



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:30 PM UTC

PDB ID : 2FSE / pdb_00002fse
Title : Crystallographic structure of a rheumatoid arthritis MHC susceptibility allele, HLA-DR1 (DRB1*0101), complexed with the immunodominant determinant of human type II collagen
Authors : Ivey, R.A.; Rosloniec, E.F.; Whittington, K.B.; Kang, A.H.; Park, H.W.
Deposited on : 2006-01-22
Resolution : 3.10 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

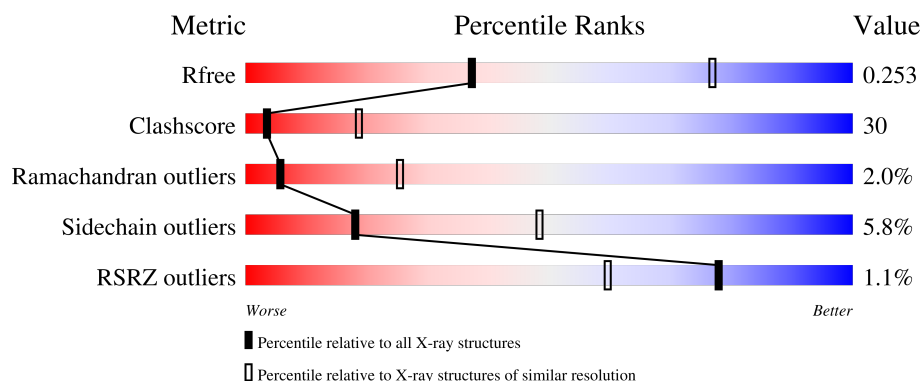
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

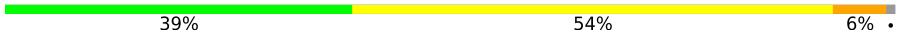
The reported resolution of this entry is 3.10 Å.

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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	178	
1	C	178	
2	B	187	
2	D	187	
3	E	14	

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Mol	Chain	Length	Quality of chain
3	F	14	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: a red segment at the top left labeled '14%', a green segment below it labeled '57%', a yellow segment labeled '29%', and a red segment at the bottom right labeled '14%'.

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6216 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 H-2 class II histocompatibility antigen, E-K alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	178	Total	C	N	O	S	0	0	0
			1465	945	240	275	5			
1	C	177	Total	C	N	O	S	0	0	0
			1455	940	239	271	5			

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	186	Total	C	N	O	S	0	0	0
			1534	967	269	292	6			
2	D	186	Total	C	N	O	S	0	0	0
			1539	970	272	291	6			

- Molecule 3 is a protein called Collagen alpha-1(II).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	14	Total	C	N	O	0	0	0
			96	59	17	20			
3	F	14	Total	C	N	O	0	0	0
			96	59	17	20			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	7	Total	O	0	0
			7	7		
4	B	10	Total	O	0	0
			10	10		
4	C	2	Total	O	0	0
			2	2		
4	D	10	Total	O	0	0
			10	10		

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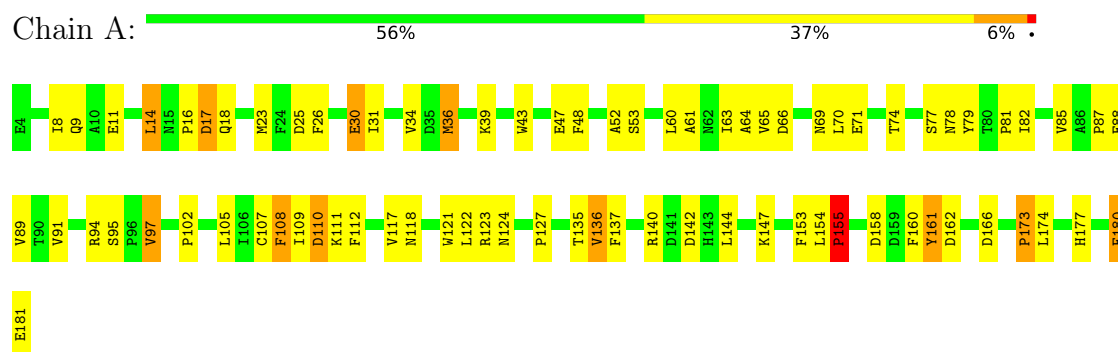
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	2	Total	O	0	0
			2	2		

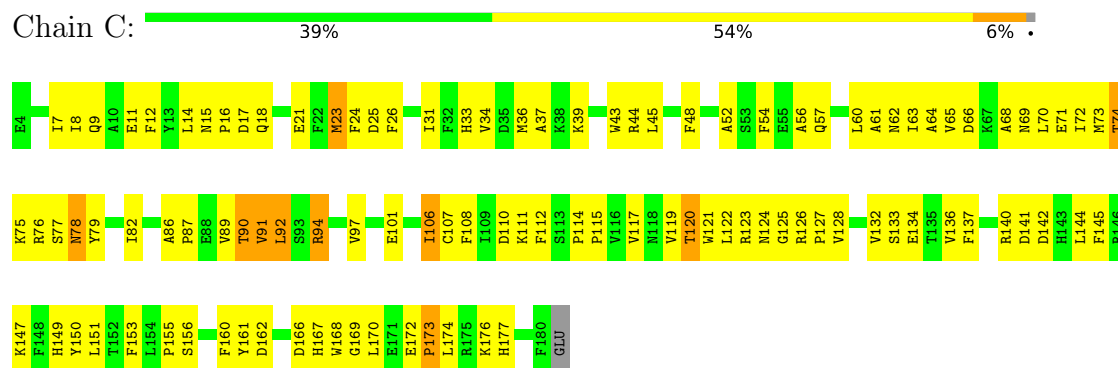
3 Residue-property plots

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: H-2 class II histocompatibility antigen, E-K alpha chain

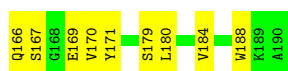


- Molecule 1: H-2 class II histocompatibility antigen, E-K alpha chain



- Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain





- Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain

Chain D: 2% 49% 42% 7% ..



