



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:35 PM UTC

PDB ID : 3D7S / pdb_00003d7s
Title : Crystal structure of Wild-Type E. Coli Asparate Transcarbamoylase at pH 8.5
at 2.80 Å Resolution
Authors : Stieglitz, K.A.; Xia, J.; Kantrowitz, E.R.
Deposited on : 2008-05-21
Resolution : 2.80 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

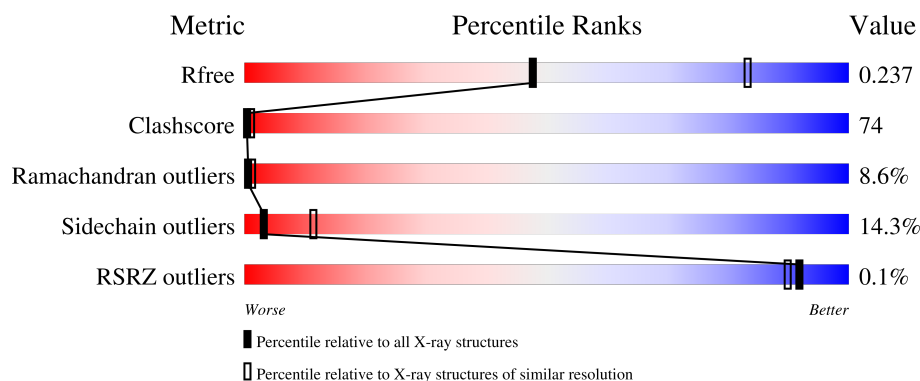
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	310	 26% 61% 11% .
1	C	310	 30% 55% 14% .
2	B	153	 12% 56% 28% .
2	D	153	 17% 54% 24% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7371 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 Aspartate carbamoyltransferase catalytic chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2415	1527	423	456	9			
1	C	310	Total	C	N	O	S	0	0	0
			2415	1527	423	456	9			

- Molecule 2 is a protein called Aspartate carbamoyltransferase regulatory chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	153	Total	C	N	O	S	0	0	0
			1201	752	213	230	6			
2	D	153	Total	C	N	O	S	0	0	0
			1201	752	213	230	6			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		

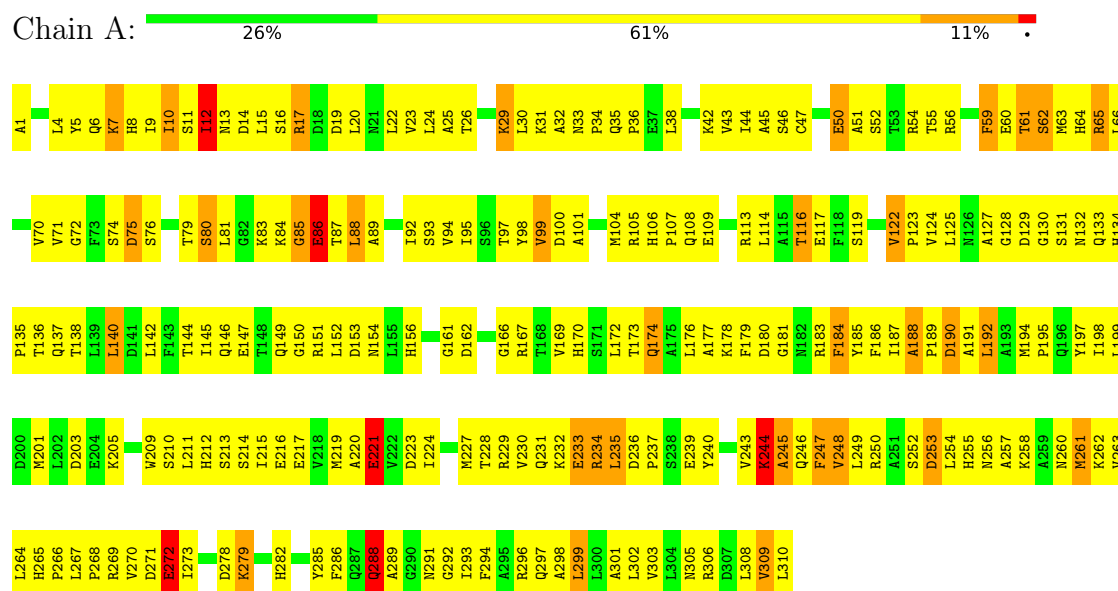
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	32	Total	O	0	0
			32	32		
4	B	28	Total	O	0	0
			28	28		
4	C	40	Total	O	0	0
			40	40		
4	D	37	Total	O	0	0
			37	37		

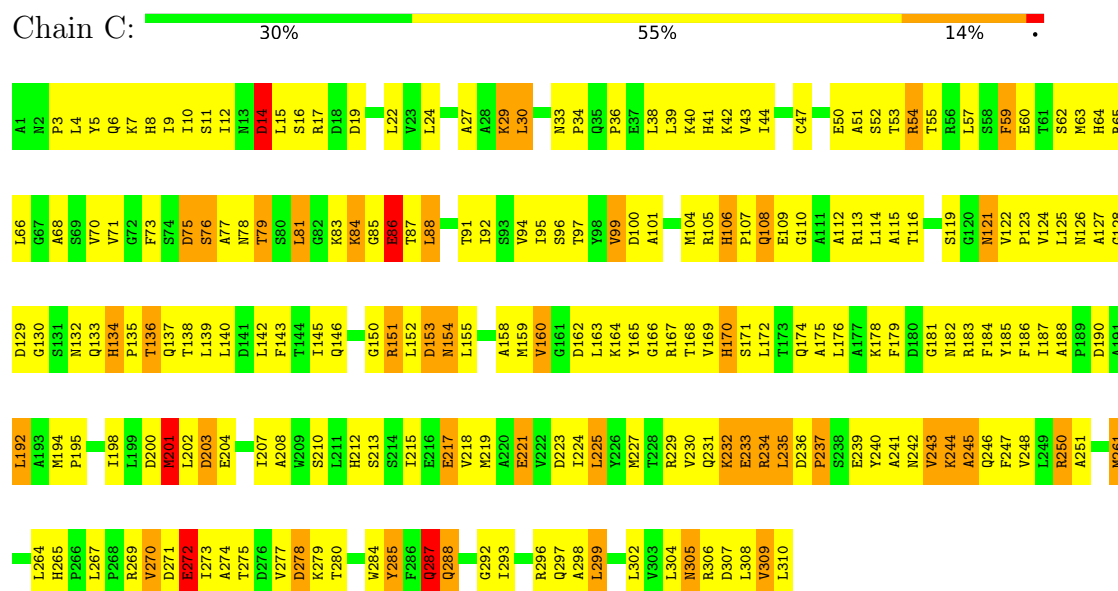
3 Residue-property plots

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.

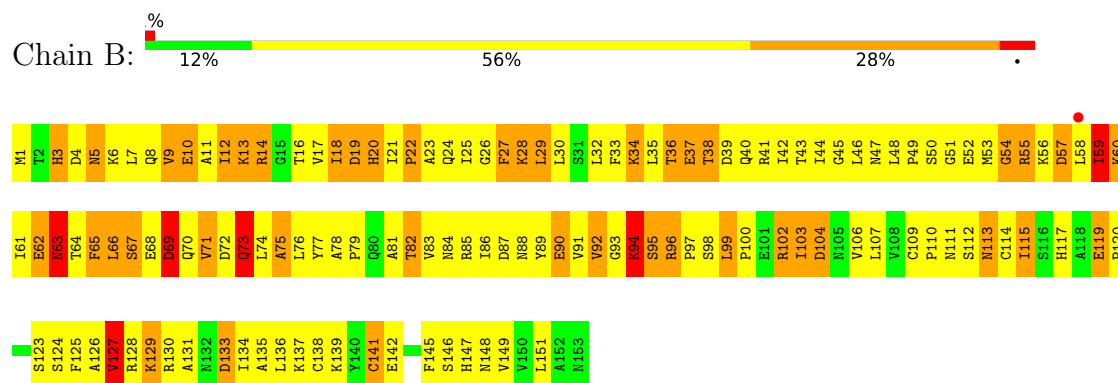
- Molecule 1: Aspartate carbamoyltransferase catalytic chain



- Molecule 1: Aspartate carbamoyltransferase catalytic chain



- Molecule 2: Aspartate carbamoyltransferase regulatory chain



- Molecule 2: Aspartate carbamoyltransferase regulatory chain



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	129.68Å 129.68Å 198.58Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.80 50.00 – 2.81	Depositor EDS
% Data completeness (in resolution range)	86.6 (50.00-2.80) 91.4 (50.00-2.81)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.31 (at 2.81Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.206 , 0.235 0.212 , 0.237	Depositor DCC
R_{free} test set	2828 reflections (10.17%)	wwPDB-VP
Wilson B-factor (Å ²)	66.2	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 88.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.428 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7371	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.91	3/2461 (0.1%)	1.30	25/3339 (0.7%)
1	C	0.90	2/2461 (0.1%)	1.27	26/3339 (0.8%)
2	B	0.69	0/1219	1.17	12/1647 (0.7%)
2	D	0.72	0/1219	1.21	11/1647 (0.7%)
All	All	0.84	5/7360 (0.1%)	1.25	74/9972 (0.7%)

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	2
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	227	MET	SD-CE	6.08	1.94	1.79
1	A	309	VAL	CA-CB	5.64	1.60	1.54
1	C	227	MET	SD-CE	5.50	1.93	1.79
1	A	219	MET	SD-CE	-5.28	1.66	1.79
1	C	201	MET	SD-CE	5.09	1.92	1.79

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	188	ALA	N-CA-C	10.28	117.47	108.22
1	A	10	ILE	N-CA-C	9.41	119.66	111.56

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	280	THR	CA-C-N	-8.48	111.39	120.47
1	C	280	THR	C-N-CA	-8.48	111.39	120.47
1	A	88	LEU	N-CA-C	-8.45	102.01	111.82
2	B	12	ILE	N-CA-C	8.41	120.73	108.53
2	D	18	ILE	N-CA-C	7.97	119.96	108.48
1	A	33	ASN	CA-C-N	7.91	128.37	119.83
1	A	33	ASN	C-N-CA	7.91	128.37	119.83
1	A	247	PHE	N-CA-C	-7.80	100.63	113.50
1	C	79	THR	N-CA-C	-7.70	103.73	113.43
1	A	35	GLN	CA-C-N	7.62	129.37	119.84
1	A	35	GLN	C-N-CA	7.62	129.37	119.84
1	C	287	GLN	N-CA-C	-7.29	103.33	111.28
1	C	106	HIS	CA-C-N	7.25	126.96	119.56
1	C	106	HIS	C-N-CA	7.25	126.96	119.56
2	B	119	GLU	CA-C-N	7.10	128.72	119.84
2	B	119	GLU	C-N-CA	7.10	128.72	119.84
1	C	221	GLU	N-CA-C	7.01	120.71	112.72
1	A	220	ALA	N-CA-C	7.00	119.57	111.02
2	B	129	LYS	N-CA-C	6.99	120.33	109.07
2	D	32	LEU	N-CA-C	6.90	118.81	111.28
1	A	61	THR	N-CA-C	-6.89	103.70	111.07
2	D	89	TYR	N-CA-C	6.87	125.43	110.80
1	C	33	ASN	CA-C-N	6.83	128.38	119.84
1	C	33	ASN	C-N-CA	6.83	128.38	119.84
1	C	51	ALA	N-CA-C	6.76	120.18	110.24
2	B	67	SER	N-CA-C	6.48	119.74	109.50
2	B	27	PHE	N-CA-C	-6.23	104.40	111.07
1	A	174	GLN	N-CA-C	-6.21	103.09	112.04
1	C	122	VAL	CA-C-N	6.16	125.92	119.76
1	C	122	VAL	C-N-CA	6.16	125.92	119.76
2	D	118	ALA	N-CA-C	-6.09	105.61	113.16
2	B	127	VAL	N-CA-C	6.05	117.30	108.53
1	C	190	ASP	N-CA-C	6.01	118.79	111.82
1	A	10	ILE	CB-CA-C	-6.00	105.74	111.44
2	D	99	LEU	N-CA-C	5.99	118.30	109.50
2	D	77	TYR	N-CA-C	5.92	117.40	111.07
1	C	160	VAL	N-CA-C	5.79	116.28	108.17
2	D	101	GLU	N-CA-C	-5.78	105.06	111.36
1	C	81	LEU	N-CA-C	-5.75	105.93	113.17
1	C	152	LEU	N-CA-C	-5.74	104.47	113.02
1	A	180	ASP	N-CA-C	5.72	119.38	110.17
1	C	204	GLU	N-CA-C	5.67	117.13	111.07

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	145	ILE	CB-CA-C	-5.63	104.49	111.70
2	B	119	GLU	N-CA-C	5.63	119.06	110.50
1	A	213	SER	N-CA-C	-5.58	107.02	113.88
1	C	207	ILE	N-CA-C	5.55	115.94	108.17
1	A	192	LEU	N-CA-C	5.54	117.98	110.88
2	B	106	VAL	N-CA-C	5.52	121.51	113.39
1	C	108	GLN	N-CA-C	5.49	118.43	109.59
1	A	184	PHE	N-CA-C	5.40	117.77	109.07
2	D	115	ILE	N-CA-C	5.35	120.47	109.34
1	C	14	ASP	N-CA-C	5.35	118.99	110.70
1	C	30	LEU	N-CA-C	-5.33	105.63	111.82
1	A	94	VAL	N-CA-C	5.32	115.42	110.42
2	B	57	ASP	N-CA-C	-5.32	102.18	110.42
1	C	184	PHE	N-CA-C	5.31	118.72	110.17
1	A	122	VAL	CA-C-N	5.30	125.24	119.78
1	A	122	VAL	C-N-CA	5.30	125.24	119.78
1	C	203	ASP	N-CA-C	-5.29	105.43	111.14
1	C	288	GLN	N-CA-C	-5.23	105.58	111.28
2	B	141	CYS	CA-CB-SG	5.22	126.41	114.40
1	A	303	VAL	N-CA-C	5.21	115.98	110.72
1	A	42	LYS	N-CA-C	-5.17	101.27	109.59
2	D	14	ARG	N-CA-C	5.16	117.50	109.60
2	D	60	LYS	N-CA-C	5.12	116.52	107.61
2	B	82	THR	N-CA-C	5.11	117.57	109.50
2	D	109	CYS	N-CA-C	-5.11	98.53	109.81
1	A	12	ILE	N-CA-C	-5.10	104.71	111.09
1	C	251	ALA	N-CA-C	5.10	117.50	111.33
1	C	139	LEU	N-CA-C	5.08	117.47	111.33
1	A	288	GLN	N-CA-C	-5.06	105.76	111.28
1	A	221	GLU	N-CA-C	5.03	119.37	112.88

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	98	TYR	Sidechain
1	C	185	TYR	Sidechain
1	C	285	TYR	Sidechain

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	2415	0	2422	293	0
1	C	2415	0	2422	294	0
2	B	1201	0	1219	252	0
2	D	1201	0	1219	255	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	A	32	0	0	23	0
4	B	28	0	0	24	0
4	C	40	0	0	40	0
4	D	37	0	0	25	0
All	All	7371	0	7282	1072	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 74.

