



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 04:18 am GMT

PDB ID : 3FHN
Title : Structure of Tip20p
Authors : Tripathi, A.; Ren, Y.; Jeffrey, P.D.; Hughson, F.M.
Deposited on : 2008-12-09
Resolution : 3.00 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

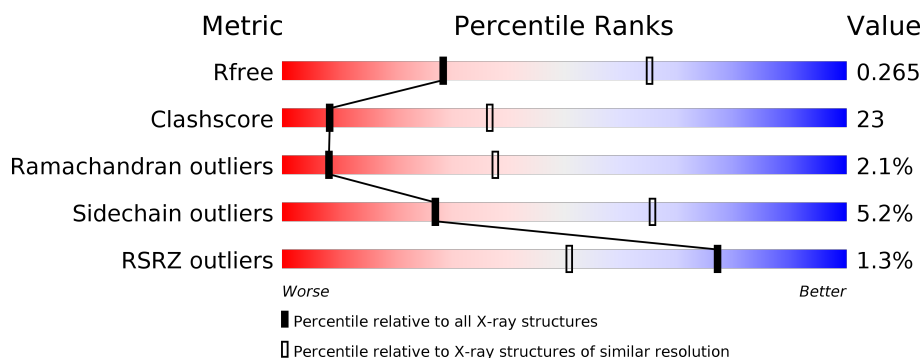
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	100719	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	706	<div> <div>%</div> <div> <div></div> <div>51%</div> <div>40%</div> <div>• 5%</div> </div> </div>
1	B	706	<div> <div>%</div> <div> <div></div> <div>57%</div> <div>35%</div> <div>• 5%</div> </div> </div>
1	C	706	<div> <div>%</div> <div> <div></div> <div>59%</div> <div>34%</div> <div>• 5%</div> </div> </div>
1	D	706	<div> <div>3%</div> <div> <div></div> <div>53%</div> <div>37%</div> <div>5% 5%</div> </div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 22040 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 Protein transport protein TIP20.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	673	Total	C	N	O	S	Se	0	0	0
			5510	3532	910	1053	5	10			
1	B	673	Total	C	N	O	S	Se	0	0	0
			5510	3532	910	1053	5	10			
1	C	673	Total	C	N	O	S	Se	0	0	0
			5510	3532	910	1053	5	10			
1	D	673	Total	C	N	O	S	Se	0	0	0
			5510	3532	910	1053	5	10			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	EXPRESSION TAG	UNP P33891