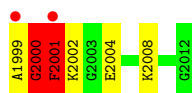
- Molecule 3: Collagen alpha-1(II)

Chain E: 7% 43% 50% 7%



- Molecule 3: Collagen alpha-1(II)

Chain F: 14% 57% 29% 14%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.81Å 109.00Å 170.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.10 20.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	82.4 (20.00-3.10) 95.6 (20.00-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 3.11Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.222 , 0.295 0.245 , 0.253	Depositor DCC
R_{free} test set	2087 reflections (9.78%)	wwPDB-VP
Wilson B-factor (Å ²)	52.0	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 48.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	6216	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% of the height of the origin peak. No significant pseudotranslation is detected.*

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	0.47	0/1509	1.03	8/2052 (0.4%)
1	C	0.47	0/1499	1.01	13/2040 (0.6%)
2	B	0.52	0/1574	0.97	2/2140 (0.1%)
2	D	0.61	1/1579 (0.1%)	1.46	33/2148 (1.5%)
3	E	0.54	0/98	1.49	4/127 (3.1%)
3	F	0.95	0/98	3.27	11/127 (8.7%)
All	All	0.53	1/6357 (0.0%)	1.20	71/8634 (0.8%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	108	PRO	N-CA	7.39	1.56	1.47

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	108	PRO	CA-N-CD	-16.85	88.41	112.00
3	F	2001	PHE	CA-C-N	16.20	145.00	121.02
3	F	2001	PHE	C-N-CA	16.20	145.00	121.02
2	D	109	LEU	CA-C-N	14.21	144.39	122.93
2	D	109	LEU	C-N-CA	14.21	144.39	122.93
2	D	103	PRO	CA-N-CD	-14.00	92.40	112.00
3	F	2000	GLY	CA-C-N	11.97	144.41	121.54
3	F	2000	GLY	C-N-CA	11.97	144.41	121.54
2	D	108	PRO	CA-C-N	-10.09	107.81	122.94
2	D	108	PRO	C-N-CA	-10.09	107.81	122.94
3	F	2001	PHE	O-C-N	9.86	135.70	122.59
2	D	110	GLN	OE1-CD-NE2	-9.14	113.46	122.60
1	A	97	VAL	N-CA-C	8.71	121.13	108.58
2	D	107	GLN	N-CA-C	8.63	128.88	109.81
2	D	5	PRO	CA-N-CD	-8.59	99.97	112.00
2	D	34	GLN	N-CA-C	-8.51	102.66	113.72
2	D	109	LEU	CA-C-O	8.18	129.53	120.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2001	PHE	CA-C-O	7.85	131.73	120.51
3	E	1001	PHE	N-CA-C	7.74	127.29	110.80
2	D	110	GLN	CA-C-N	7.52	134.32	122.74
2	D	110	GLN	C-N-CA	7.52	134.32	122.74
2	D	6	ARG	CB-CA-C	-7.17	96.15	110.42
2	D	104	THR	CB-CA-C	-7.12	96.25	110.42
1	C	78	ASN	N-CA-C	-7.07	104.60	113.23
3	F	2001	PHE	N-CA-C	6.79	125.27	110.80
2	D	108	PRO	N-CA-CB	6.76	110.35	103.25
2	D	102	TYR	N-CA-C	6.74	116.06	108.25
2	D	110	GLN	CG-CD-NE2	6.65	126.38	116.40
1	C	86	ALA	CA-C-N	6.64	127.16	119.99
1	C	86	ALA	C-N-CA	6.64	127.16	119.99
1	C	94	ARG	N-CA-C	-6.58	105.40	113.50
1	C	97	VAL	N-CA-C	6.53	117.46	108.84
2	D	102	TYR	O-C-N	6.51	126.40	121.65
2	D	107	GLN	C-N-CD	-6.42	98.67	125.00
3	E	1000	GLY	N-CA-C	6.37	128.27	113.18
1	A	110	ASP	N-CA-C	6.36	119.54	109.50
2	D	4	ARG	C-N-CD	-6.35	98.95	125.00
2	D	50	VAL	N-CA-C	-6.35	106.61	112.96
2	D	109	LEU	N-CA-C	6.13	119.40	109.40
2	D	108	PRO	CB-CA-C	-5.96	101.73	111.56
1	A	77	SER	N-CA-C	-5.85	106.12	113.72
2	D	83	TYR	N-CA-C	-5.76	104.90	111.07
1	C	15	ASN	N-CA-C	-5.76	102.90	110.39
2	B	65	LYS	N-CA-C	5.71	117.50	111.28
2	B	99	VAL	N-CA-C	5.69	116.13	108.17
1	C	74	THR	N-CA-C	-5.62	106.12	112.87
1	A	161	TYR	N-CA-C	5.58	117.90	109.41
2	D	177	HIS	CA-C-N	5.51	125.86	119.47
2	D	177	HIS	C-N-CA	5.51	125.86	119.47
2	D	111	HIS	N-CA-CB	5.49	120.30	110.80
1	C	23	MET	N-CA-C	5.47	117.50	109.24
2	D	109	LEU	O-C-N	5.42	130.27	123.23
1	A	97	VAL	CB-CA-C	-5.41	104.20	110.91
3	F	1999	ALA	CA-C-N	5.39	131.98	121.41
3	F	1999	ALA	C-N-CA	5.39	131.98	121.41
2	D	120	SER	N-CA-C	5.32	117.95	109.81
1	C	101	GLU	CA-C-N	5.29	125.29	119.89
1	C	101	GLU	C-N-CA	5.29	125.29	119.89
1	C	31	ILE	N-CA-C	-5.27	105.99	111.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2001	PHE	CA-CB-CG	5.23	119.03	113.80
1	A	78	ASN	N-CA-C	-5.19	104.96	111.92
2	D	109	LEU	CB-CA-C	5.11	119.14	109.37
2	D	105	LYS	N-CA-C	5.09	117.99	110.46
1	A	31	ILE	N-CA-C	-5.08	105.89	110.82
3	F	2008	LYS	N-CA-C	-5.07	103.36	110.50
1	C	91	VAL	N-CA-C	5.05	115.20	108.27
1	C	77	SER	N-CA-C	-5.05	107.18	113.19
1	A	91	VAL	N-CA-C	5.05	115.98	108.46
2	D	141	GLY	N-CA-C	5.01	125.06	113.18
3	E	1010	GLU	CA-C-N	-5.01	114.56	119.92
3	E	1010	GLU	C-N-CA	-5.01	114.56	119.92