All (1072) 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)
1:C:136:THR:HB	4:C:332:HOH:O	1.30	1.29
1:C:287:GLN:H	1:C:287:GLN:NE2	1.41	1.19
1:C:287:GLN:HE21	1:C:287:GLN:N	1.44	1.13
1:C:29:LYS:HD2	1:C:310:LEU:HD22	1.30	1.08
2:B:20:HIS:HA	2:B:56:LYS:HD2	1.30	1.06
2:D:126:ALA:O	2:D:136:LEU:HA	1.57	1.05
2:D:15:GLY:HA3	2:D:62:GLU:HA	1.35	1.04
2:B:111:ASN:HB3	2:B:114:CYS:HB2	1.42	1.02
2:B:30:LEU:HA	2:B:35:LEU:HD12	1.38	1.01
1:C:298:ALA:O	1:C:302:LEU:HD12	1.59	0.99
2:D:67:SER:HB3	2:D:70:GLN:HB2	1.41	0.98
1:A:162:ASP:HB2	1:A:230:VAL:HG22	1.47	0.97
1:A:229:ARG:HE	1:A:270:VAL:HB	1.27	0.97
1:C:265:HIS:HD2	1:C:267:LEU:H	1.13	0.97
1:A:79:THR:HG23	1:A:85:GLY:HA3	1.44	0.96
2:D:50:SER:HB3	2:D:56:LYS:HD3	1.46	0.96
2:D:21:ILE:HB	2:D:57:ASP:HB2	1.46	0.96