A	-3	ALA	-	EXPRESSION TAG	UNP P33891
A	-2	MSE	-	EXPRESSION TAG	UNP P33891
A	-1	GLY	-	EXPRESSION TAG	UNP P33891
A	0	SER	-	EXPRESSION TAG	UNP P33891
A	1	MSE	-	EXPRESSION TAG	UNP P33891
B	-4	GLY	-	EXPRESSION TAG	UNP P33891
B	-3	ALA	-	EXPRESSION TAG	UNP P33891
B	-2	MSE	-	EXPRESSION TAG	UNP P33891
B	-1	GLY	-	EXPRESSION TAG	UNP P33891
B	0	SER	-	EXPRESSION TAG	UNP P33891
B	1	MSE	-	EXPRESSION TAG	UNP P33891
C	-4	GLY	-	EXPRESSION TAG	UNP P33891
C	-3	ALA	-	EXPRESSION TAG	UNP P33891
C	-2	MSE	-	EXPRESSION TAG	UNP P33891
C	-1	GLY	-	EXPRESSION TAG	UNP P33891
C	0	SER	-	EXPRESSION TAG	UNP P33891
C	1	MSE	-	EXPRESSION TAG	UNP P33891
D	-4	GLY	-	EXPRESSION TAG	UNP P33891
D	-3	ALA	-	EXPRESSION TAG	UNP P33891
D	-2	MSE	-	EXPRESSION TAG	UNP P33891

Continued on next page...

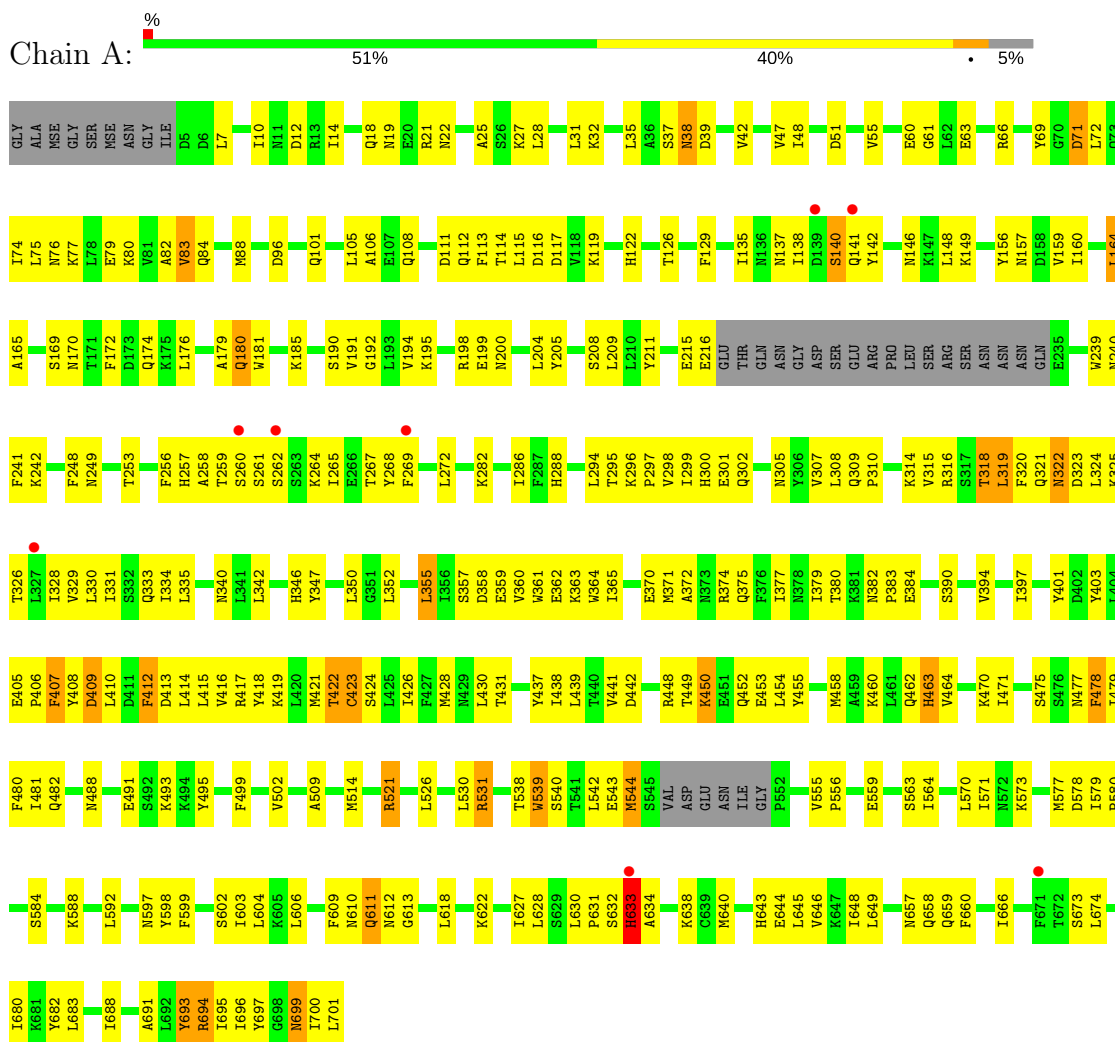
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	GLY	-	EXPRESSION TAG	UNP P33891
D	0	SER	-	EXPRESSION TAG	UNP P33891
D	1	MSE	-	EXPRESSION TAG	UNP P33891

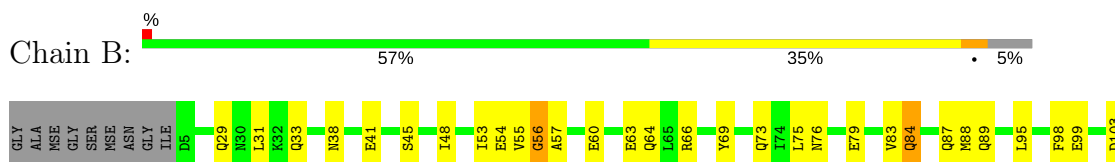
3 Residue-property plots

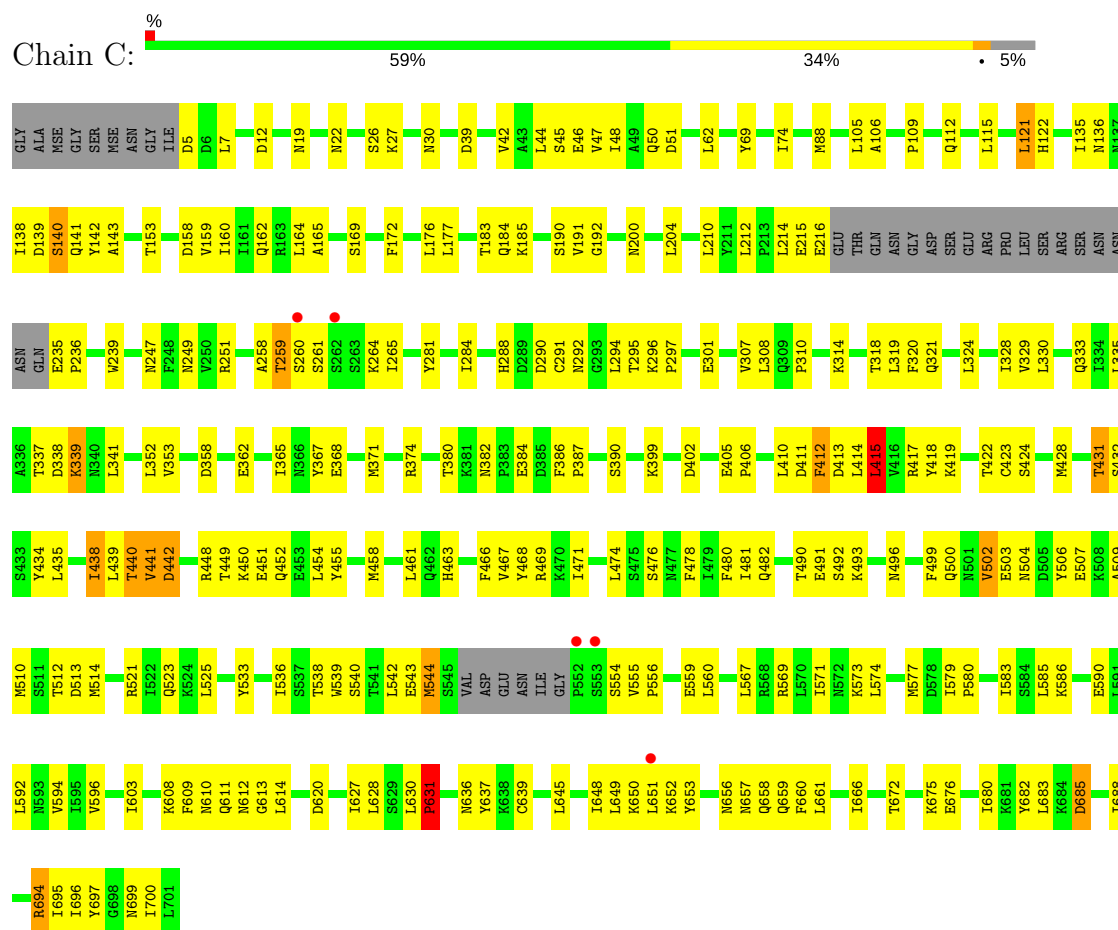
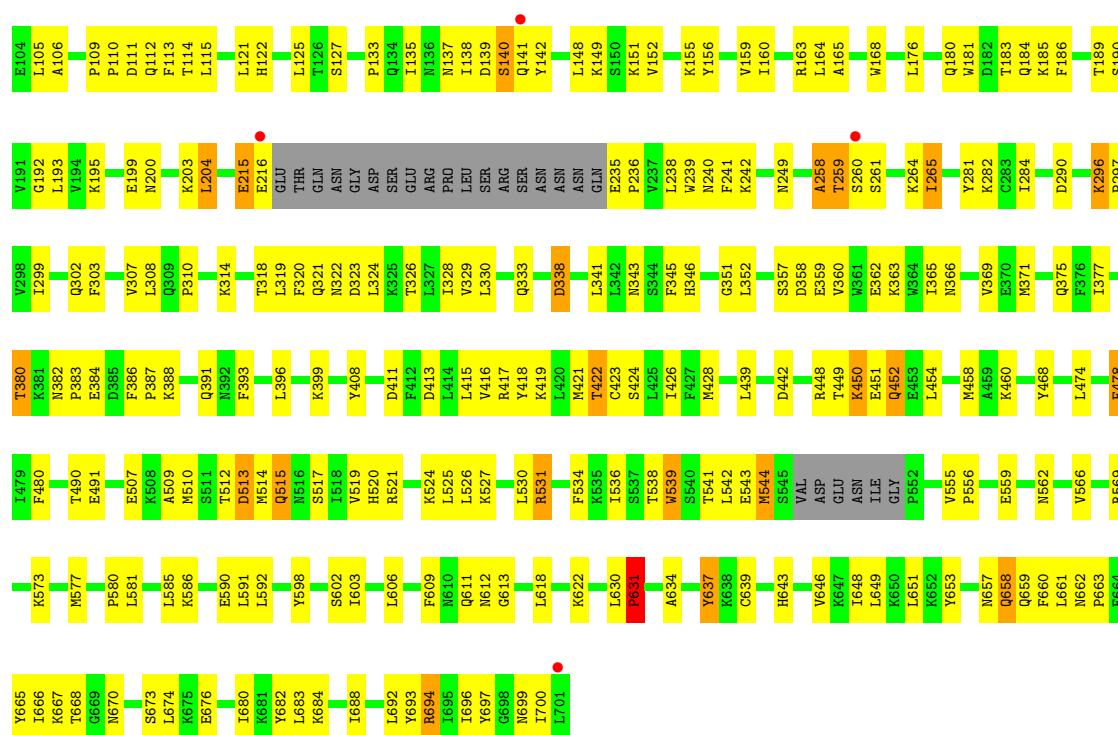
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Protein transport protein TIP20

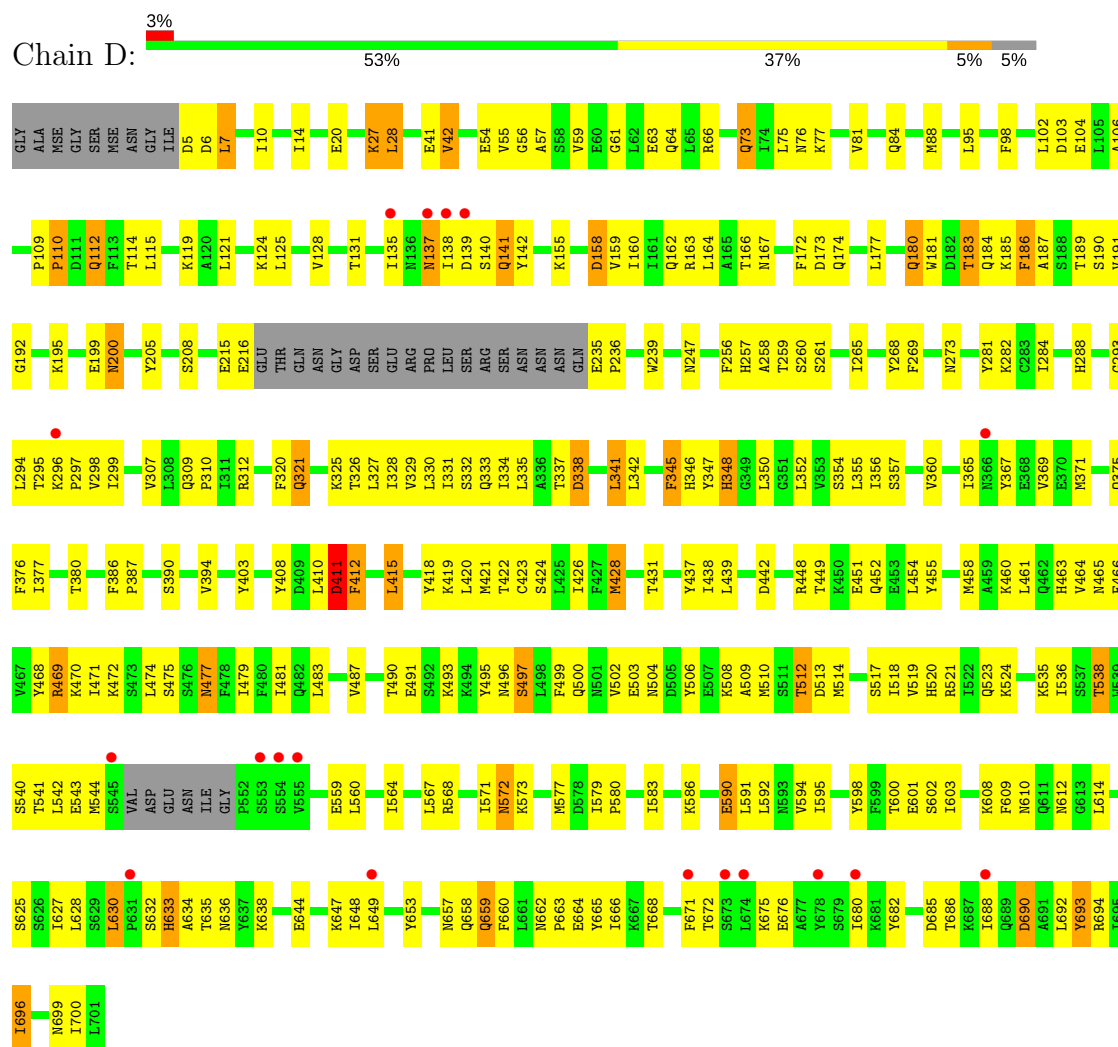


• Molecule 1: Protein transport protein TIP20





● Molecule 1: Protein transport protein TIP20



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	85.48Å 111.62Å 149.84Å 77.09° 88.12° 70.35°	Depositor
Resolution (Å)	29.90 – 3.00 48.97 – 2.99	Depositor EDS
% Data completeness (in resolution range)	98.2 (29.90-3.00) 90.3 (48.97-2.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 3.01Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.220 , 0.265 0.220 , 0.265	Depositor DCC
R_{free} test set	5002 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	73.5	Xtriage
Anisotropy	0.129	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.9	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	0.93	EDS
Total number of atoms	22040	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.75% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.42	0/5601	0.63	1/7561 (0.0%)
1	B	0.46	1/5601 (0.0%)	0.64	0/7561
1	C	0.44	0/5601	0.63	1/7561 (0.0%)
1	D	0.40	0/5601	0.60	0/7561
All	All	0.43	1/22404 (0.0%)	0.63	2/30244 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	460	LYS	CE-NZ	5.25	1.62	1.49

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	407	PHE	N-CA-C	-5.97	94.87	111.00
1	C	415	LEU	CA-CB-CG	5.13	127.10	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5510	0	5545	325	0
1	B	5510	0	5545	244	0
1	C	5510	0	5545	211	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	5510	0	5545	275	0
All	All	22040	0	22180	1020	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 23.