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	1465	0	1386	71	0
1	C	1455	0	1380	118	0
2	B	1534	0	1456	101	0
2	D	1539	0	1463	116	0
3	E	96	0	88	9	0
3	F	96	0	88	17	0
4	A	7	0	0	0	0
4	B	10	0	0	1	0
4	C	2	0	0	0	0
4	D	10	0	0	0	0
4	E	2	0	0	0	0
All	All	6216	0	5861	356	0

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 30.

All (356) 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)
2:D:110:GLN:CG	2:D:164:VAL:CG1	1.74	1.57
2:D:110:GLN:HG2	2:D:164:VAL:CG1	1.37	1.43
2:D:110:GLN:HE21	2:D:166:GLN:CG	1.38	1.34
2:D:108:PRO:C	2:D:109:LEU:HD12	1.55	1.30
2:D:110:GLN:CD	2:D:164:VAL:HG11	1.56	1.30
1:C:52:ALA:HB1	3:F:2001:PHE:CE2	1.70	1.25
1:C:82:ILE:HG22	2:D:6:ARG:O	1.36	1.22
2:D:110:GLN:NE2	2:D:166:GLN:CG	2.03	1.19
2:D:108:PRO:O	2:D:109:LEU:HD12	1.47	1.14
2:D:110:GLN:HG3	2:D:164:VAL:CG1	1.68	1.13
1:C:168:TRP:CH2	2:D:6:ARG:NH1	2.18	1.12
2:D:110:GLN:NE2	2:D:166:GLN:HG2	1.65	1.11
2:D:110:GLN:HG2	2:D:164:VAL:HG13	1.07	1.07
2:D:110:GLN:HE21	2:D:166:GLN:HG3	1.19	1.04
2:D:110:GLN:CG	2:D:164:VAL:HG11	1.53	1.03
2:D:110:GLN:HG3	2:D:164:VAL:HG12	1.41	1.03
2:D:110:GLN:CG	2:D:164:VAL:HG13	1.64	1.00
2:D:110:GLN:CG	2:D:164:VAL:HG12	1.90	0.99
2:D:110:GLN:HE21	2:D:166:GLN:HG2	1.19	0.99
2:D:110:GLN:CD	2:D:164:VAL:CG1	2.25	0.96
2:D:110:GLN:HG2	2:D:164:VAL:HG11	1.20	0.94
1:C:70:LEU:HD13	2:D:9:TRP:HB2	1.49	0.92
2:B:112:HIS:HE1	1:C:111:LYS:HB2	1.36	0.89
1:C:94:ARG:HB2	1:C:106:ILE:HD11	1.53	0.88
2:D:108:PRO:C	2:D:109:LEU:CD1	2.46	0.86
2:B:71:ARG:HH21	3:E:1007:PRO:HD3	1.40	0.85
2:B:150:ASN:HD22	2:B:154:THR:HG22	1.42	0.84
1:C:52:ALA:CB	3:F:2001:PHE:CE2	2.60	0.83
2:D:105:LYS:HD2	2:D:113:ASN:HA	1.59	0.83
2:D:110:GLN:NE2	2:D:166:GLN:CD	2.36	0.82
2:B:112:HIS:CE1	1:C:111:LYS:HB2	2.15	0.82
2:D:110:GLN:HE22	2:D:166:GLN:NE2	1.78	0.81
1:A:70:LEU:HD13	2:B:9:TRP:HB2	1.61	0.81
1:C:52:ALA:HB1	3:F:2001:PHE:CZ	2.14	0.81
1:A:8:ILE:HG12	2:B:14:GLU:HB3	1.63	0.81
1:A:53:SER:HG	3:E:999:ALA:N	1.79	0.80
1:A:65:VAL:HG13	3:E:1008:LYS:HG2	1.62	0.80
1:A:14:LEU:HD21	1:A:17:ASP:HB2	1.61	0.80
2:D:150:ASN:HB2	2:D:154:THR:HG22	1.64	0.79
1:C:168:TRP:HH2	2:D:6:ARG:NH1	1.78	0.79
2:B:105:LYS:NZ	2:B:113:ASN:HA	1.97	0.78
2:D:166:GLN:O	2:D:169:GLU:HB2	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:112:HIS:HE1	1:C:111:LYS:CB	1.96	0.78
1:C:82:ILE:CG2	2:D:6:ARG:O	2.26	0.77
1:A:82:ILE:HG22	2:B:6:ARG:O	1.85	0.76
1:A:111:LYS:HE3	1:A:140:ARG:HH21	1.51	0.75
2:D:133:ARG:HG3	2:D:171:TYR:CE1	2.21	0.75
1:C:82:ILE:HD11	2:D:34:GLN:HE22	1.51	0.75
2:D:108:PRO:O	2:D:109:LEU:CD1	2.32	0.74
2:D:55:ARG:HB2	2:D:56:PRO:HD3	1.69	0.73
1:A:17:ASP:OD2	2:B:6:ARG:HD2	1.90	0.72
2:B:145:THR:HG22	2:B:158:LEU:H	1.55	0.72
1:C:52:ALA:CB	3:F:2001:PHE:CZ	2.72	0.72
2:D:24:VAL:HG21	2:D:80:ARG:HE	1.52	0.72
1:C:170:LEU:HD13	1:C:174:LEU:HB2	1.70	0.71
2:D:110:GLN:HE22	2:D:166:GLN:CD	1.97	0.71
1:C:9:GLN:HB3	2:D:13:PHE:HB2	1.73	0.70
1:C:121:TRP:HB3	1:C:151:LEU:HD22	1.74	0.70
1:A:111:LYS:CE	1:A:140:ARG:HH21	2.05	0.70
1:C:73:MET:HE1	2:D:53:LEU:HB3	1.74	0.70
2:B:112:HIS:CE1	1:C:111:LYS:CB	2.75	0.69
2:B:26:LEU:HD22	2:B:74:ALA:HB3	1.75	0.69
2:B:114:LEU:HD22	2:B:160:MET:HB3	1.73	0.69
2:D:26:LEU:HD22	2:D:74:ALA:HB3	1.75	0.68
2:D:104:THR:HB	2:D:105:LYS:HG3	1.76	0.68
1:C:168:TRP:HH2	2:D:6:ARG:HH12	1.42	0.68
2:B:112:HIS:HA	2:B:163:THR:O	1.95	0.67
1:C:82:ILE:CG2	2:D:6:ARG:HB2	2.24	0.67
1:A:85:VAL:HG11	2:D:110:GLN:OE1	1.96	0.66
2:B:25:ARG:HH21	2:B:27:LEU:HD21	1.61	0.66
1:A:111:LYS:HE3	1:A:140:ARG:NH2	2.10	0.65
1:A:9:GLN:HB3	2:B:13:PHE:HB2	1.76	0.65
3:F:2000:GLY:O	3:F:2001:PHE:HD2	1.80	0.65
1:C:57:GLN:HA	1:C:60:LEU:HD12	1.79	0.65
1:C:168:TRP:CZ3	2:D:6:ARG:NH1	2.65	0.65
1:C:106:ILE:N	1:C:106:ILE:HD12	2.11	0.65
2:B:27:LEU:HD12	2:B:41:ASP:HA	1.80	0.64
1:C:122:LEU:HD22	1:C:125:GLY:C	2.22	0.64
1:C:168:TRP:CH2	2:D:6:ARG:CZ	2.82	0.63
1:C:82:ILE:HD11	2:D:34:GLN:NE2	2.14	0.63
1:A:14:LEU:CD2	1:A:17:ASP:HB2	2.28	0.63
2:B:40:PHE:HB2	2:B:47:TYR:CE1	2.34	0.62
2:B:180:LEU:HD13	2:B:184:VAL:HG23	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:111:HIS:O	2:B:112:HIS:HB2	1.97	0.62