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:LYS:HB2	1:A:29:LYS:NZ	1.80	0.95
1:C:269:ARG:NH2	4:C:338:HOH:O	1.98	0.95
1:C:29:LYS:HG3	1:C:310:LEU:HD13	1.48	0.95
2:B:146:SER:HB3	2:B:149:VAL:HG23	1.49	0.94
1:A:293:ILE:O	1:A:297:GLN:HB2	1.68	0.93
1:C:9:ILE:HG12	1:C:299:LEU:HD21	1.48	0.92
1:A:229:ARG:HB2	1:A:272:GLU:OE2	1.69	0.92
1:C:250:ARG:HG2	1:C:274:ALA:HB2	1.53	0.91
2:B:62:GLU:HB3	4:B:335:HOH:O	1.71	0.90
2:B:27:PHE:HA	2:B:30:LEU:CD1	2.02	0.90
2:D:13:LYS:HB2	2:D:41:ARG:NH1	1.86	0.89
2:B:100:PRO:HB2	4:B:337:HOH:O	1.70	0.89
2:D:16:THR:OG1	2:D:65:PHE:HA	1.72	0.89
2:B:45:GLY:HA2	2:D:43:THR:HG22	1.56	0.88
1:C:198:ILE:O	1:C:202:LEU:HD13	1.73	0.88
1:A:76:SER:HA	4:A:331:HOH:O	1.74	0.87
1:C:126:ASN:ND2	1:C:128:GLY:H	1.72	0.87
1:C:187:ILE:HG13	1:C:212:HIS:HB2	1.55	0.87
1:A:156:HIS:HB3	1:A:185:TYR:HE1	1.39	0.87
1:C:43:VAL:HG12	1:C:99:VAL:HG12	1.57	0.87
2:D:66:LEU:CD1	2:D:71:VAL:HG22	2.04	0.87
1:A:12:ILE:HD13	1:A:135:PRO:HA	1.57	0.86
1:C:269:ARG:NH2	1:C:278:ASP:OD2	2.08	0.86
2:B:41:ARG:HH22	2:D:49:PRO:HD2	1.39	0.86
2:B:42:ILE:HG13	2:B:61:ILE:HA	1.58	0.85
2:D:67:SER:HB3	2:D:70:GLN:CB	2.06	0.85
1:C:29:LYS:CG	1:C:310:LEU:HD13	2.06	0.85
1:A:243:VAL:C	1:A:245:ALA:H	1.85	0.84
2:B:59:ILE:O	2:B:60:LYS:HG3	1.77	0.84
2:D:7:LEU:HD22	2:D:8:GLN:H	1.42	0.84
1:C:136:THR:OG1	1:C:296:ARG:NH1	2.11	0.84
2:B:16:THR:HG22	2:B:85:ARG:HA	1.58	0.83
2:D:70:GLN:O	2:D:74:LEU:HG	1.79	0.83
1:C:162:ASP:HA	4:C:350:HOH:O	1.80	0.82
1:A:258:LYS:HZ2	1:A:260:ASN:HD21	1.25	0.81
1:C:84:LYS:HE2	1:C:84:LYS:C	2.06	0.81
2:B:129:LYS:HD2	2:B:130:ARG:O	1.81	0.81
1:C:240:TYR:CE1	1:C:244:LYS:HB2	2.14	0.81
2:D:7:LEU:HD22	2:D:9:VAL:H	1.45	0.81
2:B:134:ILE:HB	2:B:147:HIS:HB3	1.61	0.81
1:A:258:LYS:NZ	1:A:260:ASN:HD21	1.79	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:LEU:HD12	1:C:261:MET:HE1	1.62	0.81
1:A:305:ASN:HD22	1:A:308:LEU:HD23	1.46	0.80
1:C:229:ARG:HA	1:C:272:GLU:HG2	1.61	0.80
1:C:269:ARG:CZ	4:C:338:HOH:O	2.29	0.80
2:D:130:ARG:NH2	2:D:132:ASN:HB2	1.96	0.80
1:A:229:ARG:NH1	1:A:231:GLN:HA	1.97	0.79
1:C:155:LEU:O	1:C:182:ASN:HA	1.83	0.79
1:C:304:LEU:HA	4:C:340:HOH:O	1.80	0.79
1:A:229:ARG:NE	1:A:270:VAL:HB	1.98	0.79
2:D:12:ILE:HG22	2:D:13:LYS:H	1.47	0.79
2:B:70:GLN:CD	2:B:70:GLN:H	1.90	0.79
1:A:50:GLU:HG3	1:A:107:PRO:HB3	1.62	0.78
1:A:173:THR:C	4:A:336:HOH:O	2.26	0.78
2:D:41:ARG:NE	2:D:62:GLU:HB2	1.97	0.78
2:B:50:SER:HB2	2:B:56:LYS:CE	2.13	0.78
1:C:12:ILE:HA	4:C:328:HOH:O	1.83	0.78
1:A:265:HIS:CD2	1:A:267:LEU:H	2.01	0.78
1:C:183:ARG:HH11	1:C:183:ARG:HG2	1.48	0.78
2:D:41:ARG:O	2:D:41:ARG:HG3	1.84	0.78
2:D:84:ASN:OD1	2:D:91:VAL:HG13	1.82	0.77
1:C:38:LEU:HB3	4:C:335:HOH:O	1.83	0.77
1:C:265:HIS:CD2	1:C:267:LEU:H	2.02	0.77
2:D:16:THR:HG23	2:D:85:ARG:HG3	1.64	0.77
2:D:122:SER:HB3	4:D:348:HOH:O	1.84	0.77
2:D:52:GLU:HG3	4:D:332:HOH:O	1.84	0.77
1:A:229:ARG:HE	1:A:270:VAL:CB	1.97	0.77
2:B:99:LEU:CD2	2:B:127:VAL:HG11	2.14	0.77
1:C:151:ARG:HG3	1:C:151:ARG:HH11	1.50	0.77
2:D:84:ASN:HA	2:D:93:GLY:O	1.84	0.77
1:A:154:ASN:HA	1:A:181:GLY:O	1.83	0.77
2:B:66:LEU:HD12	2:B:71:VAL:HG23	1.65	0.76
2:B:126:ALA:O	2:B:136:LEU:HA	1.85	0.76
2:D:7:LEU:CD2	2:D:8:GLN:H	1.99	0.76
1:C:234:ARG:CG	1:C:234:ARG:HH11	1.99	0.76
1:A:235:LEU:HD13	1:A:240:TYR:HD2	1.51	0.76
2:B:133:ASP:C	2:B:134:ILE:HD12	2.11	0.76
1:A:29:LYS:HB2	1:A:29:LYS:HZ3	1.48	0.76
2:D:66:LEU:HD11	2:D:71:VAL:HG22	1.66	0.75
2:D:41:ARG:HE	2:D:62:GLU:HB2	1.51	0.75
2:B:82:THR:HG21	2:B:94:LYS:NZ	2.01	0.75
2:B:14:ARG:HA	4:B:325:HOH:O	1.84	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:18:ILE:HG13	4:B:329:HOH:O	1.87	0.75
1:C:12:ILE:HD12	1:C:15:LEU:HD12	1.68	0.75
2:D:67:SER:C	2:D:69:ASP:H	1.91	0.75
1:A:244:LYS:NZ	1:A:247:PHE:HB2	2.01	0.74
2:B:28:LYS:O	2:B:32:LEU:HD13	1.87	0.74
1:C:234:ARG:HH11	1:C:234:ARG:HG3	1.52	0.74
2:B:9:VAL:CG2	2:B:48:LEU:HD21	2.16	0.74
1:C:210:SER:N	4:C:333:HOH:O	2.20	0.74
2:B:70:GLN:HB2	4:B:327:HOH:O	1.88	0.74
1:C:50:GLU:HB2	1:C:107:PRO:HG3	1.69	0.74
1:C:308:LEU:HD23	1:C:309:VAL:N	2.03	0.74
1:C:192:LEU:HB3	4:C:350:HOH:O	1.87	0.74
1:A:302:LEU:HD23	1:A:308:LEU:HD12	1.68	0.74
1:C:229:ARG:HA	1:C:272:GLU:CG	2.18	0.74
1:C:231:GLN:HB3	1:C:233:GLU:OE2	1.87	0.74
2:D:106:VAL:HG23	2:D:107:LEU:HG	1.70	0.74
2:B:42:ILE:CG1	2:B:61:ILE:HA	2.18	0.73
1:A:187:ILE:HG12	1:A:212:HIS:HB2	1.71	0.73
2:B:20:HIS:HA	2:B:56:LYS:CD	2.13	0.73
1:C:159:MET:HE1	1:C:172:LEU:HD23	1.69	0.73
2:B:26:GLY:HA2	2:B:29:LEU:HG	1.71	0.73
2:D:67:SER:O	2:D:69:ASP:N	2.20	0.73
2:B:21:ILE:HG23	2:B:78:ALA:HB2	1.71	0.73
2:D:19:ASP:HA	2:D:58:LEU:CD2	2.19	0.73
1:A:65:ARG:HG3	1:A:65:ARG:HH11	1.53	0.73
1:C:163:LEU:CD2	1:C:186:PHE:HB3	2.18	0.73
1:C:183:ARG:HG3	1:C:208:ALA:HB1	1.71	0.73
2:B:14:ARG:HB3	2:B:88:ASN:OD1	1.89	0.72
2:B:66:LEU:HA	4:B:332:HOH:O	1.89	0.72
1:C:292:GLY:O	1:C:296:ARG:HG3	1.89	0.72
1:A:31:LYS:HE3	1:A:294:PHE:CE1	2.25	0.72
1:A:50:GLU:HB2	1:A:107:PRO:HD3	1.72	0.72
1:A:44:ILE:HD12	1:A:101:ALA:HB3	1.72	0.72
1:A:156:HIS:HB3	1:A:185:TYR:CE1	2.22	0.72
2:B:99:LEU:HD21	2:B:127:VAL:HG11	1.70	0.72
1:C:75:ASP:OD1	1:C:79:THR:HB	1.90	0.72
2:D:73:GLN:HE22	2:D:103:ILE:HA	1.54	0.72
1:C:113:ARG:O	1:C:116:THR:HB	1.90	0.71
2:D:109:CYS:N	2:D:125:PHE:HZ	1.89	0.71
1:A:150:GLY:HA2	4:A:323:HOH:O	1.89	0.71
2:D:66:LEU:HD22	2:D:67:SER:H	1.56	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:ASP:HB3	1:A:239:GLU:HB3	1.72	0.71
1:C:8:HIS:C	1:C:9:ILE:HD12	2.16	0.71
1:A:265:HIS:HD2	1:A:267:LEU:H	1.37	0.71
1:A:79:THR:O	1:A:80:SER:HB2	1.90	0.71
2:B:18:ILE:CD1	2:B:58:LEU:HD12	2.19	0.71
2:B:96:ARG:HB3	2:B:96:ARG:NH2	2.06	0.71
1:C:187:ILE:HB	4:C:326:HOH:O	1.91	0.71
1:C:188:ALA:HA	4:C:339:HOH:O	1.91	0.71
1:A:79:THR:HG23	1:A:85:GLY:CA	2.20	0.71
2:D:20:HIS:HE1	2:D:52:GLU:HG3	1.55	0.71
2:D:95:SER:O	2:D:96:ARG:HD2	1.91	0.71
2:B:18:ILE:HD12	2:B:58:LEU:HD12	1.72	0.70
2:D:130:ARG:NH2	2:D:132:ASN:HD22	1.89	0.70
1:A:162:ASP:CB	1:A:230:VAL:HG22	2.21	0.70
1:C:175:ALA:O	1:C:178:LYS:HB2	1.92	0.70
1:A:9:ILE:C	1:A:10:ILE:HD12	2.16	0.70
1:A:258:LYS:HZ3	1:A:258:LYS:HB3	1.56	0.69
1:A:223:ASP:O	1:A:261:MET:HA	1.92	0.69
1:A:305:ASN:ND2	1:A:308:LEU:HD23	2.06	0.69
2:B:17:VAL:HG12	2:B:61:ILE:H	1.57	0.69
2:D:100:PRO:HG2	2:D:103:ILE:HD11	1.73	0.69
2:B:43:THR:C	2:B:44:ILE:HD12	2.17	0.69
2:B:86:ILE:HA	2:B:90:GLU:O	1.92	0.69
2:B:36:THR:O	2:B:38:THR:N	2.24	0.69
1:A:60:GLU:O	1:A:63:MET:HB2	1.92	0.69
1:C:232:LYS:HD3	1:C:232:LYS:H	1.55	0.69
1:A:83:LYS:CG	1:A:84:LYS:H	2.05	0.69
1:A:256:ASN:N	4:A:339:HOH:O	2.26	0.69
2:B:20:HIS:CA	2:B:56:LYS:HD2	2.18	0.69
1:A:240:TYR:CE1	1:A:244:LYS:HD2	2.27	0.69
1:A:29:LYS:HB2	1:A:29:LYS:HZ2	1.58	0.69
2:B:50:SER:C	2:B:52:GLU:H	1.98	0.69
2:D:46:LEU:HG	4:D:323:HOH:O	1.92	0.69
2:D:73:GLN:NE2	2:D:103:ILE:HA	2.07	0.68
1:A:114:LEU:C	1:A:114:LEU:HD23	2.18	0.68
1:C:76:SER:HB2	4:C:334:HOH:O	1.91	0.68
1:A:248:VAL:HB	1:A:272:GLU:HA	1.74	0.68
1:C:163:LEU:HD21	1:C:186:PHE:HB3	1.75	0.68
2:D:19:ASP:HA	2:D:58:LEU:HD22	1.75	0.68
2:B:99:LEU:HD23	2:B:100:PRO:HD2	1.74	0.68
2:B:27:PHE:HE1	2:D:27:PHE:HE1	1.39	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:29:LYS:HD2	1:C:310:LEU:CD2	2.17	0.68
1:A:113:ARG:O	1:A:116:THR:HG22	1.94	0.68
2:B:61:ILE:HG21	2:B:64:THR:HB	1.76	0.68
1:A:31:LYS:NZ	1:A:291:ASN:OD1	2.23	0.68
1:A:244:LYS:HZ2	1:A:247:PHE:HB2	1.58	0.68
2:D:136:LEU:HD12	2:D:136:LEU:O	1.93	0.68
2:D:14:ARG:HD2	2:D:88:ASN:HA	1.75	0.68
2:D:100:PRO:HG2	2:D:103:ILE:CD1	2.23	0.68
1:A:4:LEU:HA	1:A:7:LYS:HG3	1.75	0.67
2:B:10:GLU:HB2	2:B:60:LYS:NZ	2.10	0.67
1:C:308:LEU:HD23	1:C:310:LEU:H	1.60	0.67
1:A:44:ILE:HG23	1:A:101:ALA:HB3	1.76	0.67
2:B:124:SER:HB3	2:B:139:LYS:HD3	1.75	0.67
1:C:88:LEU:HD22	1:C:92:ILE:HG12	1.77	0.67
1:A:235:LEU:N	1:A:235:LEU:HD12	2.09	0.67
1:A:244:LYS:HG3	1:A:244:LYS:O	1.94	0.67
2:B:146:SER:HB3	2:B:149:VAL:CG2	2.23	0.67
2:D:53:MET:HG2	4:D:330:HOH:O	1.94	0.67
1:A:245:ALA:HB3	1:A:247:PHE:HE1	1.59	0.67
1:C:110:GLY:HA2	2:D:140:TYR:O	1.95	0.67
2:B:36:THR:C	2:B:38:THR:H	2.02	0.66
1:A:250:ARG:NH1	1:A:252:SER:HB3	2.11	0.66
2:B:12:ILE:HG12	2:D:8:GLN:HG3	1.77	0.66
1:A:83:LYS:HG2	1:A:84:LYS:N	2.10	0.66
1:A:128:GLY:HA2	1:A:133:GLN:O	1.95	0.66
1:A:61:THR:C	1:A:63:MET:H	2.03	0.66
1:A:132:ASN:ND2	1:A:133:GLN:HG2	2.09	0.66
1:C:235:LEU:HB3	1:C:239:GLU:CD	2.20	0.66
2:D:111:ASN:HB3	2:D:114:CYS:HB2	1.78	0.66
1:A:11:SER:HA	1:A:133:GLN:HG3	1.76	0.66
1:C:63:MET:HA	4:C:316:HOH:O	1.96	0.66
1:A:51:ALA:HB2	1:A:75:ASP:H	1.59	0.66
1:A:132:ASN:HD22	1:A:132:ASN:C	2.04	0.66
2:B:66:LEU:CD1	2:B:71:VAL:HG23	2.25	0.66
1:C:296:ARG:HG2	4:C:332:HOH:O	1.95	0.66
1:A:232:LYS:O	1:A:235:LEU:HD12	1.96	0.66
1:C:250:ARG:HG2	1:C:274:ALA:CB	2.25	0.66
1:C:181:GLY:O	1:C:182:ASN:HB2	1.97	0.65
2:D:72:ASP:C	2:D:74:LEU:H	2.04	0.65
2:D:134:ILE:O	2:D:146:SER:HA	1.96	0.65
2:D:71:VAL:HA	2:D:74:LEU:HD12	1.78	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:147:HIS:O	2:B:151:LEU:HD13	1.96	0.65
1:C:243:VAL:O	1:C:246:GLN:HB3	1.97	0.65
2:D:40:GLN:O	2:D:42:ILE:HG13	1.96	0.65
2:D:66:LEU:HD13	2:D:67:SER:O	1.97	0.65
1:C:71:VAL:N	4:C:342:HOH:O	2.29	0.65
1:A:235:LEU:HD13	1:A:240:TYR:CD2	2.32	0.65
1:A:243:VAL:C	1:A:245:ALA:N	2.55	0.65
2:B:6:LYS:HE2	2:B:48:LEU:CD2	2.26	0.65
1:C:92:ILE:O	1:C:96:SER:HB2	1.96	0.65
2:D:76:LEU:HD23	2:D:77:TYR:N	2.12	0.65
2:D:124:SER:HB3	2:D:139:LYS:HE3	1.77	0.65
1:C:159:MET:CE	1:C:172:LEU:HD23	2.27	0.65
1:C:270:VAL:HG11	4:C:343:HOH:O	1.96	0.65
1:C:14:ASP:O	1:C:15:LEU:HD23	1.96	0.64
2:D:19:ASP:O	2:D:81:ALA:HB1	1.96	0.64
2:D:75:ALA:O	2:D:77:TYR:N	2.30	0.64
2:D:108:VAL:HG23	2:D:108:VAL:O	1.98	0.64
2:D:129:LYS:HG2	2:D:130:ARG:N	2.12	0.64
1:A:79:THR:O	1:A:79:THR:HG22	1.95	0.64
1:A:267:LEU:HB3	1:A:268:PRO:HA	1.78	0.64
2:B:66:LEU:HD13	2:B:67:SER:N	2.12	0.64
1:A:279:LYS:HA	1:A:279:LYS:HE2	1.79	0.64
2:B:1:MET:HB2	4:B:318:HOH:O	1.95	0.64
1:C:60:GLU:HA	1:C:63:MET:HE3	1.80	0.64
2:D:41:ARG:O	2:D:61:ILE:HA	1.97	0.64
2:B:41:ARG:C	2:B:42:ILE:HD12	2.22	0.64
1:C:15:LEU:O	1:C:178:LYS:NZ	2.29	0.64
1:C:124:VAL:C	1:C:125:LEU:HD12	2.23	0.64
1:A:83:LYS:HG2	1:A:84:LYS:H	1.61	0.64
1:A:93:SER:O	1:A:97:THR:HG23	1.97	0.64
1:C:269:ARG:O	1:C:270:VAL:HB	1.96	0.64
2:D:115:ILE:HG23	2:D:116:SER:N	2.13	0.64
2:D:136:LEU:HD11	2:D:150:VAL:HG21	1.80	0.64
2:B:66:LEU:HD13	2:B:67:SER:H	1.61	0.64
1:C:16:SER:O	1:C:19:ASP:HB2	1.99	0.63
1:A:258:LYS:NZ	1:A:258:LYS:HB3	2.13	0.63
1:A:244:LYS:HE2	1:A:244:LYS:HA	1.81	0.63
1:C:43:VAL:HG12	1:C:99:VAL:CG1	2.27	0.63
1:C:47:CYS:O	1:C:104:MET:HA	1.98	0.63
1:C:244:LYS:O	1:C:246:GLN:N	2.26	0.63
1:A:8:HIS:HA	4:A:337:HOH:O	1.99	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:9:ILE:HG12	1:C:299:LEU:CD2	2.26	0.63
1:C:109:GLU:O	2:D:115:ILE:HB	1.97	0.63
1:A:174:GLN:O	1:A:177:ALA:HB3	1.99	0.63
2:D:18:ILE:HD12	2:D:59:ILE:HB	1.81	0.63
2:B:42:ILE:HG23	2:B:60:LYS:O	1.99	0.63
2:D:17:VAL:HG13	2:D:59:ILE:O	1.99	0.63
2:B:103:ILE:HG23	2:B:103:ILE:O	1.99	0.62
2:D:15:GLY:CA	2:D:62:GLU:HA	2.23	0.62
2:D:20:HIS:H	2:D:58:LEU:CD2	2.12	0.62
2:B:96:ARG:HD2	4:B:321:HOH:O	1.99	0.62
1:C:265:HIS:HD2	1:C:267:LEU:N	1.91	0.62
2:D:87:ASP:H	2:D:92:VAL:CG1	2.12	0.62
2:B:84:ASN:HA	2:B:94:LYS:HA	1.81	0.62
2:D:72:ASP:HA	4:D:322:HOH:O	1.99	0.62
1:A:1:ALA:HA	1:A:306:ARG:HB2	1.81	0.62
