2.39	0.58
4:P:47:ILE:HG22	4:P:57:LYS:HA	1.85	0.58
4:P:160:TRP:CH2	4:P:211:GLN:HG3	2.38	0.58
1:C:238:ASP:HB3	1:C:240:THR:HG22	1.84	0.58
4:J:229:LYS:CB	4:J:230:PRO:HA	2.33	0.58
4:L:204:PRO:HG3	4:L:241:GLY:CA	2.25	0.58
1:M:253:GLN:HG3	1:M:256:ARG:HE	1.68	0.58
4:J:221:ASP:CG	4:J:222:GLU:H	2.11	0.58
1:G:178:THR:O	1:G:181:ARG:HB3	2.02	0.58
1:M:13:SER:HB3	1:M:78:LEU:HD13	1.85	0.58
2:N:81:ARG:CG	2:N:92:ILE:HG13	2.33	0.58
1:C:216:THR:HG23	1:C:260:HIS:HB2	1.85	0.58
1:G:73:THR:HG23	5:U:8:THR:HG22	1.85	0.58
4:L:147:ALA:HB2	4:L:212:VAL:HG21	1.84	0.58
1:M:219:ARG:O	1:M:220:ASP:C	2.46	0.58
1:C:35:ARG:HD2	2:D:53:ASP:OD2	2.04	0.58
1:C:72:GLN:CG	4:F:55:PRO:HB2	2.34	0.58
1:A:89:GLU:OE2	1:C:86:ASN:ND2	2.32	0.58
4:J:135:ILE:O	4:J:139:GLN:OE1	2.20	0.58
4:J:162:ASN:HA	4:J:207:HIS:CE1	2.39	0.58
4:F:153:ASP:O	4:F:155:VAL:N	2.37	0.58
1:M:10:THR:HG21	2:N:54:LEU:CD2	2.29	0.58
4:P:14:GLU:CG	4:P:117:LEU:CG	2.66	0.58
3:E:82:PRO:HA	3:E:108:VAL:CG2	2.33	0.58
4:F:97:THR:OG1	4:F:98:GLN:N	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:35:ARG:HH21	1:G:48:ARG:CD	2.17	0.58
1:G:133:TRP:CZ3	1:G:147:TRP:HZ3	2.20	0.58
2:H:24:ASN:CG	2:H:65:LEU:CD2	2.77	0.58
3:K:61:ARG:CB	3:K:78:LYS:O	2.51	0.58
3:O:182:ALA:CB	3:O:185:ASN:HB3	2.15	0.58
4:P:211:GLN:HE21	4:P:234:ILE:HG13	1.68	0.58
4:F:50:GLN:NE2	4:F:97:THR:O	2.36	0.58
1:G:123:TYR:CE2	5:U:9:VAL:HG21	2.39	0.57
1:M:170:ARG:O	1:M:174:ASN:ND2	2.37	0.57
3:E:82:PRO:O	3:E:84:ASP:HA	2.03	0.57
3:E:134:LEU:HD11	4:F:144:VAL:HG21	1.86	0.57
4:J:83:GLN:CG	4:J:84:GLN:H	2.17	0.57
3:K:175:TRP:HZ2	4:L:146:LEU:CB	2.15	0.57
3:K:185:ASN:O	3:K:188:ASN:CG	2.46	0.57
4:L:147:ALA:CB	4:L:212:VAL:HG21	2.35	0.57
4:L:201:TRP:O	4:L:204:PRO:CD	2.52	0.57
3:E:84:ASP:CB	3:E:85:SER:HB2	2.34	0.57
3:E:145:SER:HB2	3:E:189:ASN:HB3	1.86	0.57
3:E:192:ILE:HG23	3:E:193:PRO:HD3	1.84	0.57
2:N:70:PHE:CZ	2:N:72:PRO:HB3	2.39	0.57
3:I:121:GLN:O	3:I:132:VAL:O	2.23	0.57
4:J:217:LEU:HD13	4:J:221:ASP:CB	2.34	0.57
1:M:74:HIS:O	1:M:77:ASP:N	2.36	0.57
1:A:266:LEU:HD13	1:A:270:LEU:HD13	1.87	0.57
4:L:95:SER:OG	4:L:103:GLN:HB3	2.05	0.57
4:L:121:PHE:O	4:L:150:PHE:HA	2.04	0.57
3:O:27:SER:HB2	3:O:69:LYS:HD2	1.86	0.57
4:F:143:LEU:HB2	4:F:194:LEU:O	2.03	0.57
1:A:163:THR:HA	1:A:166:GLU:HB2	1.86	0.57
3:I:122:LEU:N	3:I:132:VAL:O	2.37	0.57
4:J:194:LEU:HD21	4:J:196:VAL:HG23	1.84	0.57
1:G:35:ARG:HG2	1:G:46:GLU:HB3	1.86	0.57
4:P:226:ASP:N	4:P:226:ASP:OD1	2.36	0.57
2:D:5:PRO:HB3	2:D:30:PHE:HB3	1.86	0.57
3:I:117:PRO:O	3:I:196:THR:C	2.48	0.57
4:F:118:LYS:CD	4:F:217:LEU:HD21	2.35	0.57
3:I:2:LEU:HD21	3:I:26:PRO:HB3	1.87	0.57
4:J:14:GLU:HB2	4:J:114:LEU:O	2.04	0.57
1:G:220:ASP:OD1	1:G:256:ARG:HG3	2.05	0.57
1:M:139:ALA:O	1:M:142:THR:OG1	2.22	0.57
3:I:2:LEU:HD13	3:I:26:PRO:HG3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:6:GLN:NE2	4:J:92:CYS:HB3	2.20	0.57
1:G:35:ARG:NH2	1:G:48:ARG:NE	2.53	0.57
1:M:5:MET:HE1	1:M:171:TYR:HE2	1.70	0.57
1:M:58:GLU:O	1:M:62:GLY:N	2.30	0.57
3:O:53:ASN:ND2	3:O:68:THR:OG1	2.38	0.57
3:O:187:PHE:N	3:O:187:PHE:CD2	2.73	0.57
1:C:113:TYR:CD2	1:C:113:TYR:N	2.73	0.57
1:G:12:VAL:HG11	2:H:33:SER:HB3	1.86	0.56
1:M:5:MET:HB2	1:M:28:VAL:HG12	1.87	0.56
4:P:197:SER:HB3	4:P:200:PHE:CD2	2.40	0.56
2:B:84:HIS:ND1	2:B:85:VAL:O	2.39	0.56
3:K:35:TRP:O	3:K:47:LEU:HB3	2.05	0.56
3:K:135:PHE:CE1	3:K:138:PHE:CD2	2.93	0.56
4:F:87:SER:HB3	4:F:113:VAL:HG12	1.87	0.56
1:A:204:TRP:CZ3	1:A:244:TRP:HB2	2.41	0.56
3:I:146:GLN:NE2	3:I:154:ILE:CD1	2.69	0.56
4:P:7:SER:OG	4:P:22:ARG:HD3	2.05	0.56
4:P:37:GLN:HG3	4:P:41:GLN:OE1	2.05	0.56
1:C:73:THR:HG21	5:R:6:VAL:HG23	1.86	0.56
3:E:157:LYS:NZ	3:E:170:ASN:HD21	2.03	0.56
2:B:20:SER:OG	4:L:18:ASP:OD2	2.23	0.56
4:L:170:VAL:CA	4:L:194:LEU:HD21	2.30	0.56
1:M:230:LEU:C	1:M:230:LEU:HD12	2.30	0.56
1:A:96:GLN:NE2	2:B:62:PHE:CE1	2.67	0.56
1:G:124:ILE:HD12	1:G:143:THR:HG23	1.87	0.56
1:M:5:MET:HE2	1:M:7:TYR:HE1	1.70	0.56
1:C:10:THR:HG21	2:D:54:LEU:CD2	2.35	0.56
4:L:145:CYS:SG	4:L:146:LEU:N	2.77	0.56
1:C:243:LYS:HG2	1:C:244:TRP:H	1.70	0.56
3:I:50:MET:HB3	3:I:66:LEU:HD22	1.88	0.56
3:K:185:ASN:CB	3:K:188:ASN:HD22	2.18	0.56
1:M:133:TRP:HB2	1:M:144:LYS:CG	2.36	0.56
1:C:5:MET:HB2	1:C:168:LEU:HD13	1.88	0.56
1:G:234:ARG:HB3	2:H:8:GLN:HE21	1.71	0.56
4:P:223:TRP:CZ3	4:P:229:LYS:O	2.57	0.56
4:F:150:PHE:CD1	4:F:155:VAL:HG11	2.40	0.56
3:K:62:ILE:HG22	3:K:75:LEU:HD11	1.88	0.56
4:J:29:HIS:HD2	4:J:94:SER:CA	2.13	0.56
1:G:199:ALA:N	1:G:249:VAL:O	2.39	0.56
4:F:179:GLU:HB2	4:F:187:ARG:O	2.06	0.56
4:F:230:PRO:O	4:F:231:VAL:HG22	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:GLU:HG2	1:C:86:ASN:OD1	2.05	0.55
1:C:122:ASP:OD1	2:D:60:TRP:NE1	2.36	0.55
2:D:74:GLU:HA	2:D:97:ARG:NH2	2.21	0.55
1:A:33:PHE:CD1	1:A:52:ILE:HD12	2.38	0.55
1:G:133:TRP:CZ3	1:G:147:TRP:HE3	2.21	0.55
3:K:138:PHE:CZ	3:K:157:LYS:CE	2.82	0.55
1:M:256:ARG:HD3	6:M:301:HOH:O	2.05	0.55
2:D:76:ASP:HB3	2:D:78:TYR:CE1	2.36	0.55
1:A:131:ARG:NH2	1:A:157:ARG:NH2	2.54	0.55
4:J:160:TRP:CE3	4:J:211:GLN:CB	2.90	0.55
4:J:207:HIS:HB3	4:J:240:TRP:CZ3	2.41	0.55
2:H:24:ASN:ND2	2:H:65:LEU:HD21	2.21	0.55
3:K:180:ASP:N	3:K:180:ASP:OD1	2.38	0.55
1:M:253:GLN:O	1:M:256:ARG:HG3	2.06	0.55
4:J:129:GLU:HG3	4:J:130:PRO:CD	2.34	0.55
3:K:61:ARG:HH21	3:K:84:ASP:CG	2.15	0.55
1:M:14:ARG:NH2	1:M:21:ARG:HB2	2.21	0.55
1:C:131:ARG:HH11	1:C:131:ARG:CG	2.12	0.55
2:D:56:PHE:HA	2:D:62:PHE:HA	1.86	0.55
3:I:42:LYS:NZ	3:I:43:SER:OG	2.40	0.55
4:J:11:LYS:HZ1	4:J:217:LEU:CD2	2.18	0.55
4:F:150:PHE:CE1	4:F:155:VAL:CG1	2.90	0.55
4:J:157:LEU:HD23	4:J:158:SER:N	2.22	0.55
3:K:136:THR:CB	3:K:170:ASN:O	2.51	0.55
4:L:82:THR:HG22	4:L:83:GLN:N	2.21	0.55
4:L:88:ALA:HB1	4:L:89:VAL:HG12	1.89	0.55
4:L:170:VAL:CB	4:L:194:LEU:HD21	2.35	0.55
1:M:66:LYS:HE3	3:O:29:ASN:ND2	2.21	0.55
2:N:83:ASN:OD1	2:N:84:HIS:N	2.40	0.55
2:H:37:VAL:CG2	2:H:82:VAL:HG12	2.36	0.55
4:L:124:GLU:HA	4:L:235:VAL:HG11	1.87	0.55
1:M:219:ARG:O	1:M:222:GLU:N	2.40	0.55
3:O:138:PHE:CD2	3:O:138:PHE:N	2.74	0.55
4:P:17:LYS:NZ	4:P:221:ASP:OD1	2.29	0.55
3:I:34:HIS:CE1	3:I:93:ILE:HD11	2.42	0.55
4:J:127:VAL:HG23	4:J:237:ALA:HB3	1.89	0.55
4:J:131:SER:HB2	4:J:134:GLU:HB3	1.89	0.55
1:G:192:HIS:CB	1:G:202:ARG:NH2	2.70	0.55
3:K:122:LEU:HD13	4:L:144:VAL:HG23	1.88	0.55
4:L:59:GLY:O	4:L:61:PRO:HD3	2.06	0.55
1:M:133:TRP:CB	1:M:144:LYS:HG3	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:123:ARG:HG2	3:O:124:ASP:N	2.22	0.55
4:P:83:GLN:O	4:P:113:VAL:HG11	2.06	0.55
1:C:231:VAL:HG23	1:C:232:GLU:O	2.06	0.55
2:B:18:GLY:HA2	2:B:71:THR:HG22	1.88	0.55
2:N:20:SER:HB3	4:F:18:ASP:CG	2.32	0.55
2:D:90:PRO:O	2:D:90:PRO:HG2	2.07	0.55
1:G:81:LEU:HG	5:U:9:VAL:HG11	1.88	0.54
2:N:11:SER:C	2:N:13:HIS:H	2.13	0.54
3:I:14:GLN:O	3:I:15:GLU:HB3	2.07	0.54
1:M:163:THR:HA	1:M:166:GLU:HB2	1.89	0.54
1:M:268:LYS:HB2	1:M:269:PRO:HD2	1.89	0.54
5:T:7:ALA:O	5:T:8:THR:HG23	2.06	0.54
1:A:88:SER:OG	1:A:89:GLU:N	2.40	0.54
1:G:98:MET:CE	1:G:99:TYR:CA	2.85	0.54
3:K:185:ASN:CB	3:K:188:ASN:ND2	2.69	0.54
4:P:37:GLN:HG3	4:P:41:GLN:CD	2.32	0.54
4:F:36:ARG:HB3	4:F:46:LEU:HD11	1.89	0.54
4:F:125:VAL:HG21	4:F:212:VAL:HG21	1.89	0.54
2:N:83:ASN:HB2	2:N:90:PRO:HG3	1.89	0.54
4:P:141:ALA:HB2	4:P:198:ALA:HA	1.89	0.54
3:E:136:THR:HG22	3:E:171:SER:CB	2.24	0.54
2:H:11:SER:HB2	2:H:95:TRP:CZ2	2.42	0.54
3:K:52:LEU:HD12	3:K:52:LEU:O	2.07	0.54
3:E:138:PHE:N	3:E:138:PHE:CD1	2.72	0.54
3:K:66:LEU:HD23	3:K:67:ASN:N	2.23	0.54
3:K:144:VAL:CG2	3:K:157:LYS:HZ1	2.15	0.54