1:A:65:VAL:HG12	1:A:69:ASN:ND2	2.14	0.62
1:C:52:ALA:HB1	3:F:2001:PHE:HE2	1.57	0.62
1:C:123:ARG:HG2	1:C:124:ASN:ND2	2.15	0.62
1:A:122:LEU:HD23	1:A:127:PRO:HA	1.82	0.62
1:A:65:VAL:HG12	1:A:69:ASN:HD21	1.65	0.61
1:A:105:LEU:HG	1:A:153:PHE:CE1	2.35	0.61
2:B:97:PRO:HD2	2:B:180:LEU:HD21	1.83	0.61
2:D:138:GLU:HG2	2:D:161:LEU:HD11	1.84	0.60
2:B:166:GLN:HE22	2:D:34:GLN:HG2	1.66	0.60
2:D:138:GLU:O	2:D:142:ILE:HD11	2.02	0.60
2:B:96:GLU:HA	2:B:179:SER:OG	2.02	0.60
2:B:114:LEU:CD2	2:B:160:MET:HB3	2.31	0.60
2:D:8:LEU:HD12	2:D:9:TRP:H	1.66	0.60
1:A:11:GLU:HG3	2:B:11:LEU:HB3	1.84	0.60
1:C:162:ASP:OD2	1:C:177:HIS:HA	2.02	0.59
1:C:23:MET:HG2	1:C:24:PHE:N	2.17	0.59
1:C:73:MET:HE2	2:D:53:LEU:HD22	1.85	0.59
2:B:33:ASN:O	2:B:34:GLN:HG3	2.02	0.59
1:C:76:ARG:C	1:C:78:ASN:H	2.10	0.59
1:A:34:VAL:O	1:A:36:MET:HE3	2.02	0.59
1:A:144:LEU:HD21	2:D:110:GLN:OE1	2.02	0.59
1:C:124:ASN:HA	1:C:160:PHE:CE1	2.38	0.59
2:D:169:GLU:HG2	2:D:171:TYR:CZ	2.38	0.59
2:D:82:ASN:OD1	3:F:2001:PHE:HB2	2.03	0.58
2:B:150:ASN:ND2	2:B:154:THR:HG22	2.16	0.58
1:A:142:ASP:HB2	2:D:166:GLN:OE1	2.02	0.58
2:B:105:LYS:HZ3	2:B:113:ASN:HA	1.69	0.57
1:C:21:GLU:OE1	1:C:136:VAL:HG12	2.04	0.57
2:B:24:VAL:HG23	2:B:80:ARG:NH1	2.20	0.57
2:B:112:HIS:CE1	2:B:164:VAL:CG2	2.88	0.57
2:B:145:THR:CG2	2:B:158:LEU:H	2.18	0.57
2:B:133:ARG:NH1	2:B:134:ASN:HD22	2.02	0.56
1:C:110:ASP:OD1	1:C:140:ARG:HD2	2.04	0.56
1:A:82:ILE:HG21	2:B:6:ARG:HB2	1.87	0.56
1:A:140:ARG:HG3	1:A:140:ARG:HH11	1.71	0.56
1:A:14:LEU:O	1:A:14:LEU:HD23	2.06	0.56
2:B:157:THR:O	2:B:158:LEU:HD23	2.05	0.56
2:D:81:HIS:CD2	3:F:2002:LYS:HD2	2.41	0.56
2:B:162:GLU:O	2:B:163:THR:HG23	2.06	0.55
1:C:45:LEU:HD12	1:C:48:PHE:CZ	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:21:THR:O	2:B:80:ARG:NH1	2.40	0.55
2:D:46:GLU:CD	2:D:48:ARG:HH21	2.15	0.55
1:C:73:MET:CE	2:D:53:LEU:HD22	2.37	0.54
1:C:125:GLY:O	1:C:127:PRO:HD3	2.07	0.54
1:C:14:LEU:HD13	2:D:8:LEU:HB2	1.90	0.54
1:A:39:LYS:HG3	1:A:60:LEU:HD11	1.88	0.54
3:F:2000:GLY:O	3:F:2001:PHE:CD2	2.60	0.54
2:D:93:ARG:HG2	2:D:93:ARG:HH11	1.72	0.54
1:C:66:ASP:HA	2:D:9:TRP:CZ3	2.43	0.54
2:B:64:GLN:O	2:B:67:LEU:HB3	2.08	0.54
1:A:36:MET:SD	1:A:63:ILE:HD13	2.48	0.54
1:C:106:ILE:HD12	1:C:106:ILE:H	1.72	0.54
2:B:94:ARG:NH1	2:B:94:ARG:HG3	2.23	0.53
1:A:97:VAL:O	1:A:97:VAL:HG23	2.08	0.53
1:C:7:ILE:HG13	2:D:17:PHE:HE2	1.73	0.53
1:C:43:TRP:CZ3	3:F:2001:PHE:HZ	2.26	0.53
2:D:24:VAL:CG2	2:D:80:ARG:HE	2.21	0.53
2:B:40:PHE:HB2	2:B:47:TYR:CD1	2.43	0.53
1:C:69:ASN:HA	1:C:72:ILE:HD12	1.89	0.53
2:D:110:GLN:CD	2:D:164:VAL:HG12	2.24	0.53
1:A:124:ASN:HA	1:A:160:PHE:CZ	2.44	0.53
2:B:94:ARG:HG3	2:B:94:ARG:HH11	1.72	0.53
2:B:112:HIS:CG	2:B:164:VAL:HG22	2.44	0.53
1:C:87:PRO:HD3	1:C:167:HIS:HD2	1.74	0.53
2:D:26:LEU:HG	2:D:27:LEU:N	2.20	0.53
2:B:109:LEU:HD21	2:B:167:SER:HB2	1.91	0.53
2:B:152:ASP:OD1	2:B:154:THR:HB	2.09	0.53
1:A:85:VAL:HG21	2:D:110:GLN:OE1	2.09	0.53
1:C:16:PRO:O	1:C:18:GLN:HG3	2.08	0.53
1:C:26:PHE:CE2	2:D:90:THR:HB	2.43	0.52
2:D:17:PHE:HB3	2:D:20:GLY:O	2.09	0.52
1:A:108:PHE:CD1	1:A:108:PHE:N	2.78	0.52
1:C:119:VAL:O	1:C:120:THR:HG23	2.10	0.52
1:A:109:ILE:HB	1:A:147:LYS:HB3	1.93	0.51
2:B:11:LEU:HD21	2:B:13:PHE:CZ	2.46	0.51
2:B:105:LYS:CE	2:B:113:ASN:HA	2.40	0.51
2:B:68:LEU:O	2:B:72:ARG:HG3	2.10	0.51
2:B:136:LYS:NZ	2:D:16:HIS:HE1	2.09	0.51
1:A:47:GLU:HG3	1:A:48:PHE:N	2.26	0.51
1:C:54:PHE:HD1	3:F:2001:PHE:O	1.94	0.51
1:C:133:SER:OG	1:C:150:TYR:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:VAL:HA	1:C:150:TYR:O	2.10	0.51
2:B:105:LYS:CE	2:B:112:HIS:O	2.59	0.51
2:D:110:GLN:NE2	2:D:164:VAL:CG1	2.73	0.51
1:A:117:VAL:HG12	1:A:137:PHE:CZ	2.46	0.50
1:C:8:ILE:HG23	2:D:14:GLU:HB3	1.92	0.50
2:B:71:ARG:NH2	3:E:1007:PRO:HD3	2.20	0.50
2:D:112:HIS:CD2	2:D:112:HIS:H	2.30	0.50
2:B:97:PRO:HB3	2:B:122:PHE:HB3	1.93	0.50
1:C:147:LYS:HE3	1:C:149:HIS:NE2	2.26	0.50
1:A:85:VAL:HG13	2:D:110:GLN:HB3	1.94	0.50
2:B:55:ARG:HB2	2:B:56:PRO:HD3	1.94	0.50