1:A:302:LEU:HD23	1:A:308:LEU:CD1	2.29	0.62
2:B:50:SER:C	2:B:52:GLU:N	2.57	0.62
1:C:250:ARG:CB	1:C:250:ARG:HH11	2.13	0.62
2:D:72:ASP:O	2:D:74:LEU:N	2.31	0.62
2:B:50:SER:OG	2:B:51:GLY:N	2.33	0.62
2:B:82:THR:CG2	2:B:94:LYS:HZ2	2.13	0.62
1:A:10:ILE:HD12	1:A:10:ILE:N	2.15	0.62
1:A:5:TYR:CE2	1:A:6:GLN:HG2	2.34	0.62
2:B:129:LYS:HD2	2:B:130:ARG:N	2.14	0.62
1:C:40:LYS:HG3	1:C:41:HIS:CD2	2.35	0.61
1:C:137:GLN:O	1:C:140:LEU:HG	2.00	0.61
1:A:85:GLY:O	1:A:86:GLU:HB3	2.00	0.61
1:A:229:ARG:HH11	1:A:231:GLN:HA	1.63	0.61
2:B:27:PHE:HA	2:B:30:LEU:HD13	1.81	0.61
1:C:62:SER:HB2	1:C:297:GLN:HA	1.82	0.61
2:B:126:ALA:O	2:B:136:LEU:HD23	2.01	0.61
2:D:20:HIS:CE1	2:D:52:GLU:HG3	2.35	0.61
2:B:109:CYS:SG	2:B:111:ASN:HB3	2.40	0.61
2:D:66:LEU:HD11	2:D:71:VAL:N	2.14	0.61
1:A:13:ASN:O	1:A:15:LEU:N	2.33	0.61
1:C:105:ARG:NH1	1:C:127:ALA:O	2.33	0.61
1:A:44:ILE:HB	4:A:320:HOH:O	2.00	0.61
1:C:112:ALA:CB	1:C:126:ASN:HB2	2.31	0.61
1:A:43:VAL:C	1:A:44:ILE:HD13	2.25	0.61
2:B:50:SER:HB2	2:B:56:LYS:NZ	2.16	0.61
1:A:184:PHE:O	1:A:209:TRP:HA	2.01	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:53:THR:HG23	1:C:54:ARG:H	1.66	0.61
1:C:142:LEU:O	1:C:143:PHE:C	2.44	0.61
1:A:13:ASN:C	1:A:15:LEU:H	2.09	0.60
2:B:75:ALA:O	2:B:77:TYR:N	2.34	0.60
2:B:85:ARG:O	2:B:92:VAL:HG12	2.01	0.60
1:C:5:TYR:CD1	1:C:306:ARG:HA	2.36	0.60
2:D:76:LEU:HD23	2:D:76:LEU:C	2.25	0.60
2:D:113:ASN:O	2:D:115:ILE:N	2.34	0.60
1:A:244:LYS:HA	1:A:244:LYS:CE	2.31	0.60
2:B:27:PHE:HA	2:B:30:LEU:HD12	1.82	0.60
1:C:167:ARG:HG3	1:C:168:THR:N	2.16	0.60
1:C:272:GLU:CD	1:C:272:GLU:H	2.09	0.60
2:B:18:ILE:HA	2:B:82:THR:O	2.01	0.60
2:B:30:LEU:HA	2:B:35:LEU:CD1	2.21	0.60
2:B:86:ILE:CG2	2:B:90:GLU:H	2.13	0.60
2:D:8:GLN:HG2	2:D:9:VAL:HG13	1.83	0.60
2:D:66:LEU:HD12	2:D:71:VAL:HG22	1.83	0.60
1:C:239:GLU:O	1:C:243:VAL:HG22	2.02	0.60
1:C:245:ALA:HA	1:C:248:VAL:CG1	2.32	0.60
2:B:134:ILE:HD12	2:B:134:ILE:N	2.15	0.60
1:A:269:ARG:NH2	1:A:278:ASP:OD2	2.35	0.60
2:D:72:ASP:C	2:D:100:PRO:HG3	2.26	0.60
1:A:187:ILE:CD1	1:A:215:ILE:HA	2.32	0.60
2:B:25:ILE:HG22	2:B:25:ILE:O	2.01	0.60
2:D:111:ASN:CB	4:D:345:HOH:O	2.50	0.60
2:B:43:THR:O	2:B:60:LYS:HB2	2.02	0.59
1:C:106:HIS:ND1	1:C:107:PRO:HD2	2.17	0.59
2:B:86:ILE:HG22	2:B:90:GLU:H	1.66	0.59
2:D:91:VAL:N	4:D:341:HOH:O	2.36	0.59
2:D:113:ASN:C	4:D:346:HOH:O	2.45	0.59
1:C:187:ILE:N	1:C:187:ILE:HD12	2.17	0.59
2:B:10:GLU:HB2	2:B:60:LYS:HZ1	1.67	0.59
2:B:27:PHE:CE1	2:D:27:PHE:HE1	2.21	0.59
1:A:23:VAL:O	1:A:26:THR:HB	2.02	0.59
1:C:261:MET:HG3	4:C:351:HOH:O	2.01	0.59
2:D:56:LYS:HE2	2:D:58:LEU:HD21	1.84	0.59
1:C:10:ILE:HD12	1:C:112:ALA:HB1	1.84	0.59
2:D:13:LYS:HB2	2:D:41:ARG:HH12	1.66	0.59
1:A:134:HIS:CD2	1:A:137:GLN:HB2	2.38	0.59
2:B:21:ILE:H	2:B:56:LYS:HB2	1.68	0.59
2:B:99:LEU:HD22	2:B:127:VAL:HG11	1.85	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:53:THR:HG23	1:C:54:ARG:N	2.18	0.59
1:C:236:ASP:OD1	1:C:239:GLU:HB2	2.02	0.59
1:A:124:VAL:C	1:A:125:LEU:HD12	2.28	0.59
2:B:14:ARG:HA	2:B:88:ASN:H	1.67	0.59
2:B:115:ILE:HG13	2:B:115:ILE:O	2.02	0.59
2:D:65:PHE:CE1	2:D:85:ARG:HB3	2.38	0.59
1:C:167:ARG:O	1:C:168:THR:C	2.45	0.59
2:D:102:ARG:HH22	2:D:139:LYS:HE2	1.68	0.59
1:A:216:GLU:HG3	1:A:217:GLU:H	1.67	0.58
1:C:44:ILE:HG23	1:C:101:ALA:HB3	1.84	0.58
1:C:137:GLN:OE1	1:C:140:LEU:HD11	2.03	0.58
2:B:14:ARG:HG3	2:B:63:ASN:OD1	2.04	0.58
1:C:134:HIS:CD2	1:C:137:GLN:HB2	2.38	0.58
2:D:113:ASN:HB3	4:D:346:HOH:O	2.03	0.58
1:A:70:VAL:HG13	4:A:320:HOH:O	2.03	0.58
2:B:9:VAL:HG22	2:B:48:LEU:HD21	1.84	0.58
1:C:167:ARG:HG3	1:C:168:THR:H	1.69	0.58
1:C:244:LYS:HG2	1:C:245:ALA:N	2.16	0.58
1:C:245:ALA:HB1	4:C:346:HOH:O	2.04	0.58
2:D:12:ILE:HD12	4:D:339:HOH:O	2.02	0.58
2:D:66:LEU:HD21	2:D:74:LEU:HD11	1.86	0.58
2:B:50:SER:HB2	2:B:56:LYS:HE2	1.86	0.58
1:C:30:LEU:HD13	1:C:297:GLN:HG2	1.83	0.58
1:C:44:ILE:HD12	1:C:63:MET:HG2	1.85	0.58
1:C:284:TRP:HA	1:C:287:GLN:NE2	2.18	0.58
1:A:216:GLU:HG3	1:A:217:GLU:N	2.17	0.58
2:B:35:LEU:HB2	4:B:328:HOH:O	2.02	0.58
1:C:29:LYS:CD	1:C:310:LEU:HD22	2.19	0.58
1:A:221:GLU:C	1:A:258:LYS:HD2	2.28	0.58
2:B:69:ASP:O	2:B:73:GLN:HG2	2.03	0.58
1:C:293:ILE:O	1:C:297:GLN:HB3	2.04	0.58
1:C:232:LYS:H	1:C:232:LYS:CD	2.16	0.58
1:C:163:LEU:HD13	1:C:188:ALA:HB2	1.86	0.57
1:C:225:LEU:HD12	1:C:261:MET:CE	2.33	0.57
2:D:14:ARG:O	2:D:41:ARG:NH2	2.37	0.57
2:B:26:GLY:CA	2:B:29:LEU:HG	2.34	0.57
2:B:68:GLU:O	2:B:71:VAL:HB	2.03	0.57
1:C:96:SER:OG	1:C:119:SER:HA	2.04	0.57
2:B:42:ILE:O	2:D:45:GLY:HA2	2.04	0.57
1:C:85:GLY:O	1:C:86:GLU:HB2	2.02	0.57
2:D:57:ASP:HB3	4:D:323:HOH:O	2.03	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:SER:O	1:A:75:ASP:O	2.22	0.57
2:B:68:GLU:C	2:B:71:VAL:HB	2.29	0.57
2:D:20:HIS:HE1	4:D:332:HOH:O	1.87	0.57
2:B:47:ASN:ND2	2:D:40:GLN:O	2.37	0.57
1:C:108:GLN:HB3	4:D:346:HOH:O	2.03	0.57
1:C:114:LEU:HD23	1:C:115:ALA:N	2.20	0.57
1:A:244:LYS:O	1:A:245:ALA:O	2.22	0.57
1:A:298:ALA:O	1:A:302:LEU:HG	2.04	0.57
1:A:308:LEU:HD22	1:A:310:LEU:HD11	1.86	0.57
1:C:70:VAL:HA	4:C:342:HOH:O	2.05	0.57
2:B:49:PRO:HG3	4:B:338:HOH:O	2.05	0.57
1:C:52:SER:O	1:C:55:THR:N	2.38	0.57
1:A:176:LEU:N	4:A:336:HOH:O	2.37	0.57
2:B:69:ASP:C	2:B:71:VAL:N	2.59	0.57
2:B:72:ASP:HB2	2:B:73:GLN:NE2	2.19	0.57
2:D:54:GLY:C	2:D:55:ARG:HD2	2.30	0.57
1:A:123:PRO:HA	4:A:337:HOH:O	2.03	0.56
2:D:58:LEU:O	2:D:59:ILE:HD13	2.04	0.56
2:D:110:PRO:HG2	2:D:145:PHE:CE2	2.40	0.56
1:A:29:LYS:HG2	1:A:310:LEU:OXT	2.05	0.56
1:A:129:ASP:OD1	1:A:132:ASN:HB3	2.05	0.56
1:C:160:VAL:HG22	4:C:326:HOH:O	2.05	0.56
2:D:23:ALA:O	2:D:25:ILE:HD13	2.04	0.56
2:D:26:GLY:O	2:D:29:LEU:HD12	2.05	0.56
1:A:199:LEU:HD13	1:A:209:TRP:CH2	2.40	0.56
2:B:27:PHE:HE1	2:D:27:PHE:CE1	2.22	0.56
2:D:44:ILE:HD13	2:D:44:ILE:N	2.21	0.56
2:D:66:LEU:HD11	2:D:71:VAL:H	1.71	0.56
1:A:149:GLN:HE21	1:A:224:ILE:HD11	1.69	0.56
1:A:235:LEU:CD1	1:A:240:TYR:HD2	2.17	0.56
1:C:54:ARG:HG2	1:C:54:ARG:HH11	1.69	0.56
1:A:109:GLU:OE2	1:A:130:GLY:HA3	2.06	0.56
1:A:151:ARG:HD2	1:A:153:ASP:OD1	2.06	0.56
2:B:93:GLY:O	2:B:94:LYS:HB3	2.06	0.56
1:C:91:THR:HG22	1:C:95:ILE:HD12	1.88	0.56
1:C:163:LEU:O	1:C:170:HIS:HE1	1.88	0.56
2:D:44:ILE:HA	4:D:338:HOH:O	2.06	0.56
1:A:109:GLU:CD	1:A:109:GLU:H	2.14	0.56
1:A:305:ASN:HD22	1:A:308:LEU:CD2	2.16	0.56
1:A:17:ARG:NH1	1:A:179:PHE:CD2	2.74	0.56
1:A:253:ASP:O	1:A:254:LEU:HD23	2.05	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:ARG:HD2	1:C:178:LYS:O	2.06	0.56
1:C:36:PRO:HA	1:C:65:ARG:O	2.05	0.56
1:C:169:VAL:O	1:C:170:HIS:C	2.46	0.56
1:A:12:ILE:CD1	1:A:135:PRO:HA	2.34	0.55
1:C:151:ARG:HH11	1:C:151:ARG:CG	2.19	0.55
1:C:244:LYS:CG	1:C:245:ALA:N	2.68	0.55
2:D:18:ILE:HD12	2:D:59:ILE:CB	2.36	0.55
2:D:102:ARG:CZ	2:D:124:SER:OG	2.54	0.55
1:A:51:ALA:HB2	1:A:75:ASP:N	2.21	0.55
2:D:35:LEU:O	2:D:36:THR:HG23	2.06	0.55
2:D:87:ASP:H	2:D:92:VAL:HG11	1.71	0.55
2:D:130:ARG:NH2	2:D:132:ASN:ND2	2.54	0.55
2:B:59:ILE:O	2:B:60:LYS:CG	2.54	0.55
1:C:114:LEU:HD23	1:C:114:LEU:C	2.31	0.55
1:C:284:TRP:CD1	1:C:287:GLN:HB2	2.41	0.55
2:B:42:ILE:HG12	2:B:61:ILE:HG13	1.88	0.55
2:B:82:THR:HG21	2:B:94:LYS:HZ1	1.71	0.55
2:B:130:ARG:O	2:B:131:ALA:C	2.48	0.55
1:C:234:ARG:CG	1:C:234:ARG:NH1	2.63	0.55
1:A:221:GLU:HA	1:A:258:LYS:HD2	1.89	0.55
1:C:270:VAL:HG13	1:C:271:ASP:N	2.20	0.55
2:D:4:ASP:N	2:D:4:ASP:OD2	2.39	0.55
2:D:50:SER:HB3	2:D:56:LYS:CD	2.31	0.55
2:D:66:LEU:HD13	2:D:67:SER:C	2.31	0.55
1:A:83:LYS:CG	1:A:84:LYS:N	2.68	0.55
2:B:66:LEU:HD12	2:B:71:VAL:CG2	2.34	0.55
1:C:165:TYR:CD2	1:C:234:ARG:HD2	2.41	0.55
1:C:229:ARG:NH2	4:C:323:HOH:O	2.39	0.55
2:D:59:ILE:HG22	2:D:60:LYS:N	2.20	0.55
2:B:42:ILE:HG12	2:B:61:ILE:CD1	2.37	0.55
1:C:229:ARG:HG2	1:C:230:VAL:O	2.06	0.55
1:C:308:LEU:CD2	1:C:310:LEU:H	2.20	0.55
2:D:77:TYR:O	2:D:79:PRO:HD3	2.06	0.55
1:A:50:GLU:CB	1:A:107:PRO:HD3	2.36	0.55
1:A:234:ARG:C	1:A:235:LEU:HG	2.32	0.55
1:C:66:LEU:HB3	4:C:335:HOH:O	2.06	0.55
1:C:183:ARG:HG2	1:C:183:ARG:NH1	2.21	0.55
1:C:183:ARG:HG3	1:C:208:ALA:CB	2.35	0.55
1:C:215:ILE:HD13	4:C:313:HOH:O	2.06	0.55
2:B:102:ARG:O	2:B:103:ILE:HB	2.07	0.55
2:B:134:ILE:HD13	2:B:147:HIS:ND1	2.22	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:66:LEU:HD13	2:D:67:SER:N	2.21	0.55
1:A:190:ASP:HB3	4:A:341:HOH:O	2.08	0.54
1:C:11:SER:HA	1:C:133:GLN:HG3	1.88	0.54
2:B:79:PRO:O	2:B:97:PRO:HG2	2.07	0.54
1:C:176:LEU:C	1:C:178:LYS:H	2.13	0.54
2:D:26:GLY:HA3	4:D:323:HOH:O	2.06	0.54
1:A:30:LEU:HD21	1:A:310:LEU:HD23	1.89	0.54
2:D:7:LEU:HD22	2:D:8:GLN:N	2.19	0.54
1:A:260:ASN:HD22	1:A:260:ASN:H	1.54	0.54
2:B:82:THR:HG21	2:B:94:LYS:HZ2	1.67	0.54
1:C:151:ARG:NH1	1:C:154:ASN:O	2.37	0.54
1:C:235:LEU:HB3	1:C:239:GLU:OE2	2.07	0.54
1:A:265:HIS:CD2	1:A:267:LEU:N	2.74	0.54
2:D:69:ASP:O	2:D:70:GLN:C	2.49	0.54
2:B:41:ARG:HH21	2:D:48:LEU:HB2	1.73	0.54
1:C:50:GLU:HB2	1:C:107:PRO:CG	2.38	0.54
2:D:17:VAL:HG12	2:D:18:ILE:N	2.23	0.54
2:D:103:ILE:HG22	2:D:106:VAL:CG2	2.37	0.54
1:A:151:ARG:HD2	1:A:153:ASP:O	2.08	0.54
1:A:266:PRO:O	1:A:267:LEU:HB2	2.08	0.54
1:C:11:SER:C	4:C:328:HOH:O	2.50	0.54
1:C:113:ARG:HG3	1:C:113:ARG:HH11	1.73	0.54
1:C:229:ARG:HH21	1:C:232:LYS:NZ	2.06	0.54
2:D:74:LEU:O	2:D:75:ALA:O	2.26	0.54
1:A:194:MET:SD	1:A:195:PRO:HD2	2.47	0.54
2:D:72:ASP:C	2:D:74:LEU:N	2.64	0.54
1:A:125:LEU:HD12	1:A:125:LEU:N	2.24	0.53
2:B:24:GLN:O	2:B:25:ILE:HD13	2.09	0.53
2:B:69:ASP:C	2:B:71:VAL:H	2.15	0.53
1:C:170:HIS:O	1:C:174:GLN:HG3	2.07	0.53
2:D:69:ASP:O	2:D:72:ASP:N	2.41	0.53
2:D:20:HIS:H	2:D:58:LEU:HD23	1.72	0.53
1:A:6:GLN:HG3	4:A:326:HOH:O	2.08	0.53
1:A:245:ALA:HB3	1:A:247:PHE:CE1	2.41	0.53
2:D:46:LEU:HD23	4:D:342:HOH:O	2.07	0.53
2:D:100:PRO:HB2	2:D:102:ARG:O	2.09	0.53
1:A:223:ASP:O	1:A:224:ILE:HD13	2.07	0.53
1:A:232:LYS:HA	1:A:240:TYR:CD2	2.44	0.53
1:A:236:ASP:HB3	1:A:239:GLU:CB	2.37	0.53
1:C:269:ARG:O	1:C:270:VAL:CB	2.56	0.53
2:D:151:LEU:O	2:D:152:ALA:HB2	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:ASP:OD2	1:A:76:SER:N	2.36	0.53
1:A:123:PRO:HB3	4:A:337:HOH:O	2.08	0.53
1:A:17:ARG:HH12	1:A:179:PHE:HA	1.73	0.53
1:A:250:ARG:CZ	1:A:252:SER:HB3	2.39	0.53
2:B:87:ASP:O	2:B:88:ASN:HB2	2.09	0.53
1:C:243:VAL:O	1:C:246:GLN:CB	2.57	0.53
2:D:66:LEU:CD2	2:D:70:GLN:HB3	2.38	0.53
1:C:24:LEU:O	1:C:27:ALA:HB3	2.08	0.53
2:D:23:ALA:O	2:D:24:GLN:HB2	2.09	0.53
1:A:87:THR:HB	2:B:119:GLU:OE2	2.09	0.53
1:A:269:ARG:NH1	1:A:273:ILE:O	2.42	0.53
1:C:212:HIS:HD2	1:C:217:GLU:OE1	1.92	0.53
2:D:108:VAL:O	2:D:110:PRO:N	2.41	0.53
2:B:33:PHE:O	2:B:34:LYS:C	2.51	0.53
2:B:41:ARG:O	2:B:62:GLU:HB2	2.09	0.53
1:C:39:LEU:HD12	1:C:66:LEU:CD1	2.39	0.53
1:C:81:LEU:HB3	4:C:347:HOH:O	2.08	0.53
2:B:8:GLN:O	2:B:9:VAL:HB	2.09	0.52
2:B:13:LYS:HD3	2:B:62:GLU:OE2	2.09	0.52
1:A:132:ASN:ND2	1:A:132:ASN:C	2.66	0.52
2:B:40:GLN:NE2	4:B:315:HOH:O	2.42	0.52
2:B:42:ILE:HG23	2:B:60:LYS:C	2.35	0.52
2:B:14:ARG:NH2	4:B:323:HOH:O	2.42	0.52
1:A:269:ARG:HH22	1:A:278:ASP:CG	2.16	0.52
1:C:142:LEU:O	1:C:145:ILE:N	2.42	0.52
1:C:245:ALA:HA	1:C:248:VAL:HG11	1.90	0.52
2:D:85:ARG:HG2	2:D:85:ARG:HH11	1.74	0.52
2:D:92:VAL:HG22	2:D:92:VAL:O	2.10	0.52
2:B:13:LYS:HD3	2:B:62:GLU:CD	2.35	0.52
2:D:102:ARG:C	2:D:103:ILE:HG12	2.34	0.52
1:A:70:VAL:HG12	1:A:71:VAL:N	2.24	0.52
1:A:244:LYS:HZ1	1:A:247:PHE:HB2	1.75	0.52
1:A:173:THR:O	1:A:173:THR:HG22	2.10	0.52