4:L:7:SER:O	4:L:22:ARG:HB3	2.08	0.54
4:L:150:PHE:HE1	4:L:188:TYR:C	2.15	0.54
3:O:87:THR:HA	3:O:105:SER:HA	1.89	0.54
4:F:26:ILE:C	4:F:27:SER:HG	2.04	0.54
4:F:54:ALA:CB	4:F:57:LYS:CE	2.78	0.54
4:F:98:GLN:HE21	4:F:98:GLN:CA	2.19	0.54
4:J:123:PRO:HA	4:J:150:PHE:HB3	1.88	0.54
1:M:128:GLU:OE1	1:M:128:GLU:N	2.36	0.54
1:A:12:VAL:HG22	1:A:94:THR:HG22	1.90	0.54
1:G:143:THR:CB	5:U:9:VAL:HG23	2.38	0.54
3:K:47:LEU:O	3:K:48:PHE:HD1	1.91	0.54
3:K:72:TYR:CD1	3:K:72:TYR:C	2.85	0.54
4:P:66:SER:HG	4:P:78:THR:HG1	1.56	0.54
4:P:223:TRP:CE2	4:P:229:LYS:O	2.61	0.54
4:F:155:VAL:HG12	4:F:214:PHE:HD1	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:160:LEU:HD22	4:J:169:GLY:O	2.07	0.54
1:G:91:GLY:HA3	1:G:93:HIS:CE1	2.43	0.54
4:L:150:PHE:HD1	4:L:150:PHE:C	2.16	0.54
4:L:150:PHE:CD1	4:L:150:PHE:C	2.85	0.54
1:M:66:LYS:NZ	3:O:29:ASN:CB	2.71	0.54
2:H:71:THR:O	2:H:72:PRO:O	2.26	0.54
4:L:7:SER:OG	4:L:8:PRO:HA	2.08	0.54
2:N:46:ILE:O	2:N:49:VAL:HG23	2.08	0.54
1:C:159:TYR:CD1	1:C:163:THR:HB	2.43	0.54
1:M:175:GLY:O	1:M:179:LEU:N	2.41	0.53
3:I:9:GLN:HA	3:I:104:THR:HA	1.90	0.53
4:J:98:GLN:HA	4:J:98:GLN:NE2	2.23	0.53
4:J:177:LEU:HB3	4:J:189:ALA:HB3	1.91	0.53
2:H:70:PHE:HE1	2:H:78:TYR:CG	2.26	0.53
1:C:195:SER:OG	1:C:196:ASP:N	2.39	0.53
2:B:21:ASN:OD1	2:B:22:PHE:N	2.33	0.53
1:G:138:MET:N	1:G:138:MET:SD	2.82	0.53
4:L:203:ASN:N	4:L:204:PRO:HD2	2.22	0.53
3:E:8:PRO:O	3:E:104:THR:HB	2.08	0.53
4:F:160:TRP:CD1	4:F:165:GLU:CA	2.91	0.53
4:J:160:TRP:CH2	4:J:211:GLN:CB	2.91	0.53
1:G:155:GLN:HE22	4:L:100:TRP:CD1	2.27	0.53
3:K:35:TRP:C	3:K:36:TYR:HD1	2.16	0.53
1:M:110:LEU:HD23	1:M:111:ARG:HG2	1.91	0.53
2:D:30:PHE:CE1	2:D:62:PHE:HB2	2.44	0.53
4:J:122:PRO:HG3	4:J:230:PRO:HB2	1.90	0.53
1:G:58:GLU:O	1:G:61:ASP:N	2.42	0.53
1:M:191:HIS:NE2	1:M:193:ALA:HB2	2.24	0.53
3:E:31:TYR:C	3:E:31:TYR:CD2	2.86	0.53
2:B:57:SER:O	2:B:60:TRP:N	2.41	0.53
2:B:85:VAL:O	2:B:86:THR:OG1	2.19	0.53
4:J:130:PRO:HG3	4:J:142:THR:O	2.09	0.53
1:M:154:GLU:HB3	3:O:52:LEU:HD11	1.90	0.53
3:O:4:VAL:HG21	3:O:99:TYR:O	2.08	0.53
4:P:159:TRP:O	4:P:165:GLU:HB2	2.07	0.53
3:E:84:ASP:HB3	3:E:85:SER:CB	2.39	0.53
1:A:2:SER:HB3	1:A:103:VAL:O	2.08	0.53
1:G:189:MET:HE3	1:G:274:TRP:N	2.23	0.53
4:L:191:SER:CB	4:L:193:ARG:NH2	2.70	0.53
2:N:58:LYS:NZ	6:N:102:HOH:O	2.40	0.53
3:E:136:THR:CA	3:E:138:PHE:CE1	2.86	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:160:LEU:HD23	4:J:169:GLY:O	2.09	0.53
3:K:52:LEU:HD12	3:K:52:LEU:H	1.73	0.53
2:N:54:LEU:HD23	2:N:54:LEU:C	2.34	0.53
2:N:63:TYR:CD1	2:N:63:TYR:C	2.87	0.53
1:C:59:TYR:O	1:C:63:GLU:HG2	2.09	0.53
4:F:26:ILE:O	4:F:26:ILE:HG22	2.09	0.53
3:K:59:LYS:CD	3:K:60:GLY:H	2.21	0.53
3:O:182:ALA:O	3:O:186:ALA:N	2.40	0.53
4:F:123:PRO:HB3	4:F:150:PHE:CD2	2.43	0.53
1:A:131:ARG:NH1	6:A:302:HOH:O	2.31	0.53
3:I:115:PRO:CA	3:I:137:ASP:OD2	2.56	0.53
3:O:79:GLY:C	3:O:81:GLN:OE1	2.51	0.53
3:I:74:TYR:HB3	3:I:76:TYR:CE1	2.44	0.52
1:G:99:TYR:OH	5:U:3:VAL:HG12	2.09	0.52
1:G:218:GLN:CB	1:G:223:ASP:HA	2.37	0.52
4:L:191:SER:HB2	4:L:193:ARG:HH21	1.74	0.52
1:M:63:GLU:OE1	5:T:2:LEU:HD12	2.08	0.52
3:O:29:ASN:HB2	5:T:4:PRO:HG3	1.91	0.52
4:F:118:LYS:HD2	4:F:217:LEU:HD21	1.91	0.52
4:F:217:LEU:HD12	4:F:218:SER:H	1.73	0.52
2:H:70:PHE:CZ	2:H:78:TYR:CD2	2.97	0.52
3:K:25:PHE:CE1	3:K:71:GLY:HA2	2.44	0.52
1:M:67:VAL:O	1:M:70:HIS:HB2	2.09	0.52
3:E:157:LYS:HZ2	3:E:170:ASN:HD21	1.56	0.52
4:P:11:LYS:HZ3	4:P:19:VAL:HB	1.72	0.52
4:P:70:THR:O	4:P:74:VAL:HB	2.09	0.52
4:F:140:LYS:CD	4:F:197:SER:HA	2.39	0.52
4:J:135:ILE:CA	4:J:140:LYS:O	2.52	0.52
4:L:203:ASN:N	4:L:204:PRO:CD	2.72	0.52
1:M:97:ARG:HH22	1:M:147:TRP:HH2	1.56	0.52
1:G:192:HIS:HD2	1:G:202:ARG:HD2	1.73	0.52
3:O:44:PRO:HG2	3:O:44:PRO:O	2.10	0.52
2:D:37:VAL:HG22	2:D:82:VAL:HG12	1.90	0.52
3:E:49:VAL:HG21	4:F:102:THR:CG2	2.36	0.52
4:F:193:ARG:HG3	4:F:193:ARG:NH1	2.18	0.52
4:L:13:THR:OG1	4:L:14:GLU:N	2.40	0.52
4:L:125:VAL:HG21	4:L:236:SER:O	2.10	0.52
4:L:217:LEU:HB2	4:L:230:PRO:O	2.09	0.52
4:P:61:PRO:O	6:P:301:HOH:O	2.19	0.52
1:C:74:HIS:CD2	1:C:97:ARG:HH21	2.27	0.52
2:D:74:GLU:HA	2:D:97:ARG:HH22	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:89:LEU:HD21	3:E:100:PHE:CD1	2.43	0.52
3:I:155:THR:HG21	4:J:191:SER:OG	2.09	0.52
4:J:11:LYS:NZ	4:J:217:LEU:CD2	2.73	0.52
2:N:60:TRP:HA	2:N:60:TRP:CE3	2.42	0.52
4:J:36:ARG:HB3	4:J:46:LEU:HD11	1.92	0.52
4:J:96:GLN:O	4:J:98:GLN:N	2.40	0.52
1:G:12:VAL:HA	1:G:94:THR:HA	1.92	0.52
1:G:116:TYR:HD2	1:G:116:TYR:C	2.18	0.52
2:H:55:SER:OG	2:H:56:PHE:N	2.43	0.52
3:K:135:PHE:CD1	3:K:135:PHE:C	2.85	0.52
1:M:219:ARG:N	1:M:222:GLU:O	2.41	0.52
2:N:41:LYS:O	2:N:77:GLU:O	2.27	0.52
3:E:181:PHE:CB	3:E:182:ALA:CA	2.86	0.52
4:F:6:GLN:HG3	4:F:22:ARG:O	2.10	0.52
3:I:182:ALA:O	3:I:186:ALA:HB2	2.10	0.52
1:G:218:GLN:HB2	1:G:222:GLU:C	2.35	0.52
1:C:155:GLN:HE21	3:E:51:THR:HG21	1.75	0.52
3:I:158:CYS:SG	4:J:193:ARG:NH1	2.83	0.51
1:G:98:MET:C	1:G:98:MET:SD	2.93	0.51
1:G:131:ARG:NH2	6:G:303:HOH:O	2.27	0.51
2:H:37:VAL:HG21	2:H:82:VAL:HG12	1.93	0.51
4:L:36:ARG:HD2	4:L:90:TYR:CG	2.45	0.51
4:L:130:PRO:HG2	4:L:201:TRP:CE2	2.45	0.51
3:O:61:ARG:NH1	3:O:81:GLN:HB2	2.25	0.51
3:E:157:LYS:CE	3:E:170:ASN:OD1	2.58	0.51
4:J:6:GLN:HE21	4:J:92:CYS:HB3	1.74	0.51
4:J:141:ALA:CB	4:J:196:VAL:O	2.45	0.51
1:G:125:ALA:C	1:G:134:THR:HG22	2.34	0.51
1:G:168:LEU:O	1:G:172:LEU:HG	2.11	0.51
1:G:200:THR:HG21	1:G:202:ARG:NH2	2.26	0.51
4:P:97:THR:CG2	4:P:98:GLN:N	2.73	0.51
2:D:73:THR:HG22	2:D:74:GLU:H	1.74	0.51
3:O:52:LEU:O	3:O:55:ASP:N	2.42	0.51
4:P:15:LYS:HZ2	4:P:83:GLN:HG3	1.75	0.51
3:E:30:PHE:CD2	3:E:92:PHE:HE2	2.23	0.51
4:F:201:TRP:C	4:F:204:PRO:CD	2.76	0.51
3:K:50:MET:HB3	3:K:66:LEU:CD1	2.40	0.51
3:O:134:LEU:HD12	3:O:135:PHE:H	1.74	0.51
3:O:140:SER:O	3:O:142:THR:N	2.43	0.51
2:D:54:LEU:HD21	2:D:62:PHE:HD1	1.72	0.51
3:E:84:ASP:HB3	3:E:85:SER:C	2.35	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:37:GLN:NE2	4:F:38:ARG:O	2.44	0.51
3:I:81:GLN:HG2	3:I:82:PRO:HD2	1.92	0.51
4:J:113:VAL:HG22	4:J:114:LEU:N	2.26	0.51
1:G:249:VAL:HG22	1:G:257:TYR:CZ	2.46	0.51
2:H:24:ASN:OD1	2:H:66:TYR:O	2.28	0.51
4:L:62:SER:CA	4:L:65:PHE:HE2	2.24	0.51
2:N:12:ARG:O	2:N:12:ARG:HG2	2.09	0.51
4:F:121:PHE:HE2	4:F:187:ARG:NH2	1.92	0.51
2:B:37:VAL:CG2	2:B:66:TYR:CZ	2.94	0.51
3:K:21:PHE:HE1	3:K:88:TYR:CD2	2.28	0.51
3:K:59:LYS:CD	3:K:60:GLY:N	2.73	0.51
3:K:152:VAL:HG13	3:K:153:TYR:N	2.26	0.51
4:L:161:VAL:O	4:L:162:ASN:CB	2.59	0.51
3:E:157:LYS:NZ	3:E:170:ASN:OD1	2.44	0.51
3:E:161:ASP:OD1	3:E:161:ASP:N	2.43	0.51
4:F:73:SER:OG	4:F:74:VAL:N	2.43	0.51
3:I:34:HIS:O	3:I:90:CYS:HA	2.10	0.51
1:G:101:CYS:N	1:G:164:CYS:SG	2.84	0.51
3:K:185:ASN:HB2	3:K:188:ASN:HB3	1.92	0.51
1:M:188:HIS:HD2	1:M:204:TRP:HE3	1.59	0.51
1:C:226:GLN:OE1	1:C:227:ASP:HB2	2.10	0.51
2:B:1:ILE:HG13	2:B:2:GLN:N	2.26	0.51
3:O:134:LEU:HD12	3:O:135:PHE:N	2.26	0.51
1:C:6:ARG:HA	1:C:100:GLY:HA3	1.92	0.51
2:D:70:PHE:HE1	2:D:72:PRO:HB3	1.75	0.51
3:E:21:PHE:CD2	3:E:21:PHE:N	2.79	0.51
3:I:113:GLN:OE1	3:I:113:GLN:N	2.24	0.51
1:M:9:PHE:HE2	1:M:99:TYR:CE2	2.28	0.51
3:O:181:PHE:O	3:O:182:ALA:HB3	2.11	0.51
4:P:135:ILE:HG13	4:P:141:ALA:HA	1.92	0.51
4:F:29:HIS:ND1	4:F:96:GLN:HG2	2.26	0.51
1:A:143:THR:HG21	5:Q:9:VAL:HG12	1.92	0.51
3:I:81:GLN:N	3:I:84:ASP:OD2	2.40	0.51
1:G:116:TYR:CD2	1:G:116:TYR:C	2.85	0.51
4:L:123:PRO:CG	4:L:150:PHE:HD2	2.18	0.51
4:L:215:TYR:HA	4:L:232:THR:OG1	2.11	0.51
3:E:83:GLU:OE1	3:E:162:MET:CE	2.58	0.51
3:E:187:PHE:O	3:E:192:ILE:HD12	2.11	0.51