2:B:133:ARG:HD2	2:B:169:GLU:OE2	2.11	0.50
1:C:172:GLU:O	1:C:173:PRO:C	2.55	0.50
2:B:133:ARG:NH1	2:B:134:ASN:ND2	2.60	0.49
2:B:32:TYR:CG	2:B:33:ASN:N	2.80	0.49
2:D:26:LEU:HD22	2:D:74:ALA:CB	2.42	0.49
1:A:26:PHE:CE2	2:B:90:THR:HB	2.47	0.49
1:C:8:ILE:HG12	2:D:14:GLU:HB3	1.94	0.49
1:A:94:ARG:NH1	1:A:94:ARG:HG2	2.28	0.49
2:B:83:TYR:C	2:B:83:TYR:CD1	2.90	0.49
2:D:105:LYS:HD2	2:D:113:ASN:CA	2.36	0.49
1:A:107:CYS:HB2	1:A:121:TRP:CH2	2.47	0.49
2:B:81:HIS:O	2:B:85:VAL:HG23	2.13	0.49
1:C:107:CYS:HB2	1:C:121:TRP:CH2	2.48	0.49
1:C:121:TRP:CB	1:C:151:LEU:HD22	2.42	0.49
1:C:44:ARG:HH22	2:D:152:ASP:HB3	1.78	0.49
2:D:24:VAL:HG11	2:D:79:CYS:HB3	1.95	0.49
1:A:87:PRO:HB3	1:A:112:PHE:HB3	1.95	0.48
1:C:14:LEU:O	1:C:18:GLN:N	2.46	0.48
1:C:76:ARG:C	1:C:78:ASN:N	2.70	0.48
2:D:31:ILE:HA	2:D:36:GLU:HA	1.95	0.48
1:C:166:ASP:OD2	1:C:173:PRO:HG3	2.14	0.48
2:B:31:ILE:HG12	2:B:36:GLU:HA	1.95	0.48
2:B:32:TYR:O	2:B:33:ASN:C	2.56	0.48
2:B:75:VAL:O	2:B:79:CYS:HB2	2.12	0.48
2:B:119:VAL:HB	2:B:157:THR:HG22	1.95	0.48
1:C:75:LYS:HG3	1:C:79:TYR:HE1	1.79	0.48
1:C:89:VAL:HA	1:C:108:PHE:O	2.13	0.48
1:C:73:MET:C	1:C:75:LYS:H	2.21	0.48
1:C:44:ARG:NH2	2:D:152:ASP:HB3	2.28	0.48
1:C:78:ASN:O	1:C:79:TYR:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:74:ALA:O	2:D:78:TYR:HB3	2.13	0.48
1:A:16:PRO:CD	2:B:6:ARG:HD3	2.43	0.48
1:A:11:GLU:CD	2:B:11:LEU:HD23	2.39	0.48
2:D:132:PHE:O	2:D:171:TYR:HA	2.14	0.48
1:C:12:PHE:CD1	1:C:12:PHE:C	2.92	0.48
1:C:142:ASP:OD2	1:C:144:LEU:HD12	2.13	0.48
2:D:75:VAL:O	2:D:79:CYS:HB2	2.13	0.48
1:C:43:TRP:CH2	3:F:2001:PHE:CZ	3.01	0.47
1:C:73:MET:C	1:C:75:LYS:N	2.71	0.47
1:C:87:PRO:HD3	1:C:167:HIS:CD2	2.49	0.47
1:A:16:PRO:O	1:A:18:GLN:HG3	2.14	0.47
1:C:90:THR:HB	1:C:108:PHE:HB2	1.96	0.47
2:D:150:ASN:ND2	2:D:154:THR:HG23	2.28	0.47
1:C:37:ALA:O	1:C:39:LYS:HG3	2.14	0.47
2:D:64:GLN:O	2:D:67:LEU:HB3	2.14	0.47
1:A:122:LEU:HB2	1:A:162:ASP:HB2	1.96	0.47
2:B:105:LYS:HB2	2:B:113:ASN:HB2	1.96	0.47
1:C:65:VAL:HG12	1:C:69:ASN:HD21	1.79	0.47
2:D:24:VAL:HG23	2:D:80:ARG:HH21	1.78	0.47
1:A:123:ARG:HE	1:A:161:TYR:HE2	1.63	0.47
2:B:70:GLN:C	2:B:70:GLN:CD	2.81	0.47
2:B:71:ARG:HH22	3:E:1006:GLY:HA2	1.80	0.47
2:B:107:GLN:OE1	2:B:111:HIS:HB3	2.15	0.47
1:C:119:VAL:HG12	1:C:120:THR:N	2.30	0.47
2:D:93:ARG:NH1	2:D:153:TRP:HB3	2.28	0.47
4:B:501:HOH:O	3:E:1007:PRO:HD2	2.14	0.47
1:C:124:ASN:HA	1:C:160:PHE:CZ	2.50	0.47
2:D:157:THR:O	2:D:158:LEU:HD23	2.14	0.47
2:B:105:LYS:HB2	2:B:113:ASN:CB	2.45	0.47
1:C:75:LYS:HG3	1:C:79:TYR:CE1	2.50	0.47
1:C:11:GLU:OE1	1:C:62:ASN:HB3	2.15	0.46
1:A:14:LEU:HD21	1:A:17:ASP:CB	2.41	0.46
2:B:148:VAL:HB	2:B:156:GLN:HG3	1.96	0.46
2:B:162:GLU:HG2	2:B:163:THR:N	2.30	0.46
2:D:133:ARG:HG3	2:D:171:TYR:HE1	1.73	0.46
1:C:122:LEU:O	1:C:161:TYR:HA	2.16	0.46
2:B:87:GLU:HA	2:B:91:VAL:HG23	1.97	0.46
1:C:73:MET:HA	1:C:76:ARG:HG2	1.96	0.46
1:C:82:ILE:HG22	2:D:6:ARG:HB2	1.92	0.46
1:A:36:MET:HA	1:A:36:MET:HE2	1.98	0.46
2:B:140:THR:HG22	2:B:141:GLY:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:147:LEU:HD11	2:B:155:PHE:HB3	1.98	0.46
2:B:25:ARG:HH21	2:B:27:LEU:CD2	2.27	0.46
2:D:8:LEU:HD12	2:D:9:TRP:N	2.31	0.45
2:D:36:GLU:CD	2:D:39:ARG:HH21	2.24	0.45
1:C:117:VAL:HG23	1:C:166:ASP:O	2.16	0.45
2:D:180:LEU:HD13	2:D:184:VAL:HG23	1.98	0.45
2:B:31:ILE:HG22	2:B:32:TYR:O	2.15	0.45
1:C:136:VAL:HG12	1:C:137:PHE:N	2.30	0.45
2:B:112:HIS:CE1	1:C:111:LYS:HB3	2.50	0.45
2:B:148:VAL:HB	2:B:156:GLN:CG	2.47	0.45
1:C:134:GLU:O	1:C:134:GLU:HG3	2.17	0.45
1:A:30:GLU:HG3	1:A:30:GLU:O	2.15	0.45
2:B:55:ARG:O	2:B:59:GLU:HG2	2.16	0.45
2:D:110:GLN:NE2	2:D:166:GLN:HG3	2.00	0.45
1:A:61:ALA:O	1:A:64:ALA:HB3	2.17	0.45
1:A:85:VAL:CG1	2:D:110:GLN:OE1	2.65	0.45
1:A:94:ARG:HG2	1:A:94:ARG:HH11	1.82	0.45
1:A:154:LEU:O	1:A:155:PRO:C	2.59	0.45
1:A:16:PRO:HD3	2:B:6:ARG:HD3	1.99	0.44
2:D:110:GLN:NE2	2:D:164:VAL:HG12	2.32	0.44
1:A:70:LEU:CD1	2:B:9:TRP:HB2	2.42	0.44
1:C:170:LEU:CD1	1:C:174:LEU:HB2	2.42	0.44
1:A:166:ASP:OD2	1:A:173:PRO:HG3	2.17	0.44
2:D:105:LYS:HD2	2:D:113:ASN:CB	2.47	0.44