All (1020) 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:A:531:ARG:HH21	1:B:383:PRO:HD3	1.13	1.14
1:C:183:THR:HG22	1:C:185:LYS:H	1.10	1.14
1:B:365:ILE:HD11	1:B:418:TYR:HD2	1.19	1.05
1:A:295:THR:CG2	1:A:297:PRO:HD2	1.88	1.04
1:B:183:THR:HG22	1:B:185:LYS:H	1.22	1.03
1:A:531:ARG:HB2	1:A:531:ARG:HH11	1.18	1.03
1:A:295:THR:HG22	1:A:297:PRO:CD	1.89	1.01
1:A:564:ILE:HG23	1:A:627:ILE:HD11	1.44	0.99
1:C:424:SER:HA	1:C:428:MSE:HG3	1.45	0.99
1:C:538:THR:HG22	1:C:542:LEU:HB3	1.42	0.99
1:D:583:ILE:HA	1:D:586:LYS:HD2	1.45	0.98
1:A:521:ARG:HG3	1:A:521:ARG:HH11	1.29	0.96
1:D:183:THR:HG23	1:D:185:LYS:H	1.30	0.96
1:D:544:MSE:H	1:D:612:ASN:ND2	1.64	0.95
1:C:419:LYS:O	1:C:422:THR:HG22	1.64	0.95
1:A:295:THR:HG22	1:A:297:PRO:HD2	0.96	0.95
1:B:538:THR:HG22	1:B:542:LEU:HB3	1.48	0.95
1:A:335:LEU:HD21	1:A:410:LEU:HD11	1.49	0.94
1:A:531:ARG:NH2	1:B:383:PRO:HD3	1.83	0.93
1:D:235:GLU:N	1:D:236:PRO:HA	1.85	0.92
1:A:419:LYS:O	1:A:422:THR:HG22	1.68	0.92
1:D:439:LEU:HD21	1:D:514:MSE:HE2	1.50	0.92
1:C:649:LEU:HD22	1:C:700:ILE:HD11	1.49	0.91
1:C:695:ILE:HG12	1:C:700:ILE:HD12	1.49	0.91
1:C:338:ASP:OD1	1:C:353:VAL:HG23	1.71	0.91
1:D:592:LEU:HD23	1:D:636:ASN:HD22	1.34	0.90
1:C:365:ILE:HD11	1:C:418:TYR:HB3	1.53	0.89
1:B:265:ILE:HD12	1:B:330:LEU:HD22	1.53	0.88
1:B:658:GLN:HG3	1:B:661:LEU:HD12	1.55	0.88
1:D:449:THR:HG22	1:D:451:GLU:H	1.38	0.88
1:B:419:LYS:O	1:B:422:THR:HG22	1.73	0.88
1:C:88:MSE:HE1	1:C:141:GLN:HB2	1.57	0.86

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:449:THR:HB	1:D:452:GLN:HG3	1.57	0.86
1:D:394:VAL:HG13	1:D:470:LYS:HG2	1.55	0.85
1:A:377:ILE:HD13	1:B:534:PHE:HZ	1.41	0.85
1:B:259:THR:HG22	1:B:260:SER:H	1.41	0.84
1:B:666:ILE:HD12	1:B:696:ILE:HD12	1.60	0.84
1:C:586:LYS:O	1:C:590:GLU:HG2	1.78	0.84
1:C:450:LYS:HD2	1:C:525:LEU:HD23	1.60	0.83
1:C:371:MSE:HE1	1:C:374:ARG:HH21	1.43	0.83
1:B:630:LEU:HB3	1:B:631:PRO:HD2	1.61	0.82
1:C:412:PHE:O	1:C:415:LEU:HD22	1.78	0.82
1:B:555:VAL:HG12	1:B:556:PRO:HD2	1.62	0.82
1:C:458:MSE:HE2	1:C:574:LEU:HD13	1.60	0.82
1:B:531:ARG:HH11	1:B:531:ARG:HB2	1.44	0.81
1:A:137:ASN:HB2	1:A:140:SER:OG	1.81	0.81
1:A:666:ILE:HD12	1:A:696:ILE:HD12	1.62	0.81
1:C:140:SER:C	1:C:142:TYR:H	1.85	0.81
1:D:544:MSE:H	1:D:612:ASN:HD22	1.27	0.81
1:C:648:ILE:HD11	1:C:680:ILE:HD13	1.61	0.81
1:A:599:PHE:HA	1:A:603:ILE:HD13	1.63	0.80
1:C:666:ILE:HD12	1:C:696:ILE:HD12	1.63	0.80
1:B:235:GLU:HB3	1:B:236:PRO:HD3	1.62	0.80
1:D:140:SER:C	1:D:142:TYR:H	1.82	0.79
1:B:365:ILE:HD11	1:B:418:TYR:CD2	2.11	0.79
1:A:215:GLU:HG2	1:A:216:GLU:HG3	1.64	0.79
1:C:358:ASP:O	1:C:362:GLU:HG2	1.83	0.79
1:D:455:TYR:HD1	1:D:458:MSE:HE2	1.48	0.79
1:B:630:LEU:HB2	1:B:634:ALA:HB3	1.64	0.79
1:D:672:THR:O	1:D:676:GLU:HG2	1.83	0.78
1:D:424:SER:HA	1:D:428:MSE:HB2	1.64	0.78
1:A:428:MSE:HE2	1:A:499:PHE:HA	1.64	0.78
1:D:455:TYR:CD1	1:D:458:MSE:HE2	2.19	0.78
1:D:487:VAL:HA	1:D:490:THR:HG22	1.65	0.77
1:B:329:VAL:O	1:B:333:GLN:HG3	1.84	0.77
1:C:672:THR:O	1:C:676:GLU:HG2	1.84	0.77
1:D:542:LEU:HD12	1:D:612:ASN:HB3	1.66	0.77