3:I:44:PRO:HG2	4:J:105:PHE:CD2	2.47	0.50
4:F:35:TYR:OH	4:F:103:GLN:OE1	2.20	0.50
4:F:47:ILE:CG2	4:F:48:TYR:N	2.73	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:165:GLU:C	4:F:166:VAL:HG23	2.36	0.50
1:A:207:SER:O	1:A:207:SER:OG	2.22	0.50
2:B:1:ILE:HG13	2:B:2:GLN:H	1.75	0.50
4:P:160:TRP:HA	4:P:165:GLU:HB3	1.92	0.50
4:F:83:GLN:HA	4:F:113:VAL:HG21	1.93	0.50
4:F:135:ILE:CD1	4:F:201:TRP:HZ3	2.24	0.50
3:I:2:LEU:HD23	3:I:3:ASN:H	1.77	0.50
3:I:137:ASP:CG	3:I:138:PHE:H	2.19	0.50
1:G:37:ASP:HB3	1:G:40:ALA:HB2	1.93	0.50
2:N:2:GLN:HE22	2:N:85:VAL:HB	1.76	0.50
2:N:33:SER:O	2:N:35:ILE:HD12	2.11	0.50
2:N:38:ASP:OD2	2:N:45:ARG:HB3	2.12	0.50
2:N:73:THR:HG22	2:N:76:ASP:CG	2.34	0.50
4:F:123:PRO:HA	4:F:149:GLY:HA3	1.92	0.50
4:F:170:VAL:HA	4:F:194:LEU:CD1	2.40	0.50
4:F:202:GLN:C	4:F:204:PRO:HD3	2.36	0.50
3:K:30:PHE:HD1	3:K:92:PHE:HE1	1.57	0.50
4:L:46:LEU:O	4:L:47:ILE:HG22	2.12	0.50
4:P:130:PRO:HB3	4:P:142:THR:O	2.11	0.50
3:I:154:ILE:HD12	3:I:155:THR:N	2.26	0.50
1:G:98:MET:HE1	1:G:99:TYR:C	2.37	0.50
1:G:102:ASP:HB2	1:G:111:ARG:HG3	1.93	0.50
1:M:66:LYS:NZ	3:O:29:ASN:HB2	2.25	0.50
1:M:249:VAL:HG22	1:M:257:TYR:CD1	2.46	0.50
4:P:64:ARG:CG	4:P:64:ARG:NH1	2.73	0.50
1:C:13:SER:HB3	1:C:78:LEU:HD13	1.93	0.50
4:F:203:ASN:N	4:F:204:PRO:CD	2.75	0.50
4:J:29:HIS:CD2	4:J:94:SER:O	2.64	0.50
3:K:144:VAL:CG2	3:K:157:LYS:HZ2	2.23	0.50
3:K:161:ASP:HA	3:K:168:LYS:HB3	1.93	0.50
4:L:10:ASN:OD1	4:L:109:THR:HA	2.12	0.50
4:L:89:VAL:CG1	4:L:110:ARG:CG	2.83	0.50
4:L:204:PRO:HB2	4:L:205:ARG:HA	1.93	0.50
3:E:84:ASP:HA	3:E:85:SER:HG	1.76	0.50
4:F:170:VAL:CA	4:F:194:LEU:CD1	2.90	0.50
4:F:202:GLN:C	4:F:204:PRO:CD	2.85	0.50
4:L:67:ALA:HB2	4:L:77:LEU:HD13	1.93	0.50
4:F:110:ARG:HH21	4:F:154:HIS:HA	1.77	0.50
1:A:131:ARG:NH2	6:A:302:HOH:O	2.19	0.50
1:G:189:MET:CE	1:G:274:TRP:N	2.75	0.50
4:J:150:PHE:O	4:J:187:ARG:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:70:PHE:CE1	2:H:78:TYR:CZ	3.00	0.50
4:L:146:LEU:HD12	4:L:146:LEU:O	2.12	0.50
1:C:188:HIS:ND1	1:C:188:HIS:N	2.60	0.50
1:A:147:TRP:HB3	1:A:152:VAL:HB	1.92	0.49
2:B:18:GLY:N	2:B:72:PRO:O	2.37	0.49
3:I:36:TYR:O	3:I:88:TYR:HA	2.12	0.49
2:H:96:ASP:HB3	2:H:99:MET:HB2	1.94	0.49
3:K:135:PHE:CZ	3:K:192:ILE:HD11	2.44	0.49
4:L:150:PHE:CD1	4:L:188:TYR:O	2.65	0.49
1:M:227:ASP:OD1	1:M:248:VAL:HG12	2.12	0.49
1:A:4:SER:CB	1:A:102:ASP:OD2	2.53	0.49
1:A:45:MET:HE2	1:A:63:GLU:HB3	1.94	0.49
4:J:29:HIS:HD2	4:J:94:SER:C	2.13	0.49
1:G:97:ARG:HH22	5:U:8:THR:HA	1.77	0.49
4:P:11:LYS:O	4:P:111:LEU:HD12	2.13	0.49
3:E:50:MET:HE1	3:E:57:LYS:HG3	1.95	0.49
4:J:194:LEU:HD23	4:J:195:ARG:C	2.37	0.49
1:G:195:SER:HB2	1:G:196:ASP:HA	1.93	0.49
4:L:169:GLY:C	4:L:194:LEU:HD22	2.37	0.49
2:B:89:GLN:CB	2:B:90:PRO:HD2	2.42	0.49
3:K:48:PHE:HD2	3:K:64:ALA:HB2	1.77	0.49
1:C:99:TYR:OH	5:R:3:VAL:HG12	2.12	0.49
1:C:202:ARG:HG3	1:C:244:TRP:NE1	2.26	0.49
3:E:6:GLN:OE1	3:E:103:GLY:HA2	2.11	0.49
4:F:69:ARG:HB2	4:F:75:SER:HB2	1.94	0.49
4:F:162:ASN:O	4:F:164:LYS:HG3	2.13	0.49
1:A:203:CYS:HB2	1:A:217:TRP:HZ3	1.75	0.49
2:B:52:SER:OG	2:B:65:LEU:N	2.43	0.49
4:J:84:GLN:CD	1:G:177:GLU:OE1	2.56	0.49
4:J:131:SER:HB2	4:J:134:GLU:CB	2.42	0.49
1:G:185:PRO:HB3	1:G:208:PHE:HB3	1.93	0.49
4:L:202:GLN:N	4:L:204:PRO:HD2	2.27	0.49
1:M:8:PHE:HB2	1:M:25:VAL:HG13	1.92	0.49
2:N:75:LYS:O	2:N:76:ASP:C	2.54	0.49
3:O:96:ASN:H	5:T:5:MET:HE2	1.77	0.49
1:C:25:VAL:HG21	1:C:32:GLN:HE21	1.77	0.49
4:J:162:ASN:HB2	4:J:164:LYS:NZ	2.28	0.49
1:G:142:THR:O	1:G:146:LYS:HG3	2.13	0.49
3:K:119:VAL:HA	3:K:134:LEU:O	2.13	0.49
4:L:170:VAL:CG2	4:L:194:LEU:CD2	2.87	0.49
4:P:21:LEU:HD22	4:P:109:THR:HG21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:38:ARG:O	4:P:40:GLY:HA2	2.12	0.49
4:P:129:GLU:HG3	4:P:201:TRP:CZ2	2.48	0.49
4:J:177:LEU:CD1	4:J:177:LEU:C	2.86	0.49
4:L:36:ARG:HD2	4:L:90:TYR:HA	1.94	0.49
4:F:41:GLN:O	4:F:42:GLY:C	2.55	0.49
1:A:9:PHE:HB2	1:A:97:ARG:HB3	1.95	0.49
2:H:54:LEU:HA	2:H:64:LEU:HD21	1.93	0.49
4:L:11:LYS:O	4:L:111:LEU:HA	2.13	0.49
1:M:49:ALA:HB3	1:M:52:ILE:HG22	1.94	0.49
1:M:73:THR:HG22	5:T:8:THR:HG21	1.95	0.49
5:T:3:VAL:O	5:T:4:PRO:C	2.55	0.49
3:I:115:PRO:HA	3:I:137:ASP:CG	2.38	0.49
4:J:113:VAL:O	4:J:114:LEU:CB	2.60	0.49
1:G:142:THR:OG1	6:G:302:HOH:O	2.20	0.49
3:K:133:CYS:SG	3:K:183:CYS:N	2.86	0.49
3:K:159:VAL:N	4:L:171:CYS:SG	2.85	0.49
1:M:21:ARG:NH2	1:M:37:ASP:OD2	2.38	0.49
1:A:219:ARG:HD2	1:A:257:TYR:CZ	2.47	0.49
4:J:49:PHE:CE1	4:J:54:ALA:HB2	2.47	0.49
4:J:154:HIS:N	4:J:154:HIS:CD2	2.80	0.49
4:L:46:LEU:C	4:L:47:ILE:CG2	2.85	0.49
4:F:218:SER:HG	4:F:221:ASP:CB	2.22	0.49
4:J:153:ASP:OD2	4:J:176:PRO:HG3	2.12	0.48
1:G:189:MET:HE3	1:G:274:TRP:CA	2.42	0.48
3:K:2:LEU:CB	3:K:3:ASN:HA	2.39	0.48
3:K:175:TRP:CZ2	4:L:146:LEU:CB	2.95	0.48
4:L:125:VAL:HG22	4:L:235:VAL:HG12	1.95	0.48
1:M:37:ASP:OD1	1:M:38:SER:N	2.46	0.48
2:N:3:ARG:O	2:N:30:PHE:HA	2.13	0.48
4:P:196:VAL:CG2	4:P:197:SER:H	2.06	0.48
4:F:35:TYR:CD1	4:F:43:LEU:HD21	2.48	0.48
4:F:96:GLN:C	4:F:97:THR:HG1	2.08	0.48
4:F:217:LEU:CD1	4:F:218:SER:N	2.72	0.48
4:J:11:LYS:HZ1	4:J:217:LEU:HD22	1.78	0.48
2:H:7:ILE:HG23	2:H:93:VAL:HG21	1.95	0.48
3:K:63:SER:O	3:K:75:LEU:HA	2.12	0.48
3:K:113:GLN:O	3:K:114:ASN:C	2.53	0.48
1:M:197:HIS:ND1	1:M:197:HIS:N	2.60	0.48
2:D:89:GLN:HG3	2:D:90:PRO:N	2.28	0.48
4:F:230:PRO:C	4:F:231:VAL:HG23	2.37	0.48
3:I:7:SER:HB2	3:I:8:PRO:HD3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:134:LEU:HB3	3:I:173:VAL:HA	1.94	0.48
3:I:146:GLN:CG	3:I:154:ILE:HG12	2.40	0.48
4:J:120:VAL:C	4:J:121:PHE:CG	2.91	0.48
3:K:48:PHE:HE2	3:K:63:SER:HA	1.77	0.48
4:L:141:ALA:H	4:L:198:ALA:H	1.61	0.48
1:M:259:CYS:HB3	1:M:272:LEU:CB	2.43	0.48
1:M:270:LEU:HD13	1:M:272:LEU:HD21	1.95	0.48
1:C:102:ASP:OD2	1:C:113:TYR:OH	2.29	0.48
2:N:12:ARG:O	2:N:13:HIS:CE1	2.67	0.48
1:G:35:ARG:NH2	1:G:48:ARG:CD	2.76	0.48
1:G:192:HIS:CB	1:G:202:ARG:HH22	2.23	0.48
2:H:24:ASN:ND2	2:H:65:LEU:CD2	2.76	0.48
4:L:62:SER:CA	4:L:65:PHE:CD2	2.97	0.48
1:M:73:THR:HG22	5:T:8:THR:CG2	2.43	0.48
1:M:203:CYS:HB2	1:M:217:TRP:NE1	2.28	0.48
1:M:207:SER:O	1:M:207:SER:OG	2.30	0.48
1:M:225:THR:OG1	1:M:226:GLN:N	2.47	0.48
1:C:24:ALA:HB3	1:C:36:PHE:HB3	1.96	0.48
1:C:145:HIS:HD2	6:C:305:HOH:O	1.95	0.48
3:E:124:ASP:CG	3:E:125:SER:HA	2.37	0.48
3:E:178:LYS:HG2	3:E:179:SER:OG	2.13	0.48
2:B:10:TYR:HE2	2:B:26:TYR:HB3	1.79	0.48
2:B:37:VAL:HG21	2:B:66:TYR:CD1	2.49	0.48
3:K:136:THR:HG21	3:K:171:SER:HB3	1.95	0.48
4:L:88:ALA:CB	4:L:110:ARG:HA	2.42	0.48
4:P:14:GLU:OE2	4:P:117:LEU:HD11	2.13	0.48
3:E:50:MET:HA	3:E:50:MET:HE2	1.96	0.48
4:F:160:TRP:H	4:F:209:ARG:HG3	1.78	0.48
1:A:70:HIS:HD2	5:Q:6:VAL:HG22	1.77	0.48
3:I:152:VAL:HA	3:I:176:SER:OG	2.13	0.48
1:G:191:HIS:ND1	1:G:191:HIS:C	2.72	0.48
2:H:70:PHE:HZ	2:H:78:TYR:CD2	2.31	0.48
3:O:120:TYR:HB3	4:P:131:SER:OG	2.14	0.48
3:O:123:ARG:HB2	3:O:131:SER:HB3	1.95	0.48
3:E:87:THR:HA	3:E:105:SER:HA	1.96	0.48
1:A:225:THR:OG1	1:A:226:GLN:HB2	2.14	0.48
3:I:121:GLN:HG3	4:J:131:SER:HA	1.95	0.48
1:G:163:THR:HA	1:G:166:GLU:HG2	1.95	0.48
3:K:138:PHE:H	3:K:138:PHE:HD2	1.61	0.48
4:L:160:TRP:C	4:L:161:VAL:CG2	2.85	0.48
1:M:102:ASP:HB2	1:M:111:ARG:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:45:PHE:HZ	4:J:48:TYR:HB3	1.78	0.48
1:G:10:THR:HG22	2:H:56:PHE:CE2	2.48	0.48
4:L:82:THR:CG2	4:L:83:GLN:N	2.77	0.48
4:L:130:PRO:HD2	4:L:201:TRP:CZ2	2.49	0.48
2:N:30:PHE:CE1	2:N:35:ILE:HD11	2.48	0.48
4:P:160:TRP:HH2	4:P:234:ILE:HD11	1.78	0.48
1:C:22:PHE:H	1:C:38:SER:HB3	1.78	0.48