1:C:76:ARG:NH1	2:D:56:PRO:HG2	2.33	0.44
1:C:142:ASP:C	1:C:142:ASP:OD1	2.60	0.44
1:C:36:MET:SD	1:C:63:ILE:HD13	2.57	0.44
1:A:63:ILE:O	1:A:66:ASP:HB2	2.17	0.44
1:A:102:PRO:HG3	1:A:154:LEU:HD13	2.00	0.44
2:B:133:ARG:NH2	1:C:141:ASP:O	2.51	0.44
2:B:72:ARG:O	2:B:75:VAL:HG23	2.18	0.44
2:B:105:LYS:HE2	2:B:113:ASN:CB	2.48	0.44
1:C:36:MET:SD	1:C:63:ILE:CD1	3.06	0.44
1:A:79:TYR:O	1:A:81:PRO:HD3	2.17	0.43
1:C:87:PRO:HA	1:C:112:PHE:HB3	2.00	0.43
1:A:23:MET:HE2	1:A:30:GLU:HB2	2.00	0.43
2:D:177:HIS:CG	2:D:178:PRO:HD2	2.53	0.43
1:A:180:PHE:O	1:A:181:GLU:HB2	2.18	0.43
2:B:24:VAL:HG23	2:B:80:ARG:HH12	1.82	0.43
2:B:71:ARG:NH2	3:E:1006:GLY:HA2	2.32	0.43
1:A:65:VAL:CG1	3:E:1008:LYS:HG2	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:63:ILE:HA	1:C:66:ASP:HB2	2.00	0.43
2:D:85:VAL:HG11	3:F:2001:PHE:HB3	2.00	0.43
2:B:25:ARG:NH2	2:B:27:LEU:HD21	2.31	0.43
2:B:134:ASN:HD21	2:B:169:GLU:HG2	1.83	0.43
1:C:68:ALA:O	1:C:69:ASN:C	2.61	0.43
1:C:91:VAL:C	1:C:92:LEU:HD23	2.43	0.43
1:C:124:ASN:C	1:C:126:ARG:H	2.26	0.43
2:D:13:PHE:CD2	2:D:28:GLU:HG3	2.53	0.43
2:D:106:THR:HG22	2:D:108:PRO:HD2	2.01	0.43
1:A:23:MET:HE1	1:A:25:ASP:OD2	2.18	0.43
2:D:110:GLN:NE2	2:D:166:GLN:NE2	2.51	0.43
2:D:139:GLU:OE2	2:D:139:GLU:HA	2.18	0.43
1:C:128:VAL:HG11	1:C:151:LEU:CD1	2.49	0.43
1:A:43:TRP:CH2	1:A:52:ALA:HB3	2.54	0.43
1:A:180:PHE:CE2	1:A:181:GLU:OE2	2.72	0.43
2:D:150:ASN:HD22	2:D:154:THR:HG23	1.84	0.43
2:B:104:THR:HG22	2:B:105:LYS:N	2.33	0.43
1:A:89:VAL:CG2	1:A:174:LEU:HD23	2.49	0.42
1:C:33:HIS:CD2	1:C:136:VAL:HG21	2.55	0.42
1:A:117:VAL:HG22	1:A:118:ASN:N	2.34	0.42
1:C:61:ALA:O	1:C:64:ALA:HB3	2.18	0.42
2:D:11:LEU:HD12	2:D:12:LYS:H	1.84	0.42
1:A:110:ASP:CG	1:A:111:LYS:HG3	2.44	0.42
1:A:162:ASP:OD1	1:A:177:HIS:ND1	2.44	0.42
2:B:105:LYS:HE2	2:B:113:ASN:HB3	2.02	0.42
2:B:105:LYS:HE2	2:B:113:ASN:HA	2.00	0.42
1:A:82:ILE:HD11	2:B:34:GLN:OE1	2.20	0.42
2:D:18:PHE:CD1	2:D:18:PHE:N	2.87	0.42
2:D:109:LEU:HD12	2:D:109:LEU:N	2.20	0.42
1:C:114:PRO:HB2	1:C:115:PRO:HD2	2.02	0.42
1:C:167:HIS:C	1:C:169:GLY:H	2.27	0.42
1:C:89:VAL:CG2	1:C:174:LEU:HD23	2.49	0.42
1:C:137:PHE:HB3	1:C:145:PHE:CD2	2.55	0.42
2:B:54:GLY:O	2:B:55:ARG:C	2.63	0.41
2:B:74:ALA:O	2:B:78:TYR:HB3	2.19	0.41
2:B:132:PHE:O	2:B:171:TYR:HA	2.20	0.41
1:C:122:LEU:HD23	1:C:127:PRO:N	2.34	0.41
1:C:89:VAL:HG12	1:C:176:LYS:HG3	2.02	0.41
2:B:140:THR:CG2	2:B:141:GLY:N	2.83	0.41
1:C:71:GLU:HA	1:C:74:THR:HB	2.01	0.41
1:C:107:CYS:HB2	1:C:121:TRP:CZ2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:24:VAL:HG12	2:D:25:ARG:N	2.35	0.41
2:B:11:LEU:HD21	2:B:13:PHE:HZ	1.84	0.41
1:C:36:MET:HA	1:C:36:MET:HE2	2.02	0.41
2:D:61:TRP:O	2:D:63:SER:N	2.53	0.41
1:A:135:THR:C	1:A:136:VAL:O	2.62	0.41
1:C:153:PHE:CE2	1:C:155:PRO:HG3	2.55	0.41
2:D:81:HIS:CE1	3:F:2002:LYS:HE3	2.55	0.41
3:E:1010:GLU:O	3:E:1011:PRO:C	2.63	0.41
1:A:74:THR:HG23	2:B:7:PHE:CD1	2.55	0.41
2:D:188:TRP:CE3	2:D:189:LYS:HB2	2.56	0.41
1:C:34:VAL:CG1	1:C:56:ALA:HB1	2.50	0.41
1:A:111:LYS:HE2	1:A:140:ARG:HH21	1.84	0.41
2:B:68:LEU:HD13	2:B:72:ARG:NH2	2.35	0.41
1:C:43:TRP:CH2	3:F:2001:PHE:HZ	2.39	0.40
1:C:43:TRP:HH2	3:F:2001:PHE:CZ	2.40	0.40
2:D:41:ASP:OD1	2:D:43:ASP:N	2.53	0.40
2:D:61:TRP:C	2:D:63:SER:N	2.79	0.40
2:D:109:LEU:CD1	2:D:109:LEU:N	2.80	0.40
2:B:24:VAL:CG2	2:B:80:ARG:NH1	2.85	0.40
1:C:17:ASP:O	1:C:18:GLN:HB2	2.21	0.40
1:A:108:PHE:H	1:A:108:PHE:HD1	1.69	0.40
2:B:170:VAL:HA	2:B:188:TRP:O	2.21	0.40
1:C:45:LEU:HB2	1:C:48:PHE:CE2	2.56	0.40
1:C:26:PHE:HB3	2:D:153:TRP:HH2	1.87	0.40
1:C:43:TRP:CZ3	3:F:2001:PHE:CZ	3.07	0.40
1:C:68:ALA:C	1:C:70:LEU:N	2.78	0.40
2:D:96:GLU:HA	2:D:97:PRO:HD3	1.81	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	176/178 (99%)	158 (90%)	13 (7%)	5 (3%)	4	20
1	C	175/178 (98%)	152 (87%)	22 (13%)	1 (1%)	21	52
2	B	184/187 (98%)	155 (84%)	28 (15%)	1 (0%)	24	57
2	D	184/187 (98%)	161 (88%)	16 (9%)	7 (4%)	2	15
3	E	12/14 (86%)	9 (75%)	3 (25%)	0	100	100
3	F	12/14 (86%)	9 (75%)	2 (17%)	1 (8%)	0	4
All	All	743/758 (98%)	644 (87%)	84 (11%)	15 (2%)	6	25