2:B:42:ILE:HG12	2:B:61:ILE:HD12	1.91	0.52
2:B:96:ARG:HB3	2:B:96:ARG:CZ	2.40	0.52
2:D:113:ASN:CB	4:D:346:HOH:O	2.58	0.52
2:B:21:ILE:HG23	2:B:78:ALA:CB	2.38	0.52
2:B:46:LEU:O	2:B:47:ASN:HB2	2.08	0.52
2:D:13:LYS:HB2	2:D:41:ARG:CZ	2.39	0.52
2:D:86:ILE:HG12	4:D:333:HOH:O	2.10	0.52
1:A:302:LEU:HA	1:A:308:LEU:HD12	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:96:ARG:NH1	2:B:97:PRO:HG2	2.24	0.52
2:D:66:LEU:HD22	2:D:67:SER:N	2.25	0.52
2:D:108:VAL:O	2:D:110:PRO:HD3	2.10	0.52
1:C:229:ARG:HH21	1:C:232:LYS:HZ2	1.58	0.51
2:D:66:LEU:CD1	2:D:67:SER:O	2.58	0.51
2:D:108:VAL:O	2:D:109:CYS:C	2.52	0.51
2:D:147:HIS:CE1	2:D:148:ASN:ND2	2.78	0.51
1:A:43:VAL:HG12	1:A:99:VAL:HG12	1.91	0.51
2:B:72:ASP:O	2:B:100:PRO:HD3	2.10	0.51
1:C:5:TYR:CE1	1:C:306:ARG:HA	2.45	0.51
1:C:308:LEU:HA	4:C:337:HOH:O	2.10	0.51
2:D:66:LEU:HD11	2:D:71:VAL:CG2	2.40	0.51
2:D:130:ARG:HH21	2:D:132:ASN:ND2	2.08	0.51
2:D:133:ASP:C	2:D:134:ILE:HD13	2.34	0.51
1:A:305:ASN:OD1	1:A:306:ARG:N	2.43	0.51
1:C:250:ARG:HH11	1:C:250:ARG:HB3	1.76	0.51
2:D:27:PHE:O	2:D:30:LEU:HD13	2.11	0.51
1:A:235:LEU:CB	1:A:239:GLU:OE1	2.59	0.51
1:C:94:VAL:O	1:C:97:THR:HG23	2.10	0.51
1:A:229:ARG:NH1	1:A:230:VAL:O	2.44	0.51
2:D:30:LEU:HD12	2:D:30:LEU:N	2.26	0.51
2:D:113:ASN:O	2:D:114:CYS:C	2.53	0.51
2:B:71:VAL:HG12	2:B:72:ASP:N	2.25	0.51
2:B:128:ARG:HB3	2:B:135:ALA:HB3	1.93	0.51
1:C:146:GLN:O	1:C:150:GLY:N	2.44	0.51
2:B:41:ARG:O	2:B:42:ILE:HG13	2.11	0.51
1:C:39:LEU:HD12	1:C:66:LEU:HD12	1.92	0.51
2:D:89:TYR:CD1	2:D:90:GLU:HB2	2.45	0.51
1:A:50:GLU:HG3	1:A:107:PRO:CB	2.37	0.51
2:D:17:VAL:O	2:D:83:VAL:O	2.29	0.51
2:B:17:VAL:HG12	2:B:61:ILE:N	2.25	0.51
1:C:140:LEU:HB3	1:C:292:GLY:HA2	1.92	0.51
2:D:28:LYS:HG3	2:D:32:LEU:HD23	1.92	0.51
2:D:36:THR:C	2:D:38:THR:H	2.19	0.51
1:A:261:MET:SD	1:A:262:LYS:N	2.84	0.50
1:C:41:HIS:C	1:C:42:LYS:HD2	2.36	0.50
1:C:215:ILE:HB	4:C:345:HOH:O	2.11	0.50
1:A:45:ALA:HB2	1:A:99:VAL:HG11	1.94	0.50
1:A:190:ASP:O	1:A:191:ALA:C	2.54	0.50
1:A:235:LEU:HB3	1:A:239:GLU:OE1	2.12	0.50
2:B:18:ILE:HD12	2:B:18:ILE:C	2.35	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:26:GLY:HA2	2:B:29:LEU:CG	2.40	0.50
1:C:9:ILE:CG1	1:C:299:LEU:HD21	2.31	0.50
1:C:293:ILE:O	1:C:297:GLN:CB	2.59	0.50
1:A:29:LYS:HD3	1:A:310:LEU:O	2.11	0.50
2:B:7:LEU:HD22	2:B:8:GLN:NE2	2.26	0.50
2:B:27:PHE:CA	2:B:30:LEU:HD12	2.41	0.50
2:B:110:PRO:HD2	2:B:145:PHE:CE1	2.46	0.50
1:A:310:LEU:N	1:A:310:LEU:HD12	2.26	0.50
1:C:154:ASN:HA	1:C:182:ASN:H	1.75	0.50
1:C:200:ASP:O	1:C:203:ASP:HB2	2.12	0.50
1:C:219:MET:HE2	4:C:345:HOH:O	2.10	0.50
1:C:271:ASP:O	1:C:272:GLU:C	2.54	0.50
2:D:113:ASN:CA	4:D:346:HOH:O	2.59	0.50
2:D:69:ASP:HA	2:D:72:ASP:OD1	2.12	0.50
1:A:10:ILE:N	1:A:10:ILE:CD1	2.74	0.50
1:A:17:ARG:NH1	1:A:178:LYS:O	2.44	0.50
1:C:264:LEU:HD22	1:C:288:GLN:CD	2.36	0.50
2:D:27:PHE:C	2:D:30:LEU:HD13	2.36	0.50
2:D:111:ASN:N	4:D:345:HOH:O	2.44	0.50
1:A:51:ALA:HB2	1:A:75:ASP:CA	2.42	0.50
1:A:236:ASP:OD2	1:A:237:PRO:HD2	2.12	0.50
1:A:240:TYR:HB2	4:A:322:HOH:O	2.11	0.50
2:B:18:ILE:HD13	4:B:320:HOH:O	2.10	0.50
1:C:243:VAL:O	1:C:244:LYS:C	2.55	0.50
2:D:96:ARG:HG3	2:D:96:ARG:HH11	1.77	0.50
2:B:70:GLN:CD	2:B:70:GLN:N	2.65	0.50
2:B:94:LYS:NZ	2:B:94:LYS:HB2	2.25	0.50
2:B:77:TYR:O	2:B:79:PRO:HD3	2.12	0.49
1:C:212:HIS:CD2	1:C:217:GLU:OE1	2.65	0.49
1:A:62:SER:HB2	1:A:293:ILE:O	2.11	0.49
1:A:79:THR:CG2	1:A:85:GLY:HA3	2.29	0.49
1:A:140:LEU:HB2	1:A:292:GLY:HA2	1.92	0.49
1:A:286:PHE:O	1:A:289:ALA:HB3	2.12	0.49
2:B:22:PRO:HB2	2:B:25:ILE:HB	1.94	0.49
1:C:187:ILE:CG1	1:C:212:HIS:HB2	2.36	0.49
1:A:138:THR:HA	4:A:311:HOH:O	2.12	0.49
1:A:214:SER:HB2	1:A:216:GLU:HG2	1.93	0.49
2:B:96:ARG:CZ	2:B:97:PRO:HD2	2.42	0.49
2:D:62:GLU:O	2:D:63:ASN:HB2	2.12	0.49
1:A:32:ALA:C	1:A:34:PRO:HD3	2.37	0.49
1:A:183:ARG:NH1	1:A:184:PHE:O	2.46	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:42:ILE:HG12	2:B:61:ILE:CG1	2.42	0.49
1:C:77:ALA:N	4:C:334:HOH:O	2.44	0.49
1:C:129:ASP:CG	1:C:129:ASP:O	2.55	0.49
2:D:115:ILE:CG2	2:D:116:SER:N	2.75	0.49
1:A:55:THR:O	1:A:59:PHE:HB2	2.13	0.49
1:A:61:THR:O	1:A:63:MET:N	2.43	0.49
2:B:21:ILE:O	2:B:22:PRO:O	2.31	0.49
2:B:91:VAL:C	2:B:93:GLY:H	2.21	0.49
2:D:41:ARG:HG2	2:D:62:GLU:HB3	1.93	0.49
2:D:129:LYS:HG2	2:D:130:ARG:H	1.78	0.49
1:A:34:PRO:C	1:A:36:PRO:HD3	2.38	0.49
2:B:66:LEU:HD22	4:B:332:HOH:O	2.12	0.49
1:C:124:VAL:O	1:C:125:LEU:HD12	2.12	0.49
1:C:75:ASP:OD1	1:C:79:THR:CB	2.60	0.49
2:D:85:ARG:HG2	2:D:85:ARG:NH1	2.28	0.49
1:A:249:LEU:HD12	1:A:250:ARG:H	1.77	0.49
2:B:48:LEU:C	2:B:48:LEU:HD23	2.38	0.49
1:C:84:LYS:NZ	1:C:84:LYS:H	2.10	0.49
1:C:88:LEU:HD13	1:C:114:LEU:HD22	1.94	0.49
1:C:212:HIS:CD2	1:C:218:VAL:CG1	2.96	0.49
1:C:245:ALA:HA	1:C:248:VAL:HG13	1.95	0.49
2:D:111:ASN:HB2	4:D:345:HOH:O	2.13	0.49
1:A:309:VAL:C	1:A:310:LEU:HD12	2.38	0.48
1:C:78:ASN:N	4:C:334:HOH:O	2.31	0.48
2:D:26:GLY:O	2:D:27:PHE:C	2.56	0.48
2:D:67:SER:O	2:D:70:GLN:N	2.46	0.48
1:A:5:TYR:O	1:A:6:GLN:HB2	2.12	0.48
1:C:71:VAL:HG22	4:C:342:HOH:O	2.12	0.48
1:A:240:TYR:O	1:A:244:LYS:HB2	2.13	0.48
1:A:266:PRO:O	1:A:267:LEU:CB	2.61	0.48
2:B:20:HIS:N	4:B:320:HOH:O	2.46	0.48
1:C:130:GLY:O	1:C:167:ARG:NH1	2.47	0.48
2:D:8:GLN:OE1	2:D:9:VAL:HG22	2.13	0.48
2:D:133:ASP:O	2:D:134:ILE:HD13	2.12	0.48
1:A:146:GLN:HB2	1:A:152:LEU:HD21	1.94	0.48
1:A:235:LEU:O	1:A:236:ASP:C	2.56	0.48
1:C:8:HIS:NE2	1:C:116:THR:HG23	2.29	0.48
1:A:19:ASP:O	1:A:20:LEU:C	2.57	0.48
2:B:99:LEU:HD23	2:B:100:PRO:CD	2.41	0.48
2:D:109:CYS:C	2:D:111:ASN:H	2.20	0.48
1:C:9:ILE:HG22	1:C:9:ILE:O	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:VAL:C	1:A:71:VAL:HG13	2.39	0.48
1:A:70:VAL:O	1:A:71:VAL:HG13	2.14	0.48
1:C:43:VAL:N	1:C:100:ASP:OD2	2.32	0.48
1:C:240:TYR:CD1	1:C:240:TYR:C	2.91	0.48
2:B:21:ILE:HG21	2:B:29:LEU:HD11	1.96	0.48
2:B:22:PRO:HD2	2:B:78:ALA:CB	2.44	0.48
1:C:39:LEU:HB2	1:C:66:LEU:O	2.14	0.48
2:D:1:MET:O	2:D:2:THR:CB	2.62	0.48
1:A:229:ARG:HA	1:A:272:GLU:HG2	1.96	0.48
1:A:265:HIS:HD2	1:A:267:LEU:N	2.10	0.48
1:C:132:ASN:OD1	2:D:142:GLU:OE1	2.32	0.48
1:C:305:ASN:OD1	1:C:307:ASP:C	2.57	0.48
1:A:265:HIS:CD2	1:A:266:PRO:HD2	2.48	0.47
2:D:78:ALA:O	2:D:79:PRO:C	2.57	0.47
2:B:88:ASN:C	2:B:89:TYR:CD1	2.92	0.47
1:C:240:TYR:CD1	1:C:241:ALA:N	2.82	0.47
2:D:61:ILE:HG12	2:D:62:GLU:H	1.79	0.47
2:B:26:GLY:O	2:B:29:LEU:HG	2.14	0.47
1:C:75:ASP:HA	1:C:79:THR:CB	2.45	0.47
1:C:183:ARG:NH1	4:C:333:HOH:O	2.46	0.47
1:C:243:VAL:O	1:C:244:LYS:O	2.31	0.47
2:D:66:LEU:HD22	2:D:70:GLN:HB3	1.96	0.47
2:B:46:LEU:HD22	2:B:57:ASP:CG	2.40	0.47
2:B:74:LEU:O	2:B:75:ALA:O	2.32	0.47
1:A:59:PHE:O	1:A:63:MET:HG3	2.14	0.47
2:B:95:SER:C	4:B:322:HOH:O	2.56	0.47
2:D:108:VAL:O	2:D:110:PRO:CD	2.63	0.47
1:A:30:LEU:CD2	1:A:310:LEU:HD23	2.44	0.47
1:A:79:THR:O	1:A:79:THR:CG2	2.62	0.47
1:A:234:ARG:C	1:A:235:LEU:CG	2.87	0.47
2:B:83:VAL:O	2:B:94:LYS:HA	2.15	0.47
1:C:39:LEU:HB3	1:C:68:ALA:HB2	1.97	0.47
1:C:66:LEU:HB2	4:C:316:HOH:O	2.13	0.47
1:C:229:ARG:HA	1:C:272:GLU:CD	2.40	0.47
2:D:16:THR:HG23	2:D:85:ARG:CG	2.40	0.47
1:A:20:LEU:O	1:A:24:LEU:HG	2.13	0.47
1:A:177:ALA:C	1:A:179:PHE:H	2.23	0.47
1:A:203:ASP:C	1:A:205:LYS:H	2.21	0.47
2:B:41:ARG:NH2	2:D:48:LEU:HB2	2.28	0.47
1:C:11:SER:CB	1:C:133:GLN:HG3	2.44	0.47
1:C:15:LEU:HD11	4:C:328:HOH:O	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:244:LYS:C	1:C:246:GLN:N	2.72	0.47
2:D:7:LEU:HD22	2:D:9:VAL:N	2.22	0.47
1:A:8:HIS:CD2	1:A:116:THR:OG1	2.68	0.47
2:B:134:ILE:HD13	2:B:147:HIS:CG	2.50	0.47
1:C:287:GLN:NE2	1:C:287:GLN:N	2.23	0.47
2:D:147:HIS:O	2:D:151:LEU:HG	2.15	0.47
2:B:41:ARG:NH2	2:D:49:PRO:HD2	2.19	0.47
1:C:121:ASN:ND2	1:C:121:ASN:H	2.12	0.47
2:D:21:ILE:CB	2:D:57:ASP:HB2	2.31	0.47
2:D:67:SER:C	2:D:69:ASP:N	2.61	0.47
2:D:107:LEU:HB2	2:D:125:PHE:CE1	2.50	0.47
1:A:46:SER:O	1:A:72:GLY:HA3	2.14	0.47
1:A:85:GLY:O	1:A:86:GLU:CB	2.62	0.47
2:B:54:GLY:O	2:B:55:ARG:C	2.57	0.47
2:B:69:ASP:O	2:B:71:VAL:N	2.48	0.47
2:B:83:VAL:HB	4:B:322:HOH:O	2.15	0.47
2:B:134:ILE:HD13	2:B:147:HIS:CE1	2.50	0.47
1:C:224:ILE:HD13	1:C:224:ILE:HA	1.77	0.47
2:D:66:LEU:HD21	2:D:70:GLN:HG2	1.96	0.47
1:C:59:PHE:C	1:C:63:MET:HE3	2.40	0.46
1:C:153:ASP:O	1:C:154:ASN:C	2.59	0.46
2:B:61:ILE:CG2	2:B:62:GLU:N	2.78	0.46
1:C:12:ILE:HG12	1:C:138:THR:HG21	1.98	0.46
1:C:22:LEU:HG	1:C:302:LEU:HD21	1.97	0.46
1:C:225:LEU:HB2	1:C:261:MET:HE2	1.96	0.46
2:D:16:THR:O	2:D:61:ILE:HG22	2.15	0.46
2:D:66:LEU:HD13	2:D:66:LEU:C	2.40	0.46
1:A:146:GLN:OE1	1:A:146:GLN:HA	2.15	0.46
1:A:240:TYR:HE1	1:A:244:LYS:HD2	1.75	0.46
2:B:104:ASP:HA	2:B:123:SER:O	2.16	0.46
1:C:223:ASP:O	1:C:261:MET:HA	2.15	0.46
1:C:229:ARG:NH2	1:C:232:LYS:NZ	2.63	0.46
1:A:65:ARG:HG3	1:A:65:ARG:NH1	2.27	0.46
1:A:153:ASP:O	1:A:154:ASN:C	2.55	0.46
1:A:265:HIS:HD2	1:A:266:PRO:N	2.13	0.46
2:B:18:ILE:HG22	2:B:83:VAL:HG22	1.97	0.46
2:B:82:THR:HG23	2:B:95:SER:O	2.15	0.46
1:A:16:SER:O	1:A:19:ASP:HB2	2.15	0.46
1:A:140:LEU:HB2	1:A:292:GLY:CA	2.45	0.46
1:A:244:LYS:C	1:A:245:ALA:O	2.58	0.46
2:B:129:LYS:HD2	2:B:130:ARG:H	1.80	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:21:ILE:HG21	2:D:26:GLY:HA2	1.96	0.46
2:D:103:ILE:HG22	2:D:106:VAL:HG21	1.97	0.46
1:A:47:CYS:O	1:A:104:MET:HA	2.15	0.46
1:C:22:LEU:HG	1:C:302:LEU:CD2	2.45	0.46
1:C:53:THR:O	1:C:54:ARG:C	2.58	0.46
1:C:200:ASP:HA	1:C:203:ASP:HB2	1.97	0.46
1:A:64:HIS:C	1:A:66:LEU:H	2.23	0.46
1:A:65:ARG:HH11	1:A:65:ARG:CG	2.27	0.46
1:A:151:ARG:CD	1:A:153:ASP:O	2.64	0.46
2:B:66:LEU:O	2:B:85:ARG:NH1	2.48	0.46
1:C:106:HIS:HA	1:C:107:PRO:HD3	1.78	0.46
1:C:154:ASN:HA	1:C:181:GLY:HA3	1.97	0.46
2:D:23:ALA:C	2:D:25:ILE:H	2.23	0.46
2:D:41:ARG:O	2:D:41:ARG:CG	2.61	0.46
1:A:113:ARG:HH11	1:A:113:ARG:HG3	1.80	0.46
1:A:190:ASP:OD1	1:A:190:ASP:N	2.47	0.46
1:A:229:ARG:HG2	1:A:230:VAL:N	2.30	0.46
2:B:79:PRO:O	2:B:97:PRO:CG	2.63	0.46
1:C:19:ASP:O	1:C:22:LEU:HB3	2.16	0.46
1:C:54:ARG:H	1:C:54:ARG:HG3	1.43	0.46
2:D:46:LEU:HB3	2:D:47:ASN:OD1	2.16	0.46
2:D:145:PHE:HB3	2:D:149:VAL:CG2	2.46	0.46
1:A:50:GLU:HB2	1:A:107:PRO:CD	2.44	0.46
2:B:41:ARG:HH22	2:D:49:PRO:CD	2.18	0.46
1:C:62:SER:HB2	1:C:297:GLN:CA	2.46	0.46
1:C:176:LEU:C	1:C:178:LYS:N	2.74	0.46
1:C:236:ASP:OD1	1:C:239:GLU:CB	2.63	0.46
1:C:246:GLN:C	1:C:246:GLN:OE1	2.59	0.46
1:C:271:ASP:O	1:C:273:ILE:N	2.49	0.46
1:A:186:PHE:HB2	1:A:211:LEU:HD22	1.98	0.46
2:B:58:LEU:HD12	4:B:320:HOH:O	2.16	0.46
2:B:72:ASP:C	2:B:74:LEU:H	2.23	0.46
1:C:9:ILE:HD12	1:C:9:ILE:N	2.30	0.46
1:C:198:ILE:O	1:C:201:MET:HG3	2.16	0.46
2:D:55:ARG:HD2	2:D:55:ARG:N	2.31	0.46
2:D:70:GLN:O	2:D:71:VAL:C	2.58	0.46
2:D:126:ALA:O	2:D:136:LEU:CA	2.47	0.46
1:A:229:ARG:HG3	1:A:272:GLU:HG3	1.98	0.45
1:A:299:LEU:HD13	1:A:299:LEU:HA	1.65	0.45
1:A:302:LEU:N	1:A:308:LEU:HD11	2.30	0.45
1:C:142:LEU:HB3	4:C:318:HOH:O	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:ARG:HG3	1:A:113:ARG:NH1	2.30	0.45
1:A:256:ASN:OD1	4:A:339:HOH:O	2.21	0.45
2:B:21:ILE:O	2:B:56:LYS:HB2	2.16	0.45
2:B:33:PHE:O	2:B:35:LEU:N	2.49	0.45
2:B:77:TYR:C	2:B:79:PRO:HD3	2.41	0.45
2:B:82:THR:HG22	2:B:83:VAL:N	2.31	0.45
1:C:158:ALA:HB3	1:C:225:LEU:HA	1.99	0.45
1:A:62:SER:O	1:A:62:SER:OG	2.31	0.45
1:A:108:GLN:HG2	2:B:113:ASN:ND2	2.32	0.45
1:A:176:LEU:HB2	4:A:336:HOH:O	2.15	0.45
2:D:13:LYS:C	2:D:41:ARG:HH22	2.25	0.45