1:B:649:LEU:HD22	1:B:700:ILE:HD11	1.67	0.77
1:A:316:ARG:HH12	1:A:357:SER:HB2	1.50	0.76
1:A:261:SER:HB3	1:A:264:LYS:HG3	1.67	0.76
1:D:458:MSE:HE1	1:D:573:LYS:HB3	1.67	0.76
1:A:531:ARG:HB2	1:A:531:ARG:NH1	1.96	0.76
1:D:499:PHE:O	1:D:503:GLU:HB2	1.85	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:648:ILE:HD11	1:B:680:ILE:HD13	1.67	0.76
1:B:84:GLN:HG2	1:B:135:ILE:HD13	1.67	0.76
1:A:618:LEU:HD11	1:A:646:VAL:HG21	1.67	0.76
1:A:88:MSE:HE3	1:A:141:GLN:HB2	1.67	0.75
1:C:666:ILE:HD12	1:C:696:ILE:CD1	2.17	0.75
1:D:560:LEU:O	1:D:564:ILE:HG13	1.85	0.75
1:A:448:ARG:HH22	1:B:450:LYS:HE3	1.51	0.75
1:C:630:LEU:HB3	1:C:631:PRO:HD2	1.67	0.74
1:A:371:MSE:O	1:A:375:GLN:HG3	1.87	0.74
1:D:564:ILE:HG22	1:D:627:ILE:HD11	1.68	0.74
1:C:432:SER:HB3	1:C:502:VAL:HG12	1.69	0.74
1:A:521:ARG:HG3	1:A:521:ARG:NH1	1.96	0.73
1:C:7:LEU:O	1:C:7:LEU:HD23	1.89	0.73
1:A:316:ARG:NH1	1:A:357:SER:HB2	2.03	0.73
1:D:325:LYS:HG2	1:D:367:TYR:OH	1.88	0.73
1:B:450:LYS:HB2	1:B:450:LYS:NZ	2.02	0.73
1:C:503:GLU:O	1:C:507:GLU:HG3	1.88	0.73
1:C:510:MSE:HE2	1:C:583:ILE:HD12	1.71	0.73
1:A:598:TYR:CE2	1:A:603:ILE:HD11	2.24	0.72
1:A:405:GLU:HB3	1:A:406:PRO:HD3	1.71	0.72
1:C:449:THR:HB	1:C:452:GLN:HG3	1.72	0.72
1:A:454:LEU:HG	1:A:458:MSE:HE2	1.71	0.72
1:D:648:ILE:HD13	1:D:688:ILE:HG23	1.71	0.72
1:A:649:LEU:HG	1:A:700:ILE:HD11	1.71	0.72
1:A:322:ASN:ND2	1:A:323:ASP:H	1.87	0.72
1:B:362:GLU:HG2	1:B:418:TYR:HE2	1.54	0.72
1:C:555:VAL:CG1	1:C:556:PRO:HD2	2.19	0.71
1:D:474:LEU:O	1:D:477:ASN:HB2	1.89	0.71
1:A:455:TYR:CE1	1:A:573:LYS:HG3	2.26	0.71
1:D:371:MSE:O	1:D:375:GLN:HG3	1.89	0.71
1:B:140:SER:C	1:B:142:TYR:H	1.94	0.71
1:B:651:LEU:HB3	1:B:661:LEU:HD21	1.72	0.71
1:A:571:ILE:HD12	1:A:628:LEU:HA	1.72	0.70
1:C:139:ASP:OD1	1:C:143:ALA:HB2	1.90	0.70
1:C:308:LEU:HD22	1:C:352:LEU:HD21	1.72	0.70
1:D:376:PHE:O	1:D:380:THR:HG22	1.91	0.70
1:C:696:ILE:HG22	1:C:697:TYR:CD2	2.26	0.70
1:A:325:LYS:O	1:A:328:ILE:HG22	1.91	0.70
1:B:113:PHE:HB2	1:B:164:LEU:HD11	1.73	0.70
1:B:660:PHE:HD2	1:B:665:TYR:CE2	2.10	0.70
1:B:449:THR:HG23	1:B:452:GLN:H	1.57	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:449:THR:HG22	1:C:451:GLU:H	1.57	0.69
1:B:365:ILE:O	1:B:369:VAL:HG23	1.91	0.69
1:B:555:VAL:CG1	1:B:556:PRO:HD2	2.22	0.69
1:C:259:THR:HG22	1:C:260:SER:H	1.56	0.69
1:A:449:THR:HG23	1:A:452:GLN:H	1.55	0.69
1:C:685:ASP:HA	1:C:688:ILE:HD12	1.73	0.69
1:D:350:LEU:HD11	1:D:354:SER:HB3	1.72	0.69
1:D:438:ILE:HD11	1:D:463:HIS:HB3	1.75	0.69
1:A:140:SER:C	1:A:142:TYR:H	1.94	0.69
1:C:509:ALA:HB1	1:C:514:MSE:HE2	1.75	0.68
1:C:324:LEU:HD13	1:C:367:TYR:HB2	1.75	0.68
1:A:439:LEU:HD21	1:A:514:MSE:HE2	1.75	0.68
1:A:357:SER:HB3	1:A:360:VAL:HG23	1.75	0.68
1:C:183:THR:HG22	1:C:185:LYS:N	1.96	0.68
1:A:428:MSE:CE	1:A:499:PHE:HA	2.24	0.68
1:C:371:MSE:CE	1:C:374:ARG:HH21	2.06	0.68
1:A:31:LEU:O	1:A:35:LEU:HD12	1.94	0.68
1:D:592:LEU:HD23	1:D:636:ASN:ND2	2.07	0.68
1:A:648:ILE:HD11	1:A:680:ILE:HD13	1.76	0.68
1:D:183:THR:HG23	1:D:185:LYS:N	2.07	0.68