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	107	GLN
1	A	180	PHE
2	D	141	GLY
3	F	2000	GLY
2	D	32	TYR
2	D	121	ASP
1	A	155	PRO
2	B	79	CYS
1	A	17	ASP
2	D	62	ASN
2	D	165	PRO
1	C	173	PRO
1	A	173	PRO
2	D	56	PRO
1	A	136	VAL

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	161/161 (100%)	152 (94%)	9 (6%)	19	49
1	C	160/161 (99%)	154 (96%)	6 (4%)	29	60
2	B	170/171 (99%)	163 (96%)	7 (4%)	27	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	171/171 (100%)	156 (91%)	15 (9%)	9	33
3	E	8/8 (100%)	8 (100%)	0	100	100
3	F	8/8 (100%)	6 (75%)	2 (25%)	0	2
All	All	678/680 (100%)	639 (94%)	39 (6%)	18	48

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LEU
1	A	30	GLU
1	A	36	MET
1	A	71	GLU
1	A	88	GLU
1	A	95	SER
1	A	108	PHE
1	A	155	PRO
1	A	158	ASP
2	B	10	GLN
2	B	23	ARG
2	B	27	LEU
2	B	75	VAL
2	B	92	GLN
2	B	118	SER
2	B	154	THR
1	C	25	ASP
1	C	90	THR
1	C	92	LEU
1	C	106	ILE
1	C	120	THR
1	C	156	SER
2	D	5	PRO
2	D	22	GLU
2	D	23	ARG
2	D	26	LEU
2	D	29	ARG
2	D	34	GLN
2	D	38	VAL
2	D	59	GLU
2	D	66	ASP
2	D	103	PRO
2	D	110	GLN