2:D:59:ILE:HA	4:D:338:HOH:O	2.16	0.45
2:D:69:ASP:C	2:D:71:VAL:N	2.67	0.45
1:A:229:ARG:CD	1:A:270:VAL:HB	2.47	0.45
1:A:257:ALA:N	4:A:339:HOH:O	2.49	0.45
2:D:100:PRO:HG2	2:D:103:ILE:HD13	1.97	0.45
1:A:231:GLN:O	1:A:234:ARG:HB2	2.17	0.45
1:A:190:ASP:C	1:A:192:LEU:N	2.73	0.45
2:B:26:GLY:C	2:B:29:LEU:HG	2.40	0.45
2:B:94:LYS:O	2:B:95:SER:CB	2.64	0.45
2:D:129:LYS:CG	2:D:130:ARG:N	2.78	0.45
1:A:88:LEU:O	1:A:92:ILE:HG12	2.16	0.45
1:A:136:THR:CB	1:A:296:ARG:HE	2.29	0.45
1:C:71:VAL:HG23	1:C:71:VAL:O	2.16	0.45
1:C:240:TYR:O	1:C:244:LYS:N	2.41	0.45
1:A:66:LEU:HD21	4:A:328:HOH:O	2.15	0.45
1:C:277:VAL:C	1:C:279:LYS:N	2.75	0.45
1:A:52:SER:OG	1:A:54:ARG:NH2	2.49	0.45
1:A:169:VAL:O	1:A:170:HIS:C	2.60	0.45
1:A:176:LEU:HD12	4:A:321:HOH:O	2.17	0.45
2:B:6:LYS:HE2	2:B:48:LEU:HD23	1.99	0.45
2:B:125:PHE:CE2	2:B:138:CYS:HA	2.51	0.45
2:B:146:SER:O	2:B:149:VAL:HB	2.16	0.45
1:C:73:PHE:HD1	1:C:75:ASP:H	1.63	0.45
2:D:7:LEU:CD2	2:D:8:GLN:OE1	2.65	0.45
1:A:12:ILE:HD12	1:A:12:ILE:HA	1.63	0.45
1:A:161:GLY:HA3	1:A:228:THR:OG1	2.17	0.45
1:C:142:LEU:C	4:C:318:HOH:O	2.59	0.45
1:A:248:VAL:CB	1:A:272:GLU:HA	2.44	0.44
1:C:11:SER:HB2	1:C:133:GLN:HG3	1.99	0.44
1:C:178:LYS:C	1:C:179:PHE:CD1	2.95	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:183:ARG:NH1	1:C:183:ARG:CG	2.79	0.44
2:D:18:ILE:HB	2:D:59:ILE:HB	1.98	0.44
2:D:145:PHE:HB3	2:D:149:VAL:HG21	1.98	0.44
1:A:34:PRO:O	1:A:36:PRO:HD3	2.16	0.44
2:B:44:ILE:HD12	2:B:44:ILE:N	2.32	0.44
2:B:50:SER:HB2	2:B:56:LYS:CD	2.47	0.44
2:B:72:ASP:HB3	2:B:98:SER:O	2.17	0.44
1:C:201:MET:SD	1:C:202:LEU:HD12	2.57	0.44
2:D:124:SER:CB	2:D:139:LYS:HE3	2.45	0.44
2:D:125:PHE:HB3	2:D:126:ALA:H	1.62	0.44
1:A:235:LEU:CD1	1:A:240:TYR:CD2	2.98	0.44
2:B:17:VAL:HG11	2:B:60:LYS:HA	1.98	0.44
2:B:53:MET:O	2:B:55:ARG:N	2.50	0.44
1:C:29:LYS:HG2	1:C:310:LEU:HB2	1.99	0.44
1:A:56:ARG:HG2	1:A:60:GLU:OE2	2.17	0.44
2:B:130:ARG:C	4:B:324:HOH:O	2.61	0.44
2:D:30:LEU:H	2:D:30:LEU:CD1	2.31	0.44
2:D:72:ASP:O	2:D:75:ALA:N	2.47	0.44
1:A:19:ASP:O	1:A:22:LEU:N	2.50	0.44
2:B:12:ILE:HG12	2:D:8:GLN:CG	2.45	0.44
2:B:62:GLU:O	2:B:63:ASN:C	2.60	0.44
2:B:94:LYS:HG3	2:B:95:SER:N	2.31	0.44
1:C:40:LYS:HG3	1:C:41:HIS:HD2	1.82	0.44
1:C:167:ARG:CG	1:C:168:THR:N	2.81	0.44
2:B:17:VAL:CG1	2:B:60:LYS:HA	2.47	0.44
2:B:20:HIS:O	2:B:81:ALA:HB2	2.18	0.44
2:D:20:HIS:H	2:D:58:LEU:HD21	1.81	0.44
2:D:83:VAL:CG1	2:D:85:ARG:HD3	2.47	0.44
1:A:216:GLU:HA	4:A:332:HOH:O	2.17	0.44
1:A:263:VAL:C	1:A:264:LEU:HD12	2.43	0.44
2:B:4:ASP:O	2:B:5:ASN:OD1	2.36	0.44
2:D:21:ILE:HB	2:D:57:ASP:CB	2.32	0.44
2:D:114:CYS:O	2:D:116:SER:N	2.51	0.44
1:A:75:ASP:CG	1:A:76:SER:N	2.75	0.44
1:A:114:LEU:C	1:A:114:LEU:CD2	2.86	0.44
2:B:90:GLU:HA	4:B:339:HOH:O	2.18	0.44
2:D:87:ASP:H	2:D:92:VAL:HG12	1.81	0.44
1:A:75:ASP:CG	1:A:76:SER:H	2.25	0.44
2:B:12:ILE:HG21	2:D:8:GLN:HB3	2.00	0.44
2:B:21:ILE:O	2:B:22:PRO:C	2.61	0.44
2:B:61:ILE:CG2	2:B:64:THR:HB	2.45	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:85:ARG:HG2	2:B:85:ARG:HH11	1.82	0.44
1:A:263:VAL:HG23	1:A:282:HIS:HB3	1.98	0.43
2:B:114:CYS:HA	2:B:141:CYS:HB3	1.99	0.43
1:C:29:LYS:HE2	1:C:310:LEU:HB2	2.00	0.43
2:D:83:VAL:HG23	2:D:95:SER:HB2	2.00	0.43
1:A:38:LEU:HD12	1:A:38:LEU:HA	1.65	0.43
1:A:243:VAL:O	1:A:245:ALA:N	2.50	0.43
2:B:18:ILE:HD13	2:B:21:ILE:HD11	2.00	0.43
2:B:18:ILE:HG12	2:B:21:ILE:HD11	1.99	0.43
2:B:137:LYS:O	2:B:138:CYS:C	2.61	0.43
1:C:126:ASN:HD21	1:C:128:GLY:H	1.61	0.43
1:C:128:GLY:HA2	1:C:133:GLN:O	2.19	0.43
2:D:27:PHE:O	2:D:30:LEU:HB2	2.17	0.43
2:D:61:ILE:HG12	2:D:62:GLU:N	2.33	0.43
1:A:144:THR:HG21	1:A:288:GLN:HB2	1.99	0.43
1:A:229:ARG:HE	1:A:270:VAL:CG1	2.30	0.43
1:A:272:GLU:N	1:A:272:GLU:OE1	2.51	0.43
1:C:304:LEU:HD23	4:C:340:HOH:O	2.17	0.43
2:D:8:GLN:CG	2:D:9:VAL:HG13	2.48	0.43
2:D:20:HIS:CA	2:D:56:LYS:HE3	2.49	0.43
1:A:29:LYS:HG2	1:A:310:LEU:C	2.42	0.43
1:A:64:HIS:C	1:A:66:LEU:N	2.76	0.43
1:A:76:SER:OG	1:A:80:SER:O	2.37	0.43
1:A:151:ARG:NH1	1:A:151:ARG:HG2	2.34	0.43
1:A:215:ILE:H	1:A:215:ILE:HG13	1.65	0.43
2:B:6:LYS:HE2	2:B:48:LEU:HD21	1.98	0.43
1:C:269:ARG:HH22	1:C:278:ASP:CG	2.20	0.43
1:A:129:ASP:CG	1:A:132:ASN:HB3	2.44	0.43
2:B:23:ALA:O	2:B:25:ILE:HG12	2.18	0.43
1:C:154:ASN:HA	1:C:182:ASN:N	2.34	0.43
1:C:240:TYR:OH	1:C:244:LYS:HG3	2.18	0.43
2:B:94:LYS:HZ2	2:B:94:LYS:HB2	1.82	0.43
2:B:111:ASN:ND2	2:B:113:ASN:H	2.17	0.43
1:C:307:ASP:O	1:C:307:ASP:OD2	2.37	0.43
1:A:50:GLU:HB3	1:A:105:ARG:HG2	1.99	0.43
1:A:249:LEU:N	1:A:272:GLU:O	2.51	0.43
1:A:255:HIS:C	1:A:257:ALA:H	2.26	0.43
1:A:267:LEU:HA	1:A:268:PRO:C	2.43	0.43
1:C:229:ARG:NH2	1:C:232:LYS:HZ3	2.17	0.43
2:D:30:LEU:N	2:D:30:LEU:CD1	2.81	0.43
2:D:83:VAL:HG12	2:D:85:ARG:HD3	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:102:ARG:HD3	4:D:329:HOH:O	2.19	0.43
2:B:6:LYS:HE3	2:B:9:VAL:HG23	2.01	0.43
2:B:18:ILE:CD1	2:B:21:ILE:HD11	2.48	0.43
1:C:60:GLU:N	1:C:63:MET:HE3	2.34	0.43
2:D:14:ARG:HG2	2:D:86:ILE:O	2.18	0.43
1:A:13:ASN:C	1:A:15:LEU:N	2.73	0.43
2:B:42:ILE:HA	2:B:60:LYS:O	2.19	0.43
1:C:64:HIS:C	1:C:66:LEU:N	2.76	0.43
2:D:37:GLU:O	2:D:38:THR:HG23	2.19	0.43
2:D:61:ILE:HD13	2:D:64:THR:HB	2.00	0.43
2:D:83:VAL:CG2	2:D:95:SER:HB2	2.48	0.43
1:A:105:ARG:HB2	1:A:127:ALA:HB3	2.01	0.43
1:A:187:ILE:HD12	1:A:215:ILE:HA	2.00	0.43
2:B:67:SER:O	2:B:71:VAL:HB	2.18	0.43
2:B:69:ASP:O	2:B:73:GLN:NE2	2.44	0.43
2:B:91:VAL:HG23	2:B:91:VAL:O	2.18	0.43
2:D:28:LYS:HB2	2:D:28:LYS:HE3	1.84	0.43
2:D:130:ARG:HH22	2:D:132:ASN:HD22	1.64	0.43
1:A:123:PRO:CA	4:A:337:HOH:O	2.65	0.42
2:B:18:ILE:CD1	2:B:19:ASP:N	2.82	0.42
2:B:26:GLY:O	2:B:30:LEU:HD12	2.19	0.42
2:D:99:LEU:HA	2:D:100:PRO:HD3	1.71	0.42
1:A:234:ARG:O	1:A:235:LEU:HG	2.19	0.42
2:B:21:ILE:O	2:B:56:LYS:HA	2.19	0.42
2:B:65:PHE:HD2	2:B:65:PHE:HA	1.75	0.42
2:B:131:ALA:N	4:B:324:HOH:O	2.52	0.42
1:C:242:ASN:CB	4:C:319:HOH:O	2.67	0.42
1:C:309:VAL:HG22	1:C:309:VAL:O	2.20	0.42
1:A:244:LYS:NZ	1:A:244:LYS:HA	2.34	0.42
2:B:61:ILE:HG23	2:B:62:GLU:N	2.34	0.42
1:C:194:MET:SD	1:C:195:PRO:HD2	2.59	0.42
2:D:151:LEU:O	2:D:152:ALA:CB	2.67	0.42
1:A:30:LEU:HD21	1:A:310:LEU:CD2	2.50	0.42
1:A:173:THR:HA	4:A:321:HOH:O	2.18	0.42
1:A:235:LEU:HB3	1:A:239:GLU:CD	2.43	0.42
2:B:47:ASN:OD1	2:D:39:ASP:HA	2.20	0.42
1:C:39:LEU:O	1:C:42:LYS:HG2	2.19	0.42
2:D:114:CYS:HA	2:D:141:CYS:HB3	2.01	0.42
1:A:70:VAL:O	1:A:71:VAL:CG1	2.68	0.42
1:A:119:SER:OG	1:A:122:VAL:O	2.31	0.42
1:A:246:GLN:C	1:A:247:PHE:CD1	2.98	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:67:SER:HG	2:B:70:GLN:CD	2.22	0.42
1:C:40:LYS:O	1:C:41:HIS:HB2	2.18	0.42
1:C:52:SER:O	1:C:53:THR:C	2.62	0.42
1:C:272:GLU:CD	1:C:272:GLU:N	2.76	0.42
2:B:36:THR:CG2	4:D:342:HOH:O	2.68	0.42
2:B:72:ASP:C	2:B:100:PRO:HD3	2.44	0.42
2:B:86:ILE:CG2	2:B:90:GLU:N	2.79	0.42
1:C:126:ASN:HD21	1:C:129:ASP:N	2.17	0.42
2:D:14:ARG:C	2:D:62:GLU:HG3	2.44	0.42
2:B:70:GLN:O	2:B:74:LEU:HG	2.19	0.42
1:C:164:LYS:HD3	1:C:165:TYR:CE2	2.54	0.42
1:C:167:ARG:CG	1:C:168:THR:H	2.31	0.42
2:D:146:SER:O	2:D:149:VAL:CG2	2.67	0.42
1:A:174:GLN:NE2	1:A:201:MET:HE2	2.34	0.42
2:B:44:ILE:HB	2:D:44:ILE:CD1	2.50	0.42
2:B:85:ARG:NH1	2:B:85:ARG:HG2	2.34	0.42
1:C:134:HIS:N	1:C:135:PRO:CD	2.81	0.42
1:C:200:ASP:O	1:C:203:ASP:N	2.51	0.42
1:A:24:LEU:O	1:A:25:ALA:C	2.62	0.42
1:A:183:ARG:HH22	1:A:210:SER:CB	2.33	0.42
1:A:293:ILE:O	1:A:297:GLN:CB	2.54	0.42
2:B:107:LEU:HD23	2:B:107:LEU:HA	1.85	0.42
2:B:119:GLU:HA	2:B:120:PRO:HD3	1.78	0.42
1:C:133:GLN:O	1:C:134:HIS:HB2	2.20	0.42
1:C:225:LEU:HB2	1:C:261:MET:CE	2.49	0.42
1:C:247:PHE:CD1	1:C:247:PHE:N	2.88	0.42
2:D:17:VAL:CG1	2:D:18:ILE:N	2.83	0.42
2:D:105:ASN:ND2	2:D:122:SER:HB2	2.35	0.42
2:D:136:LEU:CD1	2:D:150:VAL:HG21	2.48	0.42
1:A:138:THR:O	1:A:142:LEU:HG	2.20	0.42
2:B:73:GLN:HB3	4:B:333:HOH:O	2.19	0.42
1:C:113:ARG:HG3	1:C:113:ARG:NH1	2.33	0.42
2:D:126:ALA:HB3	2:D:137:LYS:H	1.85	0.42
1:A:172:LEU:HG	4:A:321:HOH:O	2.20	0.41
1:A:271:ASP:OD1	1:A:271:ASP:N	2.50	0.41
2:B:22:PRO:HD2	2:B:78:ALA:HB2	2.02	0.41
1:C:162:ASP:OD2	1:C:162:ASP:C	2.61	0.41
2:D:14:ARG:HB2	2:D:62:GLU:OE2	2.19	0.41
2:B:1:MET:SD	4:B:340:HOH:O	2.62	0.41
2:D:12:ILE:HG22	2:D:13:LYS:N	2.25	0.41
2:D:14:ARG:HD2	2:D:88:ASN:CA	2.47	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:GLU:CA	1:A:258:LYS:HD2	2.50	0.41
1:A:298:ALA:O	1:A:301:ALA:HB3	2.21	0.41
1:A:56:ARG:CG	1:A:60:GLU:OE2	2.69	0.41
2:B:35:LEU:O	2:B:37:GLU:N	2.53	0.41
1:C:60:GLU:CA	1:C:63:MET:HE3	2.49	0.41
1:C:110:GLY:CA	2:D:140:TYR:O	2.66	0.41
1:C:298:ALA:C	1:C:302:LEU:HD12	2.40	0.41
2:D:68:GLU:CD	2:D:85:ARG:HH12	2.29	0.41
2:B:18:ILE:HD11	2:B:59:ILE:H	1.85	0.41
1:C:155:LEU:N	1:C:182:ASN:OD1	2.52	0.41
1:C:240:TYR:CD1	1:C:244:LYS:HB2	2.55	0.41
2:D:85:ARG:HD3	2:D:85:ARG:H	1.85	0.41
1:A:88:LEU:O	1:A:89:ALA:C	2.64	0.41
2:B:50:SER:CB	2:B:56:LYS:NZ	2.82	0.41
1:C:112:ALA:HB1	1:C:126:ASN:HB2	2.03	0.41
1:C:192:LEU:HD23	4:C:350:HOH:O	2.20	0.41
1:A:23:VAL:HA	1:A:302:LEU:HD11	2.03	0.41
1:A:265:HIS:CD2	1:A:266:PRO:CD	3.04	0.41
2:B:33:PHE:O	2:B:35:LEU:HG	2.20	0.41
2:B:134:ILE:HB	2:B:147:HIS:CB	2.43	0.41
2:D:18:ILE:HD12	2:D:59:ILE:CG1	2.50	0.41
2:D:146:SER:O	2:D:149:VAL:HG23	2.20	0.41
1:A:8:HIS:ND1	1:A:124:VAL:HG22	2.36	0.41
2:B:5:ASN:HB3	2:B:6:LYS:H	1.55	0.41
2:B:18:ILE:O	2:B:19:ASP:HB2	2.19	0.41
2:B:28:LYS:HG3	2:B:32:LEU:HD22	2.02	0.41
2:B:84:ASN:O	2:B:86:ILE:HG13	2.20	0.41
2:B:92:VAL:O	2:B:92:VAL:HG13	2.21	0.41
1:C:10:ILE:HD12	1:C:112:ALA:CB	2.47	0.41
1:C:100:ASP:O	1:C:123:PRO:HD2	2.21	0.41
1:C:132:ASN:OD1	1:C:133:GLN:HG2	2.21	0.41
1:C:264:LEU:HD23	1:C:264:LEU:HA	1.86	0.41
2:D:13:LYS:C	2:D:41:ARG:NH2	2.79	0.41
2:D:38:THR:HB	2:D:39:ASP:H	1.58	0.41
2:D:59:ILE:CG2	2:D:60:LYS:N	2.84	0.41
2:D:106:VAL:HA	4:D:325:HOH:O	2.20	0.41
1:A:106:HIS:CG	1:A:107:PRO:HD2	2.56	0.41
1:A:306:ARG:H	1:A:306:ARG:HG2	1.74	0.41
1:C:84:LYS:HE2	1:C:84:LYS:O	2.19	0.41
1:C:277:VAL:O	1:C:279:LYS:N	2.54	0.41
1:C:285:TYR:N	4:C:311:HOH:O	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:134:ILE:HG12	2:D:147:HIS:CE1	2.56	0.41
1:A:95:ILE:C	1:A:97:THR:N	2.79	0.40
2:B:71:VAL:O	2:B:74:LEU:HG	2.21	0.40
1:C:30:LEU:HD12	1:C:298:ALA:HA	2.02	0.40
1:C:114:LEU:O	1:C:115:ALA:C	2.62	0.40
2:D:102:ARG:HH12	2:D:139:LYS:HG3	1.85	0.40
2:D:147:HIS:CE1	2:D:148:ASN:HD21	2.39	0.40
1:A:109:GLU:OE2	1:A:131:SER:N	2.43	0.40
2:B:66:LEU:O	2:B:85:ARG:NH2	2.55	0.40
1:C:124:VAL:O	1:C:124:VAL:HG23	2.22	0.40
1:C:163:LEU:HD23	1:C:186:PHE:HB3	2.01	0.40
1:C:201:MET:HG3	1:C:202:LEU:CD1	2.51	0.40
2:D:135:ALA:HA	2:D:145:PHE:O	2.21	0.40
1:A:65:ARG:NH1	1:A:65:ARG:CG	2.85	0.40
1:A:188:ALA:HB1	1:A:189:PRO:HD2	2.02	0.40
1:A:197:TYR:CE1	1:A:198:ILE:HG12	2.56	0.40
2:B:124:SER:O	2:B:139:LYS:HB3	2.21	0.40
1:C:11:SER:CA	1:C:133:GLN:HG3	2.50	0.40
1:C:70:VAL:HG12	1:C:71:VAL:N	2.37	0.40
2:B:26:GLY:HA2	2:B:29:LEU:CD1	2.52	0.40
2:B:33:PHE:HA	4:B:330:HOH:O	2.21	0.40
2:D:21:ILE:HD13	2:D:78:ALA:HB2	2.03	0.40
2:D:66:LEU:HD21	2:D:70:GLN:HB3	2.04	0.40
1:A:51:ALA:HB2	1:A:75:ASP:HA	2.02	0.40
1:A:100:ASP:O	1:A:101:ALA:HB2	2.21	0.40
1:A:248:VAL:O	1:A:248:VAL:HG22	2.21	0.40
2:B:134:ILE:N	2:B:134:ILE:CD1	2.84	0.40
1:C:84:LYS:HE2	1:C:84:LYS:CA	2.51	0.40
1:C:166:GLY:O	1:C:169:VAL:HB	2.22	0.40
1:C:218:VAL:HG23	1:C:219:MET:N	2.36	0.40