3:E:84:ASP:CA	3:E:85:SER:CB	2.91	0.48
4:F:123:PRO:HA	4:F:149:GLY:CA	2.44	0.48
4:F:201:TRP:O	4:F:204:PRO:CG	2.62	0.48
1:A:177:GLU:CG	1:A:178:THR:N	2.77	0.48
3:K:118:ALA:HB2	3:K:197:PHE:HB3	1.96	0.48
3:K:192:ILE:O	3:K:193:PRO:C	2.56	0.48
3:O:131:SER:OG	3:O:181:PHE:HE2	1.97	0.48
2:D:74:GLU:OE1	2:D:74:GLU:N	2.47	0.48
4:F:33:TYR:O	4:F:92:CYS:HA	2.14	0.48
4:F:130:PRO:HB3	4:F:142:THR:O	2.14	0.48
1:A:237:GLY:C	1:A:239:GLY:H	2.22	0.47
3:I:33:LEU:O	3:I:50:MET:N	2.41	0.47
4:L:161:VAL:HG12	4:L:162:ASN:H	1.78	0.47
1:C:103:VAL:HG12	1:C:109:PHE:HA	1.96	0.47
1:A:231:VAL:O	1:A:232:GLU:C	2.57	0.47
4:J:14:GLU:HA	4:J:114:LEU:O	2.14	0.47
1:G:234:ARG:CG	1:G:242:GLN:HB2	2.43	0.47
2:H:3:ARG:HH21	2:H:61:SER:HB2	1.78	0.47
3:K:124:ASP:CA	4:L:128:PHE:HA	2.45	0.47
4:L:150:PHE:CZ	4:L:155:VAL:HG11	2.49	0.47
1:M:11:SER:HA	1:M:21:ARG:O	2.14	0.47
1:M:217:TRP:HZ3	1:M:247:VAL:HG22	1.79	0.47
2:N:57:SER:C	2:N:59:ASP:H	2.15	0.47
1:C:159:TYR:HD1	1:C:163:THR:HB	1.78	0.47
4:F:153:ASP:CG	4:F:176:PRO:HG3	2.39	0.47
2:B:49:VAL:HG12	2:B:50:GLU:O	2.15	0.47
1:G:98:MET:SD	1:G:99:TYR:N	2.87	0.47
3:O:155:THR:CG2	4:P:173:ASP:OD2	2.60	0.47
1:C:66:LYS:HE3	5:R:2:LEU:HB2	1.95	0.47
4:F:60:LEU:HD22	4:F:65:PHE:HB3	1.94	0.47
4:F:201:TRP:O	4:F:204:PRO:HG3	2.14	0.47
1:A:66:LYS:HE2	3:I:29:ASN:OD1	2.14	0.47
1:G:162:GLY:O	1:G:166:GLU:CD	2.58	0.47
4:L:103:GLN:OE1	4:L:103:GLN:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:131:SER:HB2	4:L:135:ILE:HG21	1.96	0.47
1:C:27:TYR:CD2	1:C:32:GLN:HB2	2.49	0.47
1:A:63:GLU:CD	1:A:66:LYS:HZ2	2.21	0.47
1:A:202:ARG:HG3	1:A:244:TRP:NE1	2.26	0.47
1:G:68:LYS:O	1:G:72:GLN:HG2	2.15	0.47
1:M:14:ARG:HH21	1:M:21:ARG:HB2	1.78	0.47
2:D:55:SER:O	2:D:63:TYR:N	2.46	0.47
2:B:40:LEU:HD23	2:B:43:GLY:HA2	1.96	0.47
4:J:191:SER:OG	4:J:191:SER:O	2.33	0.47
4:J:231:VAL:O	4:J:232:THR:C	2.57	0.47
3:K:135:PHE:HZ	3:K:192:ILE:HG12	1.67	0.47
4:L:140:LYS:HA	4:L:197:SER:HA	1.95	0.47
1:M:203:CYS:HB2	1:M:217:TRP:CZ2	2.50	0.47
1:M:213:ILE:HD11	1:M:261:VAL:CG1	2.44	0.47
1:C:155:GLN:HG2	3:E:51:THR:HG21	1.96	0.47
1:A:49:ALA:O	1:A:52:ILE:HG22	2.15	0.47
3:I:61:ARG:NH1	3:I:84:ASP:OD2	2.48	0.47
3:I:89:LEU:HD22	3:I:100:PHE:HD2	1.79	0.47
4:J:86:ASP:N	4:J:86:ASP:OD1	2.48	0.47
4:J:223:TRP:NE1	4:J:228:ALA:O	2.47	0.47
1:G:42:SER:HB3	1:G:44:ARG:HG3	1.97	0.47
1:G:66:LYS:NZ	5:U:2:LEU:O	2.45	0.47
1:G:117:ALA:HB2	2:H:60:TRP:CE2	2.50	0.47
1:G:162:GLY:C	1:G:166:GLU:OE2	2.58	0.47
4:L:36:ARG:HB2	4:L:44:GLU:OE2	2.15	0.47
4:L:83:GLN:O	4:L:84:GLN:C	2.57	0.47
3:O:118:ALA:CB	3:O:120:TYR:CZ	2.98	0.47
3:O:153:TYR:HB3	4:P:177:LEU:HD21	1.97	0.47
4:P:118:LYS:O	4:P:120:VAL:N	2.48	0.47
4:P:154:HIS:ND1	4:P:154:HIS:N	2.60	0.47
4:P:172:THR:HG22	4:P:173:ASP:H	1.80	0.47
1:C:9:PHE:HE2	1:C:99:TYR:CE2	2.33	0.47
3:E:138:PHE:CE1	3:E:170:ASN:O	2.68	0.47
4:J:175:GLN:HG3	4:J:176:PRO:HD2	1.96	0.47
3:K:115:PRO:HG3	3:K:139:ASP:OD2	2.14	0.47
4:L:224:THR:OG1	4:L:225:GLN:N	2.48	0.47
3:O:137:ASP:HB3	3:O:169:SER:HA	1.97	0.47
3:O:168:LYS:HB3	3:O:168:LYS:HE2	1.67	0.47
4:P:84:GLN:HA	4:P:113:VAL:HG13	1.96	0.47
4:P:190:LEU:HD12	4:P:191:SER:H	1.80	0.47
4:P:223:TRP:CZ2	4:P:225:GLN:CG	2.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:83:GLN:CA	4:F:113:VAL:HG21	2.45	0.47
1:A:35:ARG:HD3	1:A:48:ARG:NE	2.14	0.47
3:I:42:LYS:HG2	3:I:43:SER:N	2.30	0.47
4:J:123:PRO:CA	4:J:150:PHE:HB3	2.45	0.47
3:K:33:LEU:HD23	3:K:91:ALA:O	2.15	0.47
3:K:193:PRO:C	3:K:195:ASP:N	2.72	0.47
3:O:112:ILE:HG22	3:O:114:ASN:H	1.80	0.47
1:C:22:PHE:H	1:C:38:SER:CB	2.27	0.47
1:C:172:LEU:HD23	1:C:179:LEU:HD13	1.97	0.47
1:C:231:VAL:CG1	1:C:244:TRP:HE3	2.17	0.47
4:F:84:GLN:CG	4:F:85:GLU:H	2.27	0.47
4:F:155:VAL:HG12	4:F:214:PHE:CD1	2.50	0.47
4:F:201:TRP:HA	4:F:204:PRO:HG3	1.96	0.47
2:B:17:ASN:HD22	2:B:74:GLU:CD	2.23	0.47
3:K:137:ASP:N	3:K:137:ASP:OD1	2.47	0.47
3:K:175:TRP:NE1	4:L:146:LEU:HD22	2.12	0.47
4:P:33:TYR:OH	4:P:95:SER:OG	2.13	0.47
3:E:13:VAL:O	3:E:108:VAL:HA	2.15	0.47
2:B:26:TYR:CE2	2:B:28:SER:HB2	2.51	0.46
1:G:187:THR:HB	1:G:272:LEU:CD2	2.32	0.46
2:N:89:GLN:O	2:N:90:PRO:C	2.56	0.46
3:O:50:MET:HE3	3:O:66:LEU:HB2	1.96	0.46
3:E:138:PHE:O	3:E:139:ASP:O	2.33	0.46
1:G:159:TYR:CE1	1:G:163:THR:OG1	2.68	0.46
1:G:163:THR:HA	1:G:166:GLU:CG	2.45	0.46
4:L:150:PHE:CE2	4:L:155:VAL:HG11	2.50	0.46
2:N:22:PHE:HD2	2:N:67:TYR:HB2	1.80	0.46
1:C:147:TRP:N	1:C:147:TRP:CD1	2.83	0.46
4:F:56:ASP:OD1	4:F:57:LYS:N	2.48	0.46
2:H:7:ILE:HD11	2:H:25:CYS:SG	2.56	0.46
3:K:38:TRP:CZ3	3:K:44:PRO:HG3	2.38	0.46
3:K:151:ASP:OD2	3:K:181:PHE:HB3	2.15	0.46
4:L:89:VAL:HG11	4:L:110:ARG:HB2	1.91	0.46
4:P:196:VAL:CG2	4:P:197:SER:N	2.73	0.46
3:E:114:ASN:HA	3:E:115:PRO:HD2	1.57	0.46
4:F:15:LYS:NZ	4:F:83:GLN:HE21	2.14	0.46
4:F:36:ARG:HE	4:F:38:ARG:NH1	2.13	0.46
3:I:121:GLN:C	3:I:132:VAL:O	2.59	0.46
2:H:3:ARG:NH2	2:H:59:ASP:O	2.43	0.46
1:M:197:HIS:C	1:M:198:GLU:CG	2.89	0.46
1:M:266:LEU:HD12	1:M:266:LEU:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:243:LYS:CG	1:C:244:TRP:H	2.28	0.46
3:K:135:PHE:C	3:K:135:PHE:HD1	2.23	0.46
3:O:7:SER:HB3	3:O:22:THR:HB	1.98	0.46
1:C:136:ALA:O	1:C:137:ASP:HB3	2.16	0.46
1:A:93:HIS:CG	1:A:119:ASP:OD1	2.68	0.46
4:J:217:LEU:CD1	4:J:221:ASP:HB3	2.41	0.46
1:G:97:ARG:HH12	5:U:6:VAL:HG12	1.74	0.46
1:G:234:ARG:HB3	2:H:8:GLN:NE2	2.31	0.46
4:L:159:TRP:CE3	4:L:170:VAL:HG13	2.50	0.46
1:M:188:HIS:CD2	1:M:204:TRP:HE3	2.33	0.46
3:O:53:ASN:CA	3:O:68:THR:HG23	2.46	0.46
4:P:24:ASP:HA	4:P:25:PRO:HD2	1.76	0.46
2:D:96:ASP:HB3	2:D:99:MET:HB3	1.97	0.46
1:A:84:TYR:OH	1:A:146:LYS:NZ	2.26	0.46
3:I:15:GLU:OE1	3:I:110:PRO:HA	2.15	0.46
1:M:128:GLU:CD	1:M:128:GLU:H	2.15	0.46
1:M:187:THR:HB	1:M:272:LEU:HD11	1.98	0.46
3:O:80:SER:C	3:O:81:GLN:NE2	2.73	0.46
4:P:130:PRO:HD2	4:P:201:TRP:CZ2	2.51	0.46
1:C:33:PHE:O	1:C:52:ILE:HG21	2.15	0.46
4:F:176:PRO:HB2	4:F:188:TYR:HB3	1.97	0.46
1:A:106:ASP:N	1:A:106:ASP:OD1	2.48	0.46
4:J:202:GLN:O	4:J:205:ARG:N	2.49	0.46
1:G:97:ARG:CD	1:G:116:TYR:CE1	2.98	0.46
1:G:154:GLU:O	1:G:157:ARG:HG2	2.16	0.46
1:M:129:ASP:OD1	1:M:129:ASP:N	2.46	0.46
1:C:106:ASP:OD1	1:C:106:ASP:N	2.47	0.46
1:C:189:MET:HG3	1:C:202:ARG:O	2.16	0.46
4:F:230:PRO:C	4:F:231:VAL:CG2	2.88	0.46
1:A:217:TRP:CD1	1:A:247:VAL:HG11	2.51	0.46
2:B:3:ARG:NH1	2:B:59:ASP:O	2.29	0.46
3:I:159:VAL:HA	3:I:169:SER:O	2.15	0.46
3:K:193:PRO:C	3:K:195:ASP:H	2.23	0.46
1:M:66:LYS:CE	3:O:29:ASN:CG	2.88	0.46
1:M:78:LEU:CD2	1:M:95:VAL:CG2	2.74	0.46
1:M:135:ALA:HB1	1:M:140:ALA:HB1	1.97	0.46
1:M:198:GLU:HB3	1:M:249:VAL:O	2.16	0.46
1:G:99:TYR:CE2	5:U:3:VAL:HG12	2.51	0.46
3:K:81:GLN:O	3:K:108:VAL:HG21	2.16	0.46
3:E:11:LEU:HD13	3:E:19:THR:HG21	1.97	0.46
2:B:5:PRO:HA	2:B:30:PHE:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:259:CYS:C	1:G:260:HIS:HD1	2.23	0.45
2:H:21:ASN:OD1	2:H:22:PHE:O	2.34	0.45
2:H:70:PHE:CE1	2:H:78:TYR:CG	3.04	0.45
3:K:158:CYS:SG	4:L:172:THR:N	2.84	0.45
1:M:14:ARG:HB3	1:M:17:ARG:HB2	1.98	0.45
1:M:96:GLN:HE22	2:N:31:HIS:HE1	1.62	0.45
3:O:50:MET:HB3	3:O:66:LEU:HD22	1.98	0.45
4:P:14:GLU:OE2	4:P:117:LEU:CD1	2.63	0.45
1:C:35:ARG:HD3	1:C:48:ARG:HD3	1.98	0.45
4:F:180:GLN:CA	4:F:186:SER:OG	2.63	0.45
4:F:195:ARG:CG	4:F:195:ARG:NH1	2.73	0.45
4:J:180:GLN:HA	4:J:181:PRO:HA	1.72	0.45
1:G:6:ARG:CB	1:G:8:PHE:HE2	2.27	0.45
1:G:98:MET:HE3	1:G:99:TYR:N	2.31	0.45
2:H:7:ILE:HD12	2:H:82:VAL:HG11	1.97	0.45
2:H:40:LEU:HD12	2:H:79:ALA:HB3	1.98	0.45
2:N:59:ASP:O	2:N:60:TRP:HB2	2.17	0.45
4:P:38:ARG:HG2	4:P:38:ARG:HH11	1.81	0.45