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Mol	Chain	Res	Type
2	D	154	THR
2	D	163	THR
2	D	169	GLU
2	D	174	GLN
3	F	2001	PHE
3	F	2004	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	33	HIS
1	A	98	ASN
1	A	118	ASN
2	B	10	GLN
2	B	19	ASN
2	B	70	GLN
2	B	134	ASN
2	B	166	GLN
2	B	174	GLN
1	C	15	ASN
1	C	69	ASN
1	C	78	ASN
1	C	167	HIS
2	D	10	GLN
2	D	16	HIS
2	D	19	ASN
2	D	34	GLN
2	D	81	HIS
2	D	107	GLN
2	D	110	GLN
2	D	174	GLN
3	F	2005	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	178/178 (100%)	-0.12	0 100 100	8, 21, 33, 39	0
1	C	177/178 (99%)	0.08	0 100 100	13, 29, 44, 49	0
2	B	186/187 (99%)	0.05	2 (1%) 78 59	9, 24, 37, 48	0
2	D	186/187 (99%)	0.20	3 (1%) 70 49	12, 28, 42, 71	0
3	E	14/14 (100%)	0.34	1 (7%) 22 12	25, 27, 33, 34	0
3	F	14/14 (100%)	1.00	2 (14%) 6 3	35, 42, 45, 45	0
All	All	755/758 (99%)	0.08	8 (1%) 78 59	8, 26, 42, 71	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	110	GLN	9.1
3	F	2001	PHE	4.2
2	D	109	LEU	4.1
2	B	112	HIS	3.2
2	B	106	THR	2.7
3	E	999	ALA	2.3
2	D	9	TRP	2.2
3	F	1999	ALA	2.1

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.