1:D:439:LEU:CD2	1:D:514:MSE:HE2	2.23	0.67
1:D:88:MSE:HE1	1:D:141:GLN:HB2	1.75	0.67
1:D:504:ASN:HB3	1:D:508:LYS:HE3	1.76	0.67
1:B:618:LEU:O	1:B:622:LYS:HG3	1.94	0.67
1:D:7:LEU:HD23	1:D:7:LEU:H	1.58	0.67
1:A:55:VAL:HG12	1:A:61:GLY:HA3	1.76	0.67
1:C:424:SER:O	1:C:428:MSE:HB2	1.94	0.67
1:A:428:MSE:HE1	1:A:502:VAL:HB	1.76	0.67
1:D:543:GLU:HA	1:D:612:ASN:ND2	2.10	0.67
1:D:259:THR:HG22	1:D:260:SER:H	1.59	0.67
1:A:478:PHE:O	1:A:481:ILE:HG12	1.94	0.67
1:C:259:THR:HG22	1:C:260:SER:N	2.10	0.67
1:D:185:LYS:HA	1:D:185:LYS:HE2	1.75	0.67
1:D:408:TYR:HA	1:D:419:LYS:HE2	1.77	0.66
1:A:322:ASN:OD1	1:A:326:THR:HG21	1.95	0.66
1:D:449:THR:HG22	1:D:451:GLU:N	2.09	0.66
1:A:282:LYS:O	1:A:286:ILE:HG13	1.95	0.66
1:B:450:LYS:HB2	1:B:450:LYS:HZ2	1.60	0.66
1:C:567:LEU:HD23	1:C:627:ILE:HD12	1.77	0.66
1:D:390:SER:O	1:D:394:VAL:HG23	1.96	0.66
1:D:55:VAL:CG1	1:D:61:GLY:HA3	2.26	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:648:ILE:HD11	1:D:680:ILE:HG12	1.76	0.66
1:D:259:THR:HG22	1:D:260:SER:N	2.10	0.66
1:B:449:THR:HG22	1:B:452:GLN:CD	2.16	0.66
1:A:544:MSE:H	1:A:612:ASN:HB3	1.60	0.65
1:C:585:LEU:HD21	1:C:631:PRO:HD3	1.76	0.65
1:D:465:ASN:OD1	1:D:580:PRO:HD3	1.95	0.65
1:A:7:LEU:CD1	1:D:77:LYS:HB3	2.27	0.65
1:B:259:THR:HG22	1:B:260:SER:N	2.11	0.65
1:A:269:PHE:CE1	1:A:352:LEU:HD11	2.32	0.65
1:D:542:LEU:CD1	1:D:612:ASN:HB3	2.26	0.65
1:B:666:ILE:HD12	1:B:696:ILE:CD1	2.25	0.65
1:B:424:SER:HA	1:B:428:MSE:HE3	1.78	0.65
1:D:140:SER:C	1:D:142:TYR:N	2.47	0.65
1:A:564:ILE:HG23	1:A:627:ILE:CD1	2.25	0.65
1:D:55:VAL:O	1:D:57:ALA:N	2.30	0.65
1:D:487:VAL:HA	1:D:490:THR:CG2	2.26	0.65
1:A:555:VAL:HG22	1:A:556:PRO:HD2	1.79	0.65
1:B:618:LEU:HD22	1:B:646:VAL:HG11	1.79	0.65
1:C:523:GLN:HG3	1:C:594:VAL:HG11	1.78	0.64
1:C:630:LEU:HD12	1:C:630:LEU:H	1.62	0.64
1:D:579:ILE:HG23	1:D:580:PRO:HD2	1.78	0.64
1:D:662:ASN:HD21	1:D:665:TYR:HB2	1.61	0.64
1:D:140:SER:O	1:D:142:TYR:N	2.30	0.64
1:D:509:ALA:HB1	1:D:514:MSE:HE3	1.79	0.64
1:B:657:ASN:C	1:B:659:GLN:H	2.00	0.64
1:C:172:PHE:CE1	1:C:200:ASN:HB3	2.32	0.64
1:C:544:MSE:CE	1:C:554:SER:HB3	2.28	0.64
1:A:413:ASP:HA	1:A:416:VAL:HG23	1.78	0.64
1:B:630:LEU:HD12	1:B:630:LEU:H	1.62	0.64
1:D:665:TYR:O	1:D:668:THR:HB	1.98	0.64
1:A:7:LEU:HD13	1:D:77:LYS:HB3	1.79	0.64
1:A:288:HIS:CD2	1:A:296:LYS:HE3	2.32	0.64
1:B:159:VAL:HG12	1:B:160:ILE:HD12	1.80	0.64
1:A:113:PHE:HB2	1:A:164:LEU:HD11	1.80	0.63
1:A:394:VAL:HG13	1:A:470:LYS:HG2	1.80	0.63
1:C:592:LEU:HD22	1:C:639:CYS:SG	2.38	0.63
1:D:564:ILE:CG2	1:D:627:ILE:HD11	2.28	0.63
1:B:454:LEU:HG	1:B:458:MSE:HE2	1.79	0.63
1:C:265:ILE:HG21	1:C:330:LEU:HD22	1.79	0.63
1:D:428:MSE:HA	1:D:428:MSE:HE3	1.79	0.63
1:B:55:VAL:CG2	1:B:56:GLY:N	2.62	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:48:ILE:HG12	1:C:69:TYR:CE2	2.33	0.63
1:B:536:ILE:HD11	1:B:559:GLU:HG2	1.80	0.63
1:C:424:SER:HA	1:C:428:MSE:CG	2.26	0.63
1:C:510:MSE:HA	1:C:514:MSE:HE3	1.80	0.63
1:D:491:GLU:HB3	1:D:493:LYS:NZ	2.13	0.63
1:A:454:LEU:HG	1:A:458:MSE:CE	2.28	0.63
1:C:538:THR:CG2	1:C:542:LEU:HB3	2.23	0.63