4:P:173:ASP:N	4:P:173:ASP:OD1	2.47	0.45
3:E:154:ILE:HG22	3:E:155:THR:N	2.31	0.45
3:I:21:PHE:CE2	3:I:77:ILE:HD11	2.51	0.45
3:I:138:PHE:CD1	3:I:138:PHE:O	2.70	0.45
1:G:59:TYR:O	1:G:63:GLU:HG2	2.17	0.45
3:K:124:ASP:H	3:K:131:SER:CB	2.29	0.45
3:E:82:PRO:HG3	3:E:110:PRO:HB3	1.98	0.45
3:E:157:LYS:HE2	3:E:170:ASN:OD1	2.16	0.45
4:J:151:TYR:HB2	4:J:187:ARG:HB3	1.97	0.45
1:G:69:ALA:O	1:G:73:THR:OG1	2.26	0.45
3:K:31:TYR:CD1	5:U:4:PRO:HB2	2.42	0.45
3:K:190:SER:O	3:K:190:SER:OG	2.34	0.45
1:M:97:ARG:NH2	1:M:147:TRP:HH2	2.13	0.45
3:O:112:ILE:HB	3:O:115:PRO:HG3	1.98	0.45
4:P:206:ASN:HD22	4:P:240:TRP:C	2.24	0.45
1:A:9:PHE:HZ	5:Q:2:LEU:HD23	1.82	0.45
1:A:22:PHE:H	1:A:38:SER:CB	2.29	0.45
2:B:89:GLN:HB2	2:B:90:PRO:CD	2.44	0.45
1:G:102:ASP:HB2	1:G:111:ARG:CG	2.47	0.45
1:M:220:ASP:HB3	1:M:221:GLY:H	1.64	0.45
3:O:166:ASP:O	3:O:167:PHE:C	2.58	0.45
4:P:160:TRP:HA	4:P:165:GLU:CB	2.46	0.45
1:C:67:VAL:HA	1:C:70:HIS:HD2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:124:ILE:HG12	1:G:135:ALA:HA	1.99	0.45
2:N:2:GLN:HE21	2:N:85:VAL:CB	2.27	0.45
3:O:102:THR:HA	3:O:103:GLY:HA3	1.74	0.45
2:D:54:LEU:HD23	2:D:54:LEU:C	2.41	0.45
4:F:138:THR:O	4:F:139:GLN:HB2	2.16	0.45
3:I:53:ASN:HA	3:I:54:GLY:HA2	1.57	0.45
2:H:7:ILE:HB	2:H:27:VAL:HG12	1.99	0.45
2:H:57:SER:O	2:H:58:LYS:C	2.60	0.45
1:C:99:TYR:CZ	5:R:3:VAL:HG12	2.52	0.45
3:E:136:THR:C	3:E:138:PHE:CD1	2.95	0.45
1:A:70:HIS:O	1:A:73:THR:OG1	2.28	0.45
2:B:3:ARG:NH1	2:B:60:TRP:O	2.50	0.45
1:G:179:LEU:N	1:G:179:LEU:HD12	2.31	0.45
1:G:235:PRO:HA	1:G:241:PHE:HA	1.98	0.45
4:P:159:TRP:HD1	4:P:209:ARG:O	1.99	0.45
3:E:84:ASP:HA	3:E:85:SER:CB	2.47	0.45
1:G:81:LEU:HG	5:U:9:VAL:CG1	2.47	0.45
1:G:179:LEU:N	1:G:179:LEU:CD1	2.80	0.45
3:K:38:TRP:CE3	3:K:42:LYS:O	2.69	0.45
3:K:136:THR:CG2	3:K:171:SER:CA	2.83	0.45
2:N:5:PRO:HD3	2:N:84:HIS:CD2	2.51	0.45
2:D:13:HIS:HB2	2:D:21:ASN:OD1	2.17	0.45
1:A:103:VAL:HG12	1:A:108:ARG:O	2.17	0.45
3:I:48:PHE:CE1	3:I:59:LYS:HG3	2.41	0.45
4:J:120:VAL:O	4:J:121:PHE:CG	2.70	0.45
1:G:81:LEU:CG	5:U:9:VAL:HG11	2.46	0.45
1:G:234:ARG:NH2	1:G:244:TRP:HE1	2.15	0.45
3:K:72:TYR:CD1	3:K:72:TYR:O	2.70	0.45
3:O:161:ASP:O	3:O:162:MET:HB3	2.16	0.45
1:C:8:PHE:HB2	1:C:25:VAL:HG13	1.99	0.45
2:D:70:PHE:CE1	2:D:72:PRO:HB3	2.52	0.45
1:A:259:CYS:HB3	1:A:272:LEU:HB2	2.00	0.44
2:B:46:ILE:HG13	2:B:47:GLU:N	2.31	0.44
3:I:138:PHE:HD1	3:I:142:THR:OG1	1.95	0.44
1:G:185:PRO:CA	1:G:208:PHE:HB3	2.46	0.44
1:G:188:HIS:HB3	1:G:204:TRP:CB	2.41	0.44
1:G:189:MET:CE	1:G:273:ARG:C	2.90	0.44
4:L:70:THR:N	4:L:75:SER:OG	2.44	0.44
4:L:154:HIS:CD2	4:L:215:TYR:CB	3.01	0.44
2:N:2:GLN:HE21	2:N:85:VAL:CG2	2.30	0.44
2:N:39:LEU:HD23	2:N:39:LEU:HA	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:97:THR:HG22	4:P:98:GLN:N	2.32	0.44
1:C:4:SER:HB3	1:C:102:ASP:CG	2.39	0.44
1:C:72:GLN:CD	4:F:48:TYR:OH	2.61	0.44
1:C:226:GLN:C	1:C:226:GLN:CD	2.85	0.44
1:C:226:GLN:CD	1:C:227:ASP:N	2.73	0.44
4:F:26:ILE:HB	4:F:29:HIS:CD2	2.52	0.44
1:A:223:ASP:O	1:A:225:THR:HG22	2.16	0.44
4:J:48:TYR:CD1	4:J:99:LEU:HD11	2.52	0.44
1:G:268:LYS:O	1:G:269:PRO:C	2.58	0.44
2:H:3:ARG:NH2	2:H:61:SER:HB2	2.32	0.44
3:K:175:TRP:CZ2	4:L:146:LEU:HB2	2.52	0.44
4:L:83:GLN:CG	4:L:84:GLN:N	2.54	0.44
3:O:1:ILE:HG13	3:O:1:ILE:O	2.17	0.44
3:O:59:LYS:O	3:O:60:GLY:C	2.58	0.44
1:C:66:LYS:CD	5:R:4:PRO:HA	2.42	0.44
4:F:29:HIS:CE1	4:F:96:GLN:HG2	2.52	0.44
4:J:119:ASN:N	4:J:119:ASN:OD1	2.50	0.44
1:G:82:ARG:NH2	1:G:89:GLU:N	2.46	0.44
1:G:157:ARG:HG3	1:G:158:ALA:N	2.31	0.44
3:K:47:LEU:O	3:K:48:PHE:CD1	2.70	0.44
3:K:195:ASP:C	3:K:195:ASP:OD1	2.60	0.44
4:L:130:PRO:HB3	4:L:142:THR:O	2.16	0.44
2:N:22:PHE:CE1	4:F:80:GLN:NE2	2.85	0.44
4:P:14:GLU:CD	4:P:117:LEU:CG	2.89	0.44
4:P:211:GLN:HE22	4:P:213:GLN:HB2	1.83	0.44
1:A:274:TRP:CE3	1:A:275:GLU:HB2	2.53	0.44
4:J:84:GLN:O	4:J:87:SER:OG	2.33	0.44
2:H:24:ASN:ND2	2:H:65:LEU:CG	2.77	0.44
4:L:10:ASN:HB3	4:L:110:ARG:O	2.17	0.44
2:N:51:HIS:HB3	2:N:66:TYR:CE1	2.52	0.44
4:P:58:SER:HA	4:P:59:GLY:HA2	1.42	0.44
1:G:156:LEU:HA	1:G:156:LEU:HD23	1.77	0.44
1:G:204:TRP:CE3	1:G:244:TRP:HB3	2.51	0.44
2:H:9:VAL:CG2	2:H:80:CYS:HB2	2.47	0.44
4:L:146:LEU:HD12	4:L:146:LEU:C	2.43	0.44
4:L:171:CYS:HB2	4:L:193:ARG:O	2.17	0.44
1:M:189:MET:SD	1:M:274:TRP:CZ3	3.10	0.44
3:E:49:VAL:HG23	4:F:102:THR:HG22	1.97	0.44
1:A:49:ALA:HA	1:A:50:PRO:HD2	1.77	0.44
3:I:66:LEU:HD12	3:I:67:ASN:N	2.32	0.44
4:J:125:VAL:O	4:J:237:ALA:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:221:ASP:CG	4:J:222:GLU:N	2.75	0.44
3:K:135:PHE:CZ	3:K:192:ILE:HD13	2.51	0.44
2:B:86:THR:O	2:B:87:LEU:HD23	2.18	0.44
3:I:137:ASP:O	3:I:138:PHE:CD2	2.70	0.44
4:L:37:GLN:HG2	4:L:89:VAL:H	1.82	0.44
1:M:195:SER:O	1:M:197:HIS:CE1	2.70	0.44
1:M:231:VAL:HG13	1:M:244:TRP:HE3	1.83	0.44
3:O:80:SER:C	3:O:81:GLN:CD	2.85	0.44
1:A:47:PRO:HB3	1:A:60:TRP:CH2	2.53	0.44
1:A:167:TRP:NE1	5:Q:1:ASN:HD22	2.16	0.44
4:J:39:LEU:HA	4:J:40:GLY:HA2	1.68	0.44
4:J:196:VAL:HG12	4:J:197:SER:N	2.33	0.44
1:M:102:ASP:CG	1:M:111:ARG:HE	2.26	0.44
3:O:31:TYR:HB2	5:T:4:PRO:HB2	2.00	0.44
4:P:45:PHE:HZ	4:P:48:TYR:HB3	1.83	0.44
1:C:37:ASP:HB3	1:C:40:ALA:HB2	2.00	0.44
3:E:160:LEU:HD23	4:F:169:GLY:O	2.18	0.44
4:F:172:THR:HG22	4:F:192:SER:HB2	2.00	0.44
3:I:61:ARG:HH12	3:I:84:ASP:CG	2.26	0.43
1:G:16:GLY:CA	1:G:17:ARG:CB	2.77	0.43
1:G:133:TRP:HZ3	1:G:147:TRP:HZ3	1.65	0.43
3:K:21:PHE:O	3:K:74:TYR:HA	2.17	0.43
3:K:136:THR:O	3:K:137:ASP:HB2	2.18	0.43
4:P:14:GLU:HG2	4:P:117:LEU:CD1	2.45	0.43
1:C:25:VAL:CG2	1:C:32:GLN:HE21	2.31	0.43
1:C:117:ALA:HB2	2:D:60:TRP:CE2	2.53	0.43
4:F:220:ASN:N	4:F:220:ASN:OD1	2.51	0.43
1:A:247:VAL:HG23	1:A:249:VAL:HG23	1.99	0.43
4:J:49:PHE:CE2	4:J:69:ARG:HB2	2.53	0.43
4:J:84:GLN:O	4:J:113:VAL:HG11	2.18	0.43
2:H:24:ASN:CG	2:H:25:CYS:N	2.76	0.43
3:K:131:SER:HA	4:L:128:PHE:HE1	1.83	0.43
3:K:160:LEU:O	3:K:168:LYS:HB3	2.18	0.43
4:L:130:PRO:HG2	4:L:201:TRP:NE1	2.32	0.43
1:M:59:TYR:O	1:M:63:GLU:HG2	2.18	0.43
4:F:135:ILE:HD13	4:F:201:TRP:HZ3	1.83	0.43
4:F:219:GLU:C	4:F:220:ASN:CG	2.85	0.43
4:J:120:VAL:O	4:J:121:PHE:CD1	2.70	0.43
1:G:127:LYS:HD2	1:G:127:LYS:HA	1.66	0.43
1:G:228:THR:HG23	1:G:228:THR:O	2.18	0.43
2:N:63:TYR:CD1	2:N:63:TYR:O	2.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:81:ARG:CD	2:N:92:ILE:CG1	2.96	0.43
3:O:123:ARG:O	4:P:129:GLU:HB3	2.19	0.43
3:O:176:SER:CB	3:O:181:PHE:O	2.66	0.43
2:D:40:LEU:HD13	2:D:81:ARG:H	1.83	0.43
4:F:33:TYR:OH	4:F:99:LEU:HA	2.19	0.43
1:A:73:THR:HB	5:Q:8:THR:HG22	2.01	0.43
1:A:189:MET:HE3	1:A:217:TRP:CH2	2.53	0.43
4:J:131:SER:O	4:J:135:ILE:HG23	2.19	0.43
3:K:63:SER:O	3:K:75:LEU:HD12	2.19	0.43
4:L:39:LEU:HA	4:L:39:LEU:HD12	1.76	0.43
1:M:162:GLY:O	1:M:166:GLU:HG3	2.17	0.43
1:M:177:GLU:N	1:M:177:GLU:OE1	2.51	0.43
1:M:227:ASP:CG	1:M:248:VAL:HG12	2.43	0.43
2:N:12:ARG:C	2:N:13:HIS:CG	2.96	0.43
4:P:64:ARG:HH11	4:P:64:ARG:HG2	1.80	0.43
1:C:188:HIS:O	1:C:204:TRP:N	2.42	0.43
3:E:53:ASN:HA	3:E:54:GLY:HA2	1.63	0.43
4:F:149:GLY:CA	4:F:150:PHE:HB3	2.35	0.43
1:A:124:ILE:HG13	1:A:134:THR:O	2.19	0.43
4:J:223:TRP:CE2	4:J:228:ALA:O	2.72	0.43
1:G:123:TYR:OH	1:G:139:ALA:O	2.36	0.43
3:O:131:SER:OG	3:O:181:PHE:CE2	2.72	0.43
4:P:223:TRP:CE2	4:P:225:GLN:HG2	2.52	0.43
4:F:218:SER:CB	4:F:221:ASP:HB2	2.44	0.43
2:H:23:LEU:HD13	2:H:70:PHE:CE1	2.53	0.43
3:K:11:LEU:O	3:K:12:HIS:ND1	2.51	0.43
4:L:34:TRP:CZ3	4:L:92:CYS:HB2	2.54	0.43
4:L:120:VAL:O	4:L:230:PRO:HG3	2.19	0.43
1:M:231:VAL:HG22	1:M:244:TRP:H	1.84	0.43
3:O:123:ARG:HG3	3:O:130:LYS:O	2.18	0.43