There are no symmetry-related clashes.

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	308/310 (99%)	246 (80%)	50 (16%)	12 (4%)	2	8
1	C	308/310 (99%)	236 (77%)	57 (18%)	15 (5%)	1	6
2	B	151/153 (99%)	92 (61%)	33 (22%)	26 (17%)	0	0
2	D	151/153 (99%)	80 (53%)	45 (30%)	26 (17%)	0	0
All	All	918/926 (99%)	654 (71%)	185 (20%)	79 (9%)	0	1

All (79) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	14	ASP
1	A	75	ASP
1	A	80	SER
1	A	86	GLU
1	A	245	ALA
2	B	3	HIS
2	B	34	LYS
2	B	37	GLU
2	B	60	LYS
2	B	75	ALA
2	B	76	LEU
2	B	94	LYS
2	B	95	SER
2	B	103	ILE
1	C	75	ASP
1	C	86	GLU
1	C	244	LYS
1	C	245	ALA
1	C	270	VAL
2	D	2	THR
2	D	13	LYS
2	D	68	GLU
2	D	75	ALA
2	D	76	LEU
2	D	89	TYR
2	D	92	VAL
2	D	114	CYS
2	D	115	ILE
2	D	152	ALA
1	A	272	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	9	VAL
2	B	11	ALA
2	B	13	LYS
2	B	22	PRO
2	B	54	GLY
2	B	59	ILE
2	B	117	HIS
1	C	272	GLU
1	C	278	ASP
2	D	29	LEU
2	D	73	GLN
2	D	88	ASN
1	A	85	GLY
2	B	5	ASN
2	B	36	THR
2	B	55	ARG
2	B	63	ASN
2	B	69	ASP
1	C	6	GLN
1	C	76	SER
1	C	134	HIS
2	D	54	GLY
2	D	105	ASN
1	A	65	ARG
2	B	73	GLN
1	C	217	GLU
2	D	5	ASN
2	D	28	LYS
1	A	62	SER
1	A	166	GLY
1	A	233	GLU
1	A	244	LYS
2	B	19	ASP
2	B	20	HIS
2	D	20	HIS
2	D	44	ILE
2	D	79	PRO
2	D	36	THR
2	D	84	ASN
2	D	133	ASP
2	B	92	VAL
1	C	309	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	237	PRO
2	B	18	ILE
1	C	3	PRO
2	D	93	GLY
2	D	110	PRO
1	C	243	VAL
2	D	12	ILE