1:A:295:THR:O	1:A:298:VAL:HB	1.99	0.62
1:A:407:PHE:O	1:A:408:TYR:HB2	1.98	0.62
1:A:618:LEU:HD13	1:A:646:VAL:HG11	1.80	0.62
1:B:517:SER:O	1:B:521:ARG:HG3	1.99	0.62
1:C:109:PRO:HG2	1:C:112:GLN:HG3	1.82	0.62
1:C:140:SER:C	1:C:142:TYR:N	2.50	0.62
1:B:343:ASN:ND2	1:C:339:LYS:HD2	2.13	0.62
1:C:512:THR:HG22	1:C:513:ASP:N	2.14	0.62
1:C:215:GLU:O	1:C:216:GLU:HB2	1.97	0.62
1:A:370:GLU:O	1:A:374:ARG:HG2	2.00	0.62
1:C:544:MSE:HE1	1:C:554:SER:HB3	1.81	0.62
1:C:555:VAL:HG12	1:C:556:PRO:HD2	1.82	0.62
1:B:630:LEU:HB3	1:B:631:PRO:CD	2.29	0.62
1:D:454:LEU:O	1:D:458:MSE:HG3	1.98	0.62
1:B:66:ARG:NH2	1:B:76:ASN:OD1	2.33	0.62
1:D:215:GLU:O	1:D:216:GLU:HB2	2.00	0.62
1:A:573:LYS:O	1:A:577:MSE:HG2	2.00	0.61
1:B:648:ILE:HD13	1:B:688:ILE:HG23	1.82	0.61
1:D:269:PHE:CE2	1:D:352:LEU:HD11	2.35	0.61
1:A:14:ILE:O	1:A:18:GLN:HG3	2.00	0.61
1:C:308:LEU:HD22	1:C:352:LEU:CD2	2.30	0.61
1:C:542:LEU:HD11	1:C:613:GLY:N	2.15	0.61
1:A:401:TYR:OH	1:A:479:ILE:HD12	2.00	0.61
1:A:185:LYS:O	1:A:185:LYS:HD3	2.00	0.61
1:A:363:LYS:HA	1:B:697:TYR:HE2	1.64	0.61
1:C:542:LEU:HD11	1:C:613:GLY:CA	2.30	0.61
1:C:636:ASN:HD22	1:C:639:CYS:H	1.48	0.61
1:D:121:LEU:HD13	1:D:160:ILE:HD13	1.82	0.61
1:C:658:GLN:HG3	1:C:661:LEU:HD12	1.82	0.61
1:A:431:THR:CG2	1:A:471:ILE:HD11	2.31	0.61
1:A:431:THR:HG23	1:A:471:ILE:HD11	1.82	0.61
1:A:509:ALA:HB1	1:A:514:MSE:HE1	1.83	0.61
1:C:261:SER:HB3	1:C:264:LYS:HD2	1.83	0.61
1:A:531:ARG:HH11	1:A:531:ARG:CB	2.05	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:660:PHE:HD2	1:B:665:TYR:HE2	1.49	0.61
1:A:335:LEU:HD22	1:A:410:LEU:HD21	1.83	0.60
1:C:318:THR:O	1:C:321:GLN:HG2	2.01	0.60
1:D:235:GLU:N	1:D:236:PRO:CA	2.61	0.60
1:A:335:LEU:CD2	1:A:410:LEU:HD11	2.29	0.60
1:A:372:ALA:HB1	1:A:430:LEU:HD11	1.83	0.60
1:B:190:SER:HB3	1:B:193:LEU:HB3	1.82	0.60
1:D:337:THR:O	1:D:341:LEU:HB2	2.00	0.60
1:A:38:ASN:HD21	1:D:6:ASP:HB2	1.66	0.60
1:A:588:LYS:HD3	1:A:628:LEU:O	2.01	0.60
1:B:358:ASP:O	1:B:362:GLU:HG3	2.02	0.60
1:C:183:THR:HG22	1:C:184:GLN:N	2.14	0.60
1:D:158:ASP:O	1:D:162:GLN:HB3	2.01	0.60
1:B:573:LYS:O	1:B:577:MSE:HG2	2.00	0.60
1:C:630:LEU:HD12	1:C:630:LEU:N	2.15	0.60
1:A:135:ILE:HG22	1:A:137:ASN:ND2	2.17	0.60
1:C:320:PHE:CE1	1:C:321:GLN:HB3	2.36	0.60
1:A:108:GLN:HG3	1:A:112:GLN:NE2	2.17	0.60
1:A:48:ILE:HG12	1:A:69:TYR:CE2	2.36	0.60
1:D:633:HIS:CD2	1:D:634:ALA:H	2.19	0.60
1:A:72:LEU:HB2	1:A:75:LEU:HD13	1.84	0.60
1:B:180:GLN:OE1	1:B:185:LYS:HD3	2.02	0.60
1:D:420:LEU:HD23	1:D:483:LEU:HD22	1.82	0.60
1:C:183:THR:CG2	1:C:185:LYS:HG2	2.31	0.60
1:C:455:TYR:CE1	1:C:573:LYS:HG3	2.37	0.60
1:D:307:VAL:O	1:D:310:PRO:HD2	2.01	0.60
1:A:405:GLU:O	1:A:407:PHE:O	2.20	0.59
1:B:451:GLU:CD	1:B:569:ARG:HH12	2.06	0.59
1:C:695:ILE:CG1	1:C:700:ILE:HD12	2.29	0.59
1:B:371:MSE:O	1:B:375:GLN:HG3	2.02	0.59
1:B:450:LYS:HD2	1:B:525:LEU:HD23	1.84	0.59
1:D:309:GLN:OE1	1:D:312:ARG:HD2	2.03	0.59
1:A:603:ILE:HD12	1:A:603:ILE:N	2.17	0.59
1:A:21:ARG:NH2	1:D:28:LEU:HD21	2.17	0.59
1:D:390:SER:HB3	1:D:466:PHE:HD2	1.67	0.59