4:P:11:LYS:HG3	4:P:12:VAL:N	2.33	0.43
4:P:160:TRP:CH2	4:P:234:ILE:HD11	2.53	0.43
3:I:20:ASN:HA	3:I:75:LEU:O	2.19	0.43
4:J:164:LYS:HE2	4:J:164:LYS:HB2	1.87	0.43
1:G:58:GLU:HA	1:G:61:ASP:HB2	2.00	0.43
1:G:214:THR:O	1:G:214:THR:CG2	2.60	0.43
3:K:21:PHE:HZ	3:K:106:LEU:HD22	1.84	0.43
3:K:29:ASN:O	3:K:94:THR:OG1	2.21	0.43
4:L:88:ALA:CB	4:L:110:ARG:HG2	2.39	0.43
1:C:160:LEU:O	1:C:165:VAL:HG23	2.18	0.43
3:E:157:LYS:HE2	3:E:157:LYS:HB3	1.75	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:157:LYS:HZ1	3:E:170:ASN:CG	2.27	0.43
3:E:163:ARG:HD3	3:E:163:ARG:HA	1.63	0.43
4:F:22:ARG:HG2	4:F:76:THR:HG22	2.01	0.43
1:A:66:LYS:CD	5:Q:4:PRO:HA	2.48	0.43
2:B:58:LYS:C	2:B:60:TRP:H	2.26	0.43
4:J:84:GLN:OE1	1:G:177:GLU:OE1	2.37	0.43
1:G:17:ARG:HH11	1:G:17:ARG:CG	2.14	0.43
1:G:97:ARG:HE	1:G:116:TYR:HE1	0.61	0.43
3:K:47:LEU:HA	3:K:47:LEU:HD12	1.77	0.43
1:M:92:SER:O	1:M:92:SER:OG	2.25	0.43
4:P:182:ALA:O	4:P:183:LEU:C	2.62	0.43
3:E:37:ARG:HB2	3:E:47:LEU:HD11	2.01	0.43
3:I:2:LEU:HD23	3:I:3:ASN:N	2.33	0.43
3:I:25:PHE:HB2	3:I:26:PRO:HD2	2.01	0.43
3:I:34:HIS:ND1	3:I:93:ILE:HD11	2.34	0.43
1:G:77:ASP:CG	1:G:97:ARG:NH2	2.77	0.43
1:G:97:ARG:NH1	5:U:7:ALA:O	2.46	0.43
4:L:159:TRP:CE2	4:L:194:LEU:HG	2.54	0.43
4:L:226:ASP:HA	4:L:227:ARG:C	2.42	0.43
1:M:53:GLU:HA	1:M:60:TRP:HZ2	1.84	0.43
3:O:34:HIS:NE2	3:O:93:ILE:HD11	2.33	0.43
2:D:82:VAL:O	2:D:90:PRO:CB	2.65	0.43
3:E:125:SER:C	3:E:126:LYS:HD2	2.43	0.43
3:E:136:THR:C	3:E:138:PHE:CE1	2.97	0.43
4:F:194:LEU:HD12	4:F:194:LEU:HA	1.81	0.43
1:A:172:LEU:HD23	1:A:179:LEU:HD13	2.01	0.43
3:K:4:VAL:HG11	3:K:92:PHE:HB3	2.00	0.43
4:L:82:THR:HG21	4:L:113:VAL:HG22	2.00	0.43
1:M:256:ARG:HB3	6:M:301:HOH:O	2.19	0.43
3:O:53:ASN:HA	3:O:54:GLY:HA2	1.66	0.43
4:F:32:LEU:O	4:F:49:PHE:N	2.46	0.43
4:F:193:ARG:CG	4:F:193:ARG:NH1	2.72	0.43
1:A:228:THR:HA	1:A:247:VAL:HG12	2.01	0.42
2:B:25:CYS:HB2	2:B:39:LEU:HD21	1.99	0.42
4:J:211:GLN:HA	4:J:236:SER:HB3	2.00	0.42
4:J:217:LEU:O	4:J:231:VAL:HG12	2.19	0.42
3:K:122:LEU:HG	4:L:130:PRO:HA	2.00	0.42
3:K:134:LEU:CD2	4:L:142:THR:HG21	2.49	0.42
1:M:59:TYR:HH	1:M:171:TYR:HH	1.36	0.42
1:M:78:LEU:HB3	1:M:82:ARG:NH2	2.33	0.42
1:M:233:THR:HG22	1:M:243:LYS:HD3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:63:SER:O	3:O:75:LEU:HD12	2.19	0.42
3:O:111:ASN:OD1	3:O:112:ILE:N	2.43	0.42
1:C:154:GLU:HB3	3:E:52:LEU:HD11	2.01	0.42
1:A:46:GLU:HG3	1:A:47:PRO:HD2	2.00	0.42
1:A:77:ASP:OD1	5:Q:9:VAL:HG22	2.18	0.42
3:I:154:ILE:HD12	3:I:154:ILE:C	2.44	0.42
4:J:194:LEU:HD23	4:J:194:LEU:C	2.39	0.42
3:K:111:ASN:OD1	3:K:112:ILE:N	2.52	0.42
4:L:88:ALA:HB1	4:L:89:VAL:CG1	2.49	0.42
1:M:146:LYS:HZ2	4:P:97:THR:HG1	1.60	0.42
4:P:6:GLN:OE1	4:P:108:GLY:N	2.52	0.42
1:A:69:ALA:HB1	3:I:96:ASN:ND2	2.34	0.42
4:J:58:SER:O	4:J:58:SER:OG	2.32	0.42
1:G:49:ALA:HB1	1:G:51:TRP:NE1	2.35	0.42
1:G:218:GLN:CB	1:G:222:GLU:O	2.62	0.42
3:K:96:ASN:ND2	4:L:48:TYR:OH	2.52	0.42
4:L:175:GLN:H	4:L:175:GLN:HG2	1.59	0.42
1:C:31:THR:HG23	1:C:209:TYR:CE1	2.54	0.42
1:C:63:GLU:OE2	1:C:66:LYS:NZ	2.49	0.42
4:F:217:LEU:HD12	4:F:218:SER:N	2.34	0.42
4:J:4:VAL:HG11	4:J:105:PHE:O	2.19	0.42
4:J:151:TYR:HA	4:J:152:PRO:HA	1.84	0.42
1:G:32:GLN:O	1:G:49:ALA:HB2	2.19	0.42
1:M:25:VAL:HG11	2:N:55:SER:OG	2.20	0.42
1:C:201:LEU:O	1:C:246:ALA:HA	2.19	0.42
1:A:107:TRP:CZ2	1:A:172:LEU:HD13	2.54	0.42
1:A:128:GLU:H	1:A:128:GLU:HG2	1.39	0.42
1:A:149:ALA:C	1:A:151:HIS:H	2.26	0.42
3:I:11:LEU:HD12	3:I:21:PHE:CE1	2.55	0.42
3:I:36:TYR:N	3:I:89:LEU:O	2.48	0.42
3:I:146:GLN:HB3	3:I:147:SER:H	1.39	0.42
3:I:177:ASN:OD1	3:I:178:LYS:N	2.51	0.42
4:L:170:VAL:CB	4:L:194:LEU:CD2	2.95	0.42
1:M:4:SER:OG	1:M:6:ARG:NH1	2.52	0.42
1:M:225:THR:O	1:M:228:THR:HG22	2.20	0.42
3:E:11:LEU:HD12	3:E:106:LEU:HD13	2.01	0.42
1:A:76:VAL:O	1:A:80:THR:HG22	2.20	0.42
1:A:209:TYR:CD1	1:A:210:PRO:HA	2.54	0.42
4:J:43:LEU:HD23	4:J:44:GLU:N	2.34	0.42
1:G:70:HIS:O	1:G:74:HIS:N	2.49	0.42
1:M:73:THR:HG21	5:T:6:VAL:CG2	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:30:PHE:CE2	2:N:63:TYR:HA	2.55	0.42
3:O:187:PHE:H	3:O:187:PHE:HD2	1.66	0.42
4:P:26:ILE:HB	4:P:29:HIS:HD2	1.82	0.42
3:E:167:PHE:HD2	3:E:168:LYS:H	0.61	0.42
1:A:75:ARG:HE	1:A:75:ARG:HB2	1.74	0.42
1:A:150:ALA:HB3	1:A:152:VAL:HG23	2.01	0.42
4:J:15:LYS:HA	4:J:82:THR:O	2.19	0.42
1:G:64:THR:O	1:G:68:LYS:HG3	2.20	0.42
3:K:94:THR:HG23	3:K:95:GLY:N	2.35	0.42
3:K:115:PRO:CG	3:K:139:ASP:OD2	2.68	0.42
4:L:14:GLU:C	4:L:16:GLY:H	2.27	0.42
1:C:73:THR:HG23	5:R:8:THR:CG2	2.49	0.42
1:C:192:HIS:CE1	1:C:202:ARG:NH1	2.78	0.42
1:C:259:CYS:HB3	1:C:272:LEU:HB2	2.00	0.42
3:E:31:TYR:C	3:E:31:TYR:HD2	2.26	0.42
1:A:66:LYS:HD3	5:Q:4:PRO:HA	2.02	0.42
1:A:152:VAL:HA	1:A:155:GLN:OE1	2.19	0.42
3:K:61:ARG:CG	3:K:78:LYS:O	2.65	0.42
1:M:114:HIS:HB3	1:M:126:LEU:HB3	2.02	0.42
2:N:11:SER:O	2:N:13:HIS:N	2.53	0.42
2:N:40:LEU:HB3	2:N:43:GLY:CA	2.49	0.42
4:P:38:ARG:O	4:P:41:GLN:NE2	2.52	0.42
4:P:64:ARG:HB3	4:P:80:GLN:O	2.20	0.42
1:C:217:TRP:HZ3	1:C:257:TYR:HB3	1.85	0.42
1:A:173:GLU:HA	1:A:176:LYS:HD3	2.02	0.42
3:I:47:LEU:HD12	3:I:47:LEU:HA	1.90	0.42
4:J:47:ILE:CD1	4:J:60:LEU:HD21	2.05	0.42
4:J:238:GLU:HG3	4:J:239:ALA:H	1.80	0.42
1:G:61:ASP:O	1:G:65:ARG:HG3	2.20	0.42
3:O:52:LEU:HD23	3:O:52:LEU:HA	1.85	0.42
3:O:80:SER:N	3:O:81:GLN:NE2	2.68	0.42
3:E:6:GLN:CD	3:E:103:GLY:HA2	2.44	0.42
3:E:117:PRO:HB2	3:E:196:THR:HA	2.02	0.42
2:B:55:SER:OG	2:B:56:PHE:N	2.52	0.42
3:I:63:SER:OG	3:I:76:TYR:HB2	2.19	0.42
4:J:46:LEU:HD22	4:J:60:LEU:HA	2.02	0.42
1:G:218:GLN:HB3	1:G:223:ASP:OD1	2.20	0.42
3:K:152:VAL:CG1	3:K:153:TYR:N	2.83	0.42
4:L:122:PRO:HA	4:L:123:PRO:HD3	1.87	0.42
1:M:69:ALA:O	1:M:73:THR:OG1	2.29	0.42
1:M:142:THR:O	1:M:146:LYS:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:176:SER:HB2	3:O:181:PHE:O	2.20	0.42
4:P:121:PHE:HA	4:P:122:PRO:HD3	1.81	0.42
4:F:45:PHE:HZ	4:F:48:TYR:HD2	1.67	0.42
4:F:96:GLN:C	4:F:97:THR:HG23	2.43	0.42
4:F:227:ARG:C	4:F:228:ALA:O	2.62	0.42
4:J:143:LEU:HB3	4:J:194:LEU:HB3	2.02	0.41
1:G:8:PHE:HB2	1:G:25:VAL:HG13	2.01	0.41
1:G:200:THR:HG21	1:G:202:ARG:CZ	2.49	0.41
3:K:115:PRO:CB	3:K:139:ASP:OD2	2.67	0.41
3:K:158:CYS:SG	3:K:159:VAL:N	2.93	0.41
4:L:6:GLN:HE21	4:L:6:GLN:HB2	1.64	0.41
4:L:141:ALA:N	4:L:198:ALA:H	2.18	0.41
1:M:219:ARG:CD	1:M:224:GLN:NE2	2.70	0.41
1:C:202:ARG:HG2	1:C:244:TRP:NE1	2.28	0.41
2:D:84:HIS:CG	2:D:85:VAL:H	2.38	0.41
2:B:74:GLU:OE1	2:B:74:GLU:HA	2.20	0.41
3:I:132:VAL:HG12	3:I:173:VAL:HG13	2.01	0.41
1:G:19:GLU:O	1:G:20:PRO:C	2.62	0.41
1:G:70:HIS:CD2	5:U:2:LEU:HD23	2.55	0.41
4:L:88:ALA:HB1	4:L:110:ARG:CA	2.46	0.41
4:P:119:ASN:HB3	4:P:151:TYR:CE2	2.55	0.41
2:D:28:SER:OG	2:D:29:GLY:N	2.53	0.41
3:E:83:GLU:OE1	3:E:162:MET:HE1	2.20	0.41
4:F:203:ASN:N	4:F:204:PRO:HD3	2.35	0.41
4:F:230:PRO:O	4:F:231:VAL:HG23	2.19	0.41
1:A:11:SER:HA	1:A:22:PHE:HA	2.02	0.41
1:A:73:THR:HG23	3:I:96:ASN:ND2	2.35	0.41
1:A:98:MET:HE1	1:A:113:TYR:HB2	2.02	0.41
4:J:112:LEU:HG	4:J:113:VAL:O	2.20	0.41
4:J:196:VAL:O	4:J:197:SER:C	2.61	0.41
1:G:72:GLN:HG2	1:G:72:GLN:H	1.57	0.41
4:L:175:GLN:HA	4:L:176:PRO:HD3	1.83	0.41
4:P:36:ARG:O	4:P:44:GLU:HB2	2.21	0.41
4:P:125:VAL:HG12	4:P:237:ALA:HB2	2.01	0.41
1:C:52:ILE:HD12	1:C:52:ILE:HA	1.89	0.41
2:D:34:ASP:C	2:D:35:ILE:HG13	2.44	0.41
1:A:13:SER:HB3	1:A:93:HIS:H	1.85	0.41
1:G:98:MET:CE	1:G:99:TYR:N	2.84	0.41
1:G:211:ALA:HB2	1:G:241:PHE:HE2	1.84	0.41
3:K:135:PHE:CE1	3:K:138:PHE:CG	3.08	0.41