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	261/261 (100%)	233 (89%)	28 (11%)	6	21
1	C	261/261 (100%)	223 (85%)	38 (15%)	3	11
2	B	137/137 (100%)	109 (80%)	28 (20%)	1	4
2	D	137/137 (100%)	117 (85%)	20 (15%)	3	11
All	All	796/796 (100%)	682 (86%)	114 (14%)	3	11

All (114) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LYS
1	A	12	ILE
1	A	17	ARG
1	A	29	LYS
1	A	50	GLU
1	A	59	PHE
1	A	81	LEU
1	A	86	GLU
1	A	99	VAL
1	A	116	THR
1	A	117	GLU
1	A	140	LEU
1	A	147	GLU
1	A	167	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	190	ASP
1	A	221	GLU
1	A	233	GLU
1	A	234	ARG
1	A	235	LEU
1	A	244	LYS
1	A	248	VAL
1	A	253	ASP
1	A	261	MET
1	A	272	GLU
1	A	279	LYS
1	A	285	TYR
1	A	288	GLN
1	A	299	LEU
2	B	3	HIS
2	B	10	GLU
2	B	14	ARG
2	B	28	LYS
2	B	29	LEU
2	B	38	THR
2	B	39	ASP
2	B	59	ILE
2	B	62	GLU
2	B	63	ASN
2	B	65	PHE
2	B	66	LEU
2	B	69	ASP
2	B	71	VAL
2	B	73	GLN
2	B	90	GLU
2	B	94	LYS
2	B	96	ARG
2	B	99	LEU
2	B	102	ARG
2	B	104	ASP
2	B	112	SER
2	B	113	ASN
2	B	115	ILE
2	B	127	VAL
2	B	133	ASP
2	B	142	GLU
2	B	148	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	4	LEU
1	C	7	LYS
1	C	14	ASP
1	C	29	LYS
1	C	34	PRO
1	C	54	ARG
1	C	57	LEU
1	C	59	PHE
1	C	83	LYS
1	C	84	LYS
1	C	86	GLU
1	C	87	THR
1	C	88	LEU
1	C	99	VAL
1	C	121	ASN
1	C	136	THR
1	C	151	ARG
1	C	153	ASP
1	C	154	ASN
1	C	170	HIS
1	C	171	SER
1	C	192	LEU
1	C	201	MET
1	C	213	SER
1	C	221	GLU
1	C	225	LEU
1	C	232	LYS
1	C	233	GLU
1	C	234	ARG
1	C	235	LEU
1	C	237	PRO
1	C	250	ARG
1	C	261	MET
1	C	272	GLU
1	C	275	THR
1	C	287	GLN
1	C	299	LEU
1	C	305	ASN
2	D	4	ASP
2	D	7	LEU
2	D	12	ILE
2	D	20	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	29	LEU
2	D	30	LEU
2	D	32	LEU
2	D	44	ILE
2	D	48	LEU
2	D	52	GLU
2	D	68	GLU
2	D	69	ASP
2	D	71	VAL
2	D	82	THR
2	D	90	GLU
2	D	95	SER
2	D	98	SER
2	D	103	ILE
2	D	136	LEU
2	D	149	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	21	ASN
1	A	41	HIS
1	A	64	HIS
1	A	132	ASN
1	A	134	HIS
1	A	260	ASN
1	A	265	HIS
1	A	297	GLN
2	B	5	ASN
2	B	73	GLN
2	B	111	ASN
2	B	113	ASN
1	C	35	GLN
1	C	41	HIS
1	C	121	ASN
1	C	126	ASN
1	C	132	ASN
1	C	146	GLN
1	C	174	GLN
1	C	212	HIS
1	C	255	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	265	HIS
1	C	287	GLN
2	D	20	HIS
2	D	70	GLN
2	D	73	GLN
2	D	80	GLN
2	D	84	ASN
2	D	113	ASN
2	D	132	ASN
2	D	148	ASN

5.3.3 RNA [i](#)

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	310/310 (100%)	-1.35	0 100 100	30, 50, 85, 117	0
1	C	310/310 (100%)	-1.38	0 100 100	30, 50, 88, 114	0
2	B	153/153 (100%)	-0.89	1 (0%) 84 77	42, 106, 149, 161	0
2	D	153/153 (100%)	-0.89	0 100 100	45, 107, 137, 154	0
All	All	926/926 (100%)	-1.21	1 (0%) 92 90	30, 57, 131, 161	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	58	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ZN	B	313	1/1	1.00	0.02	91,91,91,91	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ZN	D	314	1/1	1.00	0.03	99,99,99,99	0

6.5 Other polymers [i](#)

There are no such residues in this entry.