3:K:188:ASN:O	3:K:189:ASN:HB2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:21:LEU:HD12	4:L:21:LEU:N	2.35	0.41
1:M:99:TYR:OH	5:T:3:VAL:HG12	2.20	0.41
2:N:10:TYR:HE2	2:N:26:TYR:HB3	1.85	0.41
4:P:160:TRP:HD1	4:P:165:GLU:CG	2.23	0.41
1:C:218:GLN:HG2	1:C:260:HIS:HD2	1.79	0.41
1:C:243:LYS:HG2	1:C:244:TRP:N	2.33	0.41
4:J:134:GLU:HA	4:J:137:HIS:HB2	2.01	0.41
1:G:11:SER:O	1:G:95:VAL:N	2.53	0.41
1:G:173:GLU:CD	1:G:176:LYS:NZ	2.78	0.41
1:G:266:LEU:HD23	1:G:266:LEU:HA	1.77	0.41
4:L:33:TYR:O	4:L:92:CYS:HA	2.21	0.41
1:M:203:CYS:CB	1:M:217:TRP:HE1	2.31	0.41
1:M:234:ARG:HE	1:M:234:ARG:HB2	1.62	0.41
3:O:30:PHE:CD2	3:O:68:THR:HG22	2.55	0.41
3:O:85:SER:OG	3:O:108:VAL:HG22	2.20	0.41
4:P:60:LEU:O	4:P:61:PRO:C	2.63	0.41
3:E:144:VAL:HG21	3:E:155:THR:O	2.19	0.41
4:F:51:GLY:O	4:F:69:ARG:NH1	2.52	0.41
1:A:52:ILE:HD13	1:A:60:TRP:CH2	2.55	0.41
1:A:242:GLN:NE2	2:B:12:ARG:O	2.46	0.41
3:I:133:CYS:SG	3:I:182:ALA:C	3.03	0.41
1:G:64:THR:HG22	1:G:68:LYS:CE	2.51	0.41
1:G:157:ARG:CG	1:G:158:ALA:N	2.83	0.41
1:G:262:GLN:HA	1:G:269:PRO:HB3	2.01	0.41
4:L:154:HIS:O	4:L:215:TYR:HD2	2.02	0.41
4:L:218:SER:O	4:L:219:GLU:HB2	2.20	0.41
1:M:96:GLN:HE21	2:N:31:HIS:HE1	1.66	0.41
3:O:140:SER:O	3:O:141:GLN:C	2.59	0.41
1:C:185:PRO:HD2	1:C:266:LEU:HG	2.03	0.41
3:E:125:SER:HB3	3:E:126:LYS:HD2	2.03	0.41
3:E:136:THR:N	3:E:138:PHE:HE1	2.18	0.41
4:F:140:LYS:HD3	4:F:197:SER:HA	2.02	0.41
2:H:3:ARG:O	2:H:30:PHE:HA	2.20	0.41
3:K:95:GLY:O	3:K:96:ASN:HB3	2.20	0.41
3:K:155:THR:O	3:K:172:ALA:HB1	2.20	0.41
1:M:95:VAL:HG22	1:M:118:TYR:HD1	1.84	0.41
1:M:102:ASP:HB2	1:M:111:ARG:CG	2.51	0.41
2:N:7:ILE:HA	2:N:27:VAL:HG12	2.03	0.41
4:P:13:THR:HB	4:P:17:LYS:HZ2	1.85	0.41
4:P:29:HIS:ND1	4:P:96:GLN:HA	2.36	0.41
3:I:76:TYR:N	3:I:76:TYR:CD1	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:188:ASN:ND2	3:I:192:ILE:CD1	2.83	0.41
1:G:33:PHE:CD1	1:G:34:VAL:HG13	2.56	0.41
3:K:11:LEU:HG	3:K:21:PHE:HE2	1.85	0.41
3:K:136:THR:HA	3:K:138:PHE:CE2	2.55	0.41
4:L:225:GLN:HB3	4:L:226:ASP:H	1.67	0.41
1:C:82:ARG:HD3	1:C:89:GLU:HA	2.03	0.41
1:C:92:SER:O	1:C:93:HIS:HD2	2.04	0.41
4:F:60:LEU:HA	4:F:61:PRO:HD3	1.97	0.41
4:F:124:GLU:N	4:F:148:THR:O	2.48	0.41
1:A:23:ILE:HD12	2:B:54:LEU:HB3	2.02	0.41
1:A:248:VAL:HG21	6:A:303:HOH:O	2.21	0.41
4:J:4:VAL:CG1	4:J:106:GLY:HA2	2.51	0.41
1:G:82:ARG:HH21	1:G:89:GLU:CA	2.31	0.41
1:G:97:ARG:CZ	1:G:116:TYR:HE1	2.21	0.41
1:G:134:THR:O	1:G:134:THR:HG23	2.20	0.41
1:G:192:HIS:HD2	1:G:202:ARG:CD	2.34	0.41
1:G:230:LEU:HD12	1:G:230:LEU:HA	1.83	0.41
3:K:35:TRP:O	3:K:47:LEU:CB	2.69	0.41
3:K:79:GLY:O	3:K:81:GLN:HG2	2.21	0.41
3:K:116:ASP:OD1	3:K:137:ASP:OD2	2.39	0.41
4:L:90:TYR:HB2	4:L:109:THR:CG2	2.49	0.41
4:L:160:TRP:C	4:L:161:VAL:HG23	2.45	0.41
1:M:49:ALA:HB1	1:M:51:TRP:NE1	2.36	0.41
2:N:22:PHE:HE1	4:F:80:GLN:NE2	2.19	0.41
4:P:45:PHE:CZ	4:P:48:TYR:HB3	2.56	0.41
1:C:100:GLY:C	1:C:113:TYR:CD2	2.98	0.41
1:C:200:THR:HA	1:C:247:VAL:O	2.21	0.41
4:F:154:HIS:CD2	4:F:154:HIS:N	2.88	0.41
5:R:2:LEU:HD12	5:R:2:LEU:N	2.36	0.41
1:A:45:MET:HG2	1:A:67:VAL:HG11	2.03	0.41
1:A:93:HIS:CB	1:A:119:ASP:OD1	2.67	0.41
3:I:133:CYS:SG	3:I:182:ALA:O	2.79	0.41
1:G:235:PRO:HG2	2:H:65:LEU:HD12	2.03	0.41
2:H:57:SER:C	2:H:59:ASP:N	2.79	0.41
1:M:22:PHE:CD1	1:M:71:SER:HA	2.56	0.41
1:M:222:GLU:H	1:M:222:GLU:HG3	1.70	0.41
4:P:200:PHE:HD1	4:P:200:PHE:HA	1.74	0.41
4:F:8:PRO:O	4:F:109:THR:HG22	2.20	0.41
4:F:35:TYR:HB3	4:F:43:LEU:HD21	2.02	0.41
1:A:31:THR:HG23	1:A:209:TYR:CE1	2.56	0.40
4:J:50:GLN:NE2	4:J:97:THR:O	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:69:ARG:NH1	4:J:73:SER:O	2.55	0.40
4:J:129:GLU:HA	4:J:130:PRO:HD3	1.89	0.40
1:G:35:ARG:HH21	1:G:48:ARG:NE	2.18	0.40
1:G:55:GLU:C	1:G:57:PRO:HD2	2.46	0.40
2:H:7:ILE:HD12	2:H:82:VAL:CG1	2.51	0.40
2:H:65:LEU:HD23	2:H:66:TYR:N	2.36	0.40
3:K:81:GLN:C	3:K:108:VAL:HG11	2.46	0.40
3:K:185:ASN:HB2	3:K:188:ASN:CB	2.50	0.40
4:L:97:THR:CB	4:L:98:GLN:NE2	2.84	0.40
1:M:167:TRP:CZ3	1:M:170:ARG:HD3	2.56	0.40
2:N:37:VAL:HG21	2:N:66:TYR:CD2	2.56	0.40
3:O:121:GLN:HA	3:O:132:VAL:O	2.21	0.40
1:C:231:VAL:O	1:C:243:LYS:HE2	2.22	0.40
2:D:27:VAL:HG23	2:D:30:PHE:HE2	1.86	0.40
4:F:87:SER:HA	4:F:111:LEU:O	2.21	0.40
1:A:177:GLU:HG2	1:A:178:THR:N	2.36	0.40
3:I:10:SER:O	3:I:10:SER:OG	2.38	0.40
3:I:146:GLN:NE2	3:I:154:ILE:HG21	2.37	0.40
1:G:54:GLN:C	1:G:56:GLY:H	2.28	0.40
2:H:41:LYS:C	2:H:43:GLY:H	2.29	0.40
3:K:87:THR:HA	3:K:105:SER:HA	2.03	0.40
3:K:161:ASP:OD1	3:K:168:LYS:HB3	2.21	0.40
4:L:46:LEU:C	4:L:47:ILE:HG23	2.46	0.40
4:L:88:ALA:HB2	4:L:111:LEU:N	2.37	0.40
4:L:124:GLU:O	4:L:147:ALA:HA	2.20	0.40
1:C:35:ARG:NH1	2:D:53:ASP:OD1	2.45	0.40
1:C:121:LYS:HD2	1:C:121:LYS:HA	1.73	0.40
1:C:202:ARG:HG2	1:C:244:TRP:CD1	2.56	0.40
1:A:9:PHE:N	1:A:97:ARG:O	2.48	0.40
1:A:70:HIS:NE2	5:Q:6:VAL:HG13	2.35	0.40
1:G:2:SER:HA	1:G:103:VAL:O	2.21	0.40
2:H:71:THR:OG1	2:H:72:PRO:CD	2.66	0.40
4:L:161:VAL:CG1	4:L:162:ASN:N	2.84	0.40
1:M:79:GLY:O	1:M:82:ARG:HB2	2.22	0.40
2:N:11:SER:HB3	2:N:95:TRP:CZ2	2.56	0.40
3:O:53:ASN:HB2	3:O:68:THR:H	1.87	0.40
4:P:118:LYS:O	4:P:119:ASN:C	2.64	0.40
1:C:73:THR:HG23	5:R:8:THR:HG22	2.03	0.40
1:A:13:SER:HB3	1:A:93:HIS:N	2.36	0.40
1:A:29:ASP:HB3	1:A:30:ASP:H	1.61	0.40
1:A:69:ALA:O	3:I:96:ASN:ND2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:THR:OG1	1:A:217:TRP:N	2.54	0.40
2:B:33:SER:HB3	2:B:62:PHE:CD2	2.56	0.40
4:J:98:GLN:NE2	4:J:98:GLN:CA	2.82	0.40
3:K:35:TRP:O	3:K:36:TYR:HD1	2.04	0.40
3:K:131:SER:OG	3:K:132:VAL:N	2.47	0.40
3:K:136:THR:HG22	3:K:171:SER:CB	2.43	0.40
1:M:185:PRO:HD2	1:M:266:LEU:HD11	2.03	0.40
1:M:217:TRP:CZ3	1:M:247:VAL:HG22	2.56	0.40
3:E:61:ARG:HH12	3:E:81:GLN:HB3	1.86	0.40
1:G:4:SER:O	1:G:29:ASP:N	2.42	0.40
1:G:27:TYR:HE2	2:H:55:SER:HG	1.64	0.40
1:G:187:THR:CB	1:G:272:LEU:HD21	2.35	0.40
2:H:24:ASN:CG	2:H:25:CYS:H	2.30	0.40
3:K:136:THR:CG2	3:K:171:SER:HB3	2.50	0.40
4:P:151:TYR:CD1	4:P:152:PRO:HA	2.57	0.40
5:T:5:MET:HE3	5:T:5:MET:HB2	1.89	0.40
1:C:231:VAL:CG1	1:C:244:TRP:CE3	3.00	0.40
3:E:66:LEU:HD23	3:E:67:ASN:N	2.36	0.40
4:F:36:ARG:HD2	4:F:90:TYR:CZ	2.56	0.40
4:F:36:ARG:HH11	4:F:46:LEU:HD21	1.87	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:12:HIS:ND1	3:O:10:SER:OG[1_556]	1.92	0.28
3:K:12:HIS:CG	3:O:10:SER:OG[1_556]	2.00	0.20
3:K:189:ASN:OD1	4:P:181:PRO:CG[1_556]	2.09	0.11
3:I:10:SER:OG	3:I:12:HIS:ND1[3_655]	2.14	0.06
3:K:189:ASN:OD1	4:P:181:PRO:CD[1_556]	2.17	0.03

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	272/276 (99%)	255 (94%)	17 (6%)	0	100	100
1	C	272/276 (99%)	248 (91%)	23 (8%)	1 (0%)	30	62
1	G	264/276 (96%)	239 (90%)	25 (10%)	0	100	100
1	M	271/276 (98%)	242 (89%)	29 (11%)	0	100	100
2	B	97/100 (97%)	84 (87%)	13 (13%)	0	100	100
2	D	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
2	H	92/100 (92%)	82 (89%)	9 (10%)	1 (1%)	11	44
2	N	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
3	E	179/205 (87%)	152 (85%)	26 (14%)	1 (1%)	21	55
3	I	175/205 (85%)	137 (78%)	37 (21%)	1 (1%)	21	55
3	K	188/205 (92%)	158 (84%)	26 (14%)	4 (2%)	5	31
3	O	181/205 (88%)	160 (88%)	20 (11%)	1 (1%)	21	55
4	F	234/245 (96%)	197 (84%)	34 (14%)	3 (1%)	9	40
4	J	214/245 (87%)	185 (86%)	28 (13%)	1 (0%)	24	58
4	L	214/245 (87%)	183 (86%)	29 (14%)	2 (1%)	14	48
4	P	227/245 (93%)	192 (85%)	32 (14%)	3 (1%)	9	40
5	Q	7/9 (78%)	5 (71%)	2 (29%)	0	100	100
5	R	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
5	T	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
5	U	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	3104/3340 (93%)	2707 (87%)	379 (12%)	18 (1%)	21	55

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	I	122	LEU
4	J	114	LEU
3	K	147	SER
3	K	150	SER
4	L	174	PRO
4	P	229	LYS
4	F	181	PRO
3	K	153	TYR
3	O	178	LYS

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Mol	Chain	Res	Type
3	E	190	SER
4	P	139	GLN
2	H	71	THR
3	K	115	PRO
4	P	119	ASN
4	L	203	ASN
1	C	235	PRO
4	F	203	ASN
4	F	180	GLN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	231/232 (100%)	222 (96%)	9 (4%)	28	55
1	C	231/232 (100%)	216 (94%)	15 (6%)	15	42
1	G	226/232 (97%)	205 (91%)	21 (9%)	8	32
1	M	225/232 (97%)	206 (92%)	19 (8%)	10	34
2	B	93/95 (98%)	89 (96%)	4 (4%)	26	51
2	D	93/95 (98%)	80 (86%)	13 (14%)	3	19
2	H	86/95 (90%)	79 (92%)	7 (8%)	11	35
2	N	92/95 (97%)	86 (94%)	6 (6%)	15	42
3	E	158/185 (85%)	129 (82%)	29 (18%)	1	9
3	I	155/185 (84%)	138 (89%)	17 (11%)	6	27
3	K	158/185 (85%)	137 (87%)	21 (13%)	4	21
3	O	159/185 (86%)	137 (86%)	22 (14%)	3	20
4	F	198/212 (93%)	176 (89%)	22 (11%)	6	27
4	J	189/212 (89%)	167 (88%)	22 (12%)	5	25
4	L	174/212 (82%)	154 (88%)	20 (12%)	5	25
4	P	189/212 (89%)	170 (90%)	19 (10%)	7	29
5	Q	8/8 (100%)	7 (88%)	1 (12%)	4	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	R	8/8 (100%)	8 (100%)	0	100	100
5	T	8/8 (100%)	8 (100%)	0	100	100
5	U	8/8 (100%)	7 (88%)	1 (12%)	4	22
All	All	2689/2928 (92%)	2421 (90%)	268 (10%)	7	29

All (268) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ARG
1	A	52	ILE
1	A	66	LYS
1	A	98	MET
1	A	113	TYR
1	A	119	ASP
1	A	128	GLU
1	A	230	LEU
1	A	270	LEU
2	B	16	GLU
2	B	35	ILE
2	B	54	LEU
2	B	88	SER
3	I	1	ILE
3	I	13	VAL
3	I	14	GLN
3	I	15	GLU
3	I	39	GLU
3	I	49	VAL
3	I	78	LYS
3	I	80	SER
3	I	81	GLN
3	I	89	LEU
3	I	131	SER
3	I	133	CYS
3	I	138	PHE
3	I	144	VAL
3	I	152	VAL
3	I	159	VAL
3	I	179	SER
4	J	29	HIS
4	J	30	THR
4	J	60	LEU

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Mol	Chain	Res	Type
4	J	84	GLN
4	J	86	ASP
4	J	97	THR
4	J	114	LEU
4	J	120	VAL
4	J	131	SER
4	J	135	ILE
4	J	139	GLN
4	J	161	VAL
4	J	167	HIS
4	J	177	LEU
4	J	178	LYS
4	J	201	TRP
4	J	205	ARG
4	J	223	TRP
4	J	229	LYS
4	J	230	PRO
4	J	233	GLN
4	J	238	GLU
5	Q	5	MET
1	G	28	VAL
1	G	29	ASP
1	G	39	ASP
1	G	48	ARG
1	G	52	ILE
1	G	58	GLU
1	G	95	VAL
1	G	98	MET
1	G	124	ILE
1	G	127	LYS
1	G	138	MET
1	G	148	GLU
1	G	160	LEU
1	G	161	GLU
1	G	186	LYS
1	G	189	MET
1	G	191	HIS
1	G	226	GLN
1	G	248	VAL
1	G	264	GLU
1	G	268	LYS
2	H	3	ARG

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Mol	Chain	Res	Type
2	H	23	LEU
2	H	35	ILE
2	H	48	LYS
2	H	69	GLU
2	H	80	CYS
2	H	81	ARG
3	K	2	LEU
3	K	11	LEU
3	K	42	LYS
3	K	43	SER
3	K	52	LEU
3	K	53	ASN
3	K	61	ARG
3	K	70	GLU
3	K	80	SER
3	K	102	THR
3	K	112	ILE
3	K	126	LYS
3	K	128	SER
3	K	145	SER
3	K	149	ASP
3	K	155	THR
3	K	157	LYS
3	K	168	LYS
3	K	169	SER
3	K	178	LYS
3	K	180	ASP
4	L	6	GLN
4	L	9	SER
4	L	44	GLU
4	L	85	GLU
4	L	96	GLN
4	L	118	LYS
4	L	135	ILE
4	L	142	THR
4	L	143	LEU
4	L	145	CYS
4	L	148	THR
4	L	150	PHE
4	L	157	LEU
4	L	175	GLN
4	L	179	GLU

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Mol	Chain	Res	Type
4	L	193	ARG
4	L	196	VAL
4	L	217	LEU
4	L	234	ILE
4	L	238	GLU
5	U	6	VAL
1	M	5	MET
1	M	17	ARG
1	M	25	VAL
1	M	29	ASP
1	M	31	THR
1	M	88	SER
1	M	148	GLU
1	M	155	GLN
1	M	165	VAL
1	M	194	VAL
1	M	196	ASP
1	M	197	HIS
1	M	215	LEU
1	M	222	GLU
1	M	264	GLU
1	M	266	LEU
1	M	268	LYS
1	M	272	LEU
1	M	274	TRP
2	N	9	VAL
2	N	16	GLU
2	N	37	VAL
2	N	44	GLU
2	N	59	ASP
2	N	70	PHE
3	O	14	GLN
3	O	19	THR
3	O	58	LYS
3	O	69	LYS
3	O	80	SER
3	O	97	GLN
3	O	109	ILE
3	O	116	ASP
3	O	134	LEU
3	O	138	PHE
3	O	140	SER

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Mol	Chain	Res	Type
3	O	143	ASN
3	O	156	ASP
3	O	164	SER
3	O	166	ASP
3	O	168	LYS
3	O	170	ASN
3	O	171	SER
3	O	179	SER
3	O	187	PHE
3	O	188	ASN
3	O	192	ILE
4	P	5	SER
4	P	11	LYS
4	P	64	ARG
4	P	68	GLU
4	P	72	GLU
4	P	97	THR
4	P	101	GLU
4	P	113	VAL
4	P	154	HIS
4	P	166	VAL
4	P	167	HIS
4	P	171	CYS
4	P	179	GLU
4	P	191	SER
4	P	205	ARG
4	P	226	ASP
4	P	227	ARG
4	P	231	VAL
4	P	238	GLU
1	C	25	VAL
1	C	43	GLN
1	C	48	ARG
1	C	67	VAL
1	C	113	TYR
1	C	131	ARG
1	C	188	HIS
1	C	192	HIS
1	C	194	VAL
1	C	224	GLN
1	C	226	GLN
1	C	227	ASP

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Mol	Chain	Res	Type
1	C	231	VAL
1	C	249	VAL
1	C	275	GLU
2	D	7	ILE
2	D	9	VAL
2	D	11	SER
2	D	38	ASP
2	D	45	ARG
2	D	48	LYS
2	D	58	LYS
2	D	74	GLU
2	D	89	GLN
2	D	90	PRO
2	D	91	LYS
2	D	92	ILE
2	D	98	ASP
3	E	5	GLU
3	E	11	LEU
3	E	14	GLN
3	E	21	PHE
3	E	40	THR
3	E	61	ARG
3	E	62	ILE
3	E	63	SER
3	E	68	THR
3	E	83	GLU
3	E	85	SER
3	E	97	GLN
3	E	104	THR
3	E	111	ASN
3	E	126	LYS
3	E	134	LEU
3	E	136	THR
3	E	137	ASP
3	E	138	PHE
3	E	152	VAL
3	E	157	LYS
3	E	161	ASP
3	E	173	VAL
3	E	178	LYS
3	E	179	SER
3	E	180	ASP

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Mol	Chain	Res	Type
3	E	183	CYS
3	E	189	ASN
3	E	191	ILE
4	F	4	VAL
4	F	12	VAL
4	F	13	THR
4	F	32	LEU
4	F	39	LEU
4	F	49	PHE
4	F	70	THR
4	F	85	GLU
4	F	89	VAL
4	F	115	GLU
4	F	139	GLN
4	F	140	LYS
4	F	160	TRP
4	F	170	VAL
4	F	185	ASP
4	F	193	ARG
4	F	195	ARG
4	F	217	LEU
4	F	220	ASN
4	F	222	GLU
4	F	232	THR
4	F	238	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	218	GLN
2	B	13	HIS
3	I	96	ASN
3	I	141	GLN
3	I	188	ASN
4	J	29	HIS
4	J	80	GLN
4	J	119	ASN
4	J	154	HIS
4	J	207	HIS
1	G	72	GLN
1	G	93	HIS

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Mol	Chain	Res	Type
1	G	188	HIS
1	G	192	HIS
1	G	255	GLN
3	K	14	GLN
3	K	34	HIS
3	K	81	GLN
3	K	177	ASN
3	K	188	ASN
4	L	203	ASN
1	M	93	HIS
1	M	96	GLN
1	M	224	GLN
1	M	253	GLN
2	N	2	GLN
2	N	8	GLN
2	N	13	HIS
2	N	17	ASN
2	N	31	HIS
3	O	97	GLN
3	O	185	ASN
4	P	83	GLN
4	P	206	ASN
5	T	1	ASN
1	C	70	HIS
1	C	96	GLN
3	E	81	GLN
3	E	97	GLN
4	F	29	HIS
4	F	80	GLN
4	F	83	GLN
4	F	98	GLN
4	F	154	HIS
4	F	167	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	274/276 (99%)	-0.09	0 100 100	33, 56, 82, 107	0
1	C	274/276 (99%)	-0.13	0 100 100	35, 51, 83, 100	0
1	G	270/276 (97%)	0.18	1 (0%) 88 70	57, 80, 102, 122	0
1	M	273/276 (98%)	0.07	0 100 100	51, 77, 111, 119	0
2	B	99/100 (99%)	0.08	0 100 100	45, 72, 108, 123	0
2	D	100/100 (100%)	0.01	0 100 100	40, 66, 90, 113	0
2	H	96/100 (96%)	0.18	0 100 100	59, 88, 110, 115	0
2	N	100/100 (100%)	0.16	0 100 100	57, 87, 107, 116	0
3	E	187/205 (91%)	0.18	1 (0%) 87 67	36, 63, 114, 131	0
3	I	185/205 (90%)	0.16	1 (0%) 87 67	41, 72, 115, 126	0
3	K	192/205 (93%)	0.42	5 (2%) 57 32	55, 89, 129, 140	0
3	O	187/205 (91%)	0.27	2 (1%) 78 52	58, 91, 134, 151	0
4	F	238/245 (97%)	0.20	0 100 100	38, 80, 125, 132	0
4	J	226/245 (92%)	0.28	2 (0%) 81 56	25, 88, 129, 141	0
4	L	226/245 (92%)	0.39	5 (2%) 62 35	74, 106, 127, 136	0
4	P	235/245 (95%)	0.27	4 (1%) 69 41	50, 95, 133, 154	0
5	Q	9/9 (100%)	0.32	0 100 100	43, 48, 51, 53	0
5	R	9/9 (100%)	0.16	0 100 100	40, 41, 44, 46	0
5	T	9/9 (100%)	0.36	0 100 100	59, 63, 71, 72	0
5	U	9/9 (100%)	0.38	0 100 100	63, 67, 72, 73	0
All	All	3198/3340 (95%)	0.16	21 (0%) 84 61	25, 79, 122, 154	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	K	134	LEU	3.9
3	K	127	SER	3.5
4	P	126	ALA	3.4
3	K	173	VAL	3.2
4	P	144	VAL	2.9
4	P	37	GLN	2.8
4	J	144	VAL	2.6
4	J	152	PRO	2.6
3	I	172	ALA	2.6
3	K	144	VAL	2.5
4	L	157	LEU	2.5
3	O	133	CYS	2.5
3	E	190	SER	2.5
4	L	106	GLY	2.4
1	G	97	ARG	2.3
4	L	49	PHE	2.2
3	K	175	TRP	2.2
3	O	154	ILE	2.1
4	L	194	LEU	2.1
4	L	36	ARG	2.0
4	P	190	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.