1:A:657:ASN:C	1:A:659:GLN:H	2.04	0.59
1:A:645:LEU:HD12	1:A:683:LEU:HD21	1.83	0.59
1:D:183:THR:CG2	1:D:185:LYS:HB2	2.32	0.59
1:D:479:ILE:HG13	1:D:483:LEU:HD12	1.83	0.59
1:D:544:MSE:N	1:D:612:ASN:ND2	2.46	0.59
1:D:520:HIS:HB3	1:D:524:LYS:NZ	2.17	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:540:SER:C	1:A:610:ASN:HD22	2.06	0.59
1:B:190:SER:O	1:B:192:GLY:N	2.35	0.59
1:A:449:THR:HG22	1:A:452:GLN:HG3	1.83	0.59
1:C:478:PHE:O	1:C:482:GLN:HG2	2.03	0.59
1:A:455:TYR:HD1	1:A:458:MSE:HE3	1.67	0.59
1:C:88:MSE:CE	1:C:141:GLN:HB2	2.31	0.59
1:D:320:PHE:O	1:D:320:PHE:HD1	1.86	0.59
1:B:539:TRP:O	1:B:609:PHE:HA	2.03	0.58
1:D:590:GLU:O	1:D:594:VAL:HG23	2.02	0.58
1:D:649:LEU:HD22	1:D:700:ILE:HD12	1.84	0.58
1:A:428:MSE:CE	1:A:502:VAL:HB	2.33	0.58
1:A:530:LEU:HD13	1:A:598:TYR:CE2	2.38	0.58
1:A:543:GLU:HG2	1:A:543:GLU:O	2.03	0.58
1:C:579:ILE:HG23	1:C:580:PRO:HD2	1.84	0.58
1:A:140:SER:C	1:A:142:TYR:N	2.57	0.58
1:A:666:ILE:CD1	1:A:696:ILE:HD12	2.33	0.58
1:D:538:THR:O	1:D:542:LEU:HD23	2.03	0.58
1:A:408:TYR:HA	1:A:419:LYS:HE2	1.84	0.58
1:A:406:PRO:O	1:A:409:ASP:HB2	2.02	0.58
1:B:543:GLU:O	1:B:543:GLU:HG2	2.03	0.58
1:D:190:SER:O	1:D:192:GLY:N	2.28	0.58
1:A:195:LYS:NZ	1:A:198:ARG:HH21	2.02	0.58
1:A:584:SER:O	1:A:588:LYS:HG3	2.03	0.58
1:C:105:LEU:HD13	1:C:121:LEU:HD11	1.86	0.58
1:D:394:VAL:CG1	1:D:470:LYS:HG2	2.31	0.58
1:A:449:THR:HG22	1:A:452:GLN:OE1	2.04	0.58
1:C:249:ASN:OD1	1:C:310:PRO:HB3	2.03	0.58
1:D:332:SER:O	1:D:335:LEU:HB3	2.04	0.58
1:A:571:ILE:CD1	1:A:628:LEU:HA	2.34	0.58
1:B:258:ALA:CB	1:B:264:LYS:HZ3	2.17	0.58
1:B:359:GLU:O	1:B:363:LYS:HG2	2.04	0.58
1:A:618:LEU:CD1	1:A:646:VAL:HG21	2.34	0.58
1:C:657:ASN:C	1:C:659:GLN:H	2.07	0.58
1:A:377:ILE:HD13	1:B:534:PHE:CZ	2.32	0.57
1:A:449:THR:HG22	1:A:452:GLN:CG	2.34	0.57
1:A:96:ASP:OD1	1:A:148:LEU:HD21	2.04	0.57
1:C:439:LEU:O	1:C:440:THR:HG23	2.04	0.57
1:D:124:LYS:O	1:D:128:VAL:HG23	2.04	0.57
1:A:176:LEU:HD22	1:A:181:TRP:CD1	2.39	0.57
1:B:29:GLN:O	1:B:33:GLN:HG3	2.04	0.57
1:D:512:THR:HG22	1:D:513:ASP:N	2.19	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:ALA:HB1	1:A:514:MSE:CE	2.35	0.57
1:C:106:ALA:HB2	1:C:159:VAL:HG11	1.86	0.57
1:D:660:PHE:HD2	1:D:665:TYR:CE2	2.23	0.57
1:A:542:LEU:HD11	1:A:613:GLY:N	2.20	0.57
1:C:46:GLU:O	1:C:50:GLN:HG2	2.03	0.57
1:A:449:THR:CG2	1:A:452:GLN:HG3	2.35	0.57
1:D:649:LEU:HD13	1:D:700:ILE:HD11	1.85	0.57
1:C:7:LEU:C	1:C:7:LEU:HD23	2.24	0.57
1:D:160:ILE:O	1:D:164:LEU:HG	2.05	0.57
1:D:536:ILE:HD11	1:D:559:GLU:HG3	1.87	0.57
1:C:509:ALA:CB	1:C:514:MSE:HE2	2.35	0.57
1:A:84:GLN:NE2	1:A:135:ILE:HG21	2.19	0.57
1:A:542:LEU:HD11	1:A:613:GLY:CA	2.34	0.57
1:A:606:LEU:HD13	1:B:377:ILE:HD11	1.86	0.57
1:A:538:THR:HG22	1:A:542:LEU:HD23	1.87	0.56
1:D:609:PHE:HB2	1:D:614:LEU:HD13	1.86	0.56
1:A:406:PRO:C	1:A:407:PHE:O	2.38	0.56
1:B:555:VAL:HG12	1:B:556:PRO:CD	2.33	0.56
1:D:509:ALA:HB1	1:D:514:MSE:CE	2.35	0.56
1:C:183:THR:CG2	1:C:184:GLN:N	2.68	0.56
1:A:77:LYS:HE3	1:D:7:LEU:HB3	1.86	0.56
1:B:530:LEU:HD13	1:B:598:TYR:CE2	2.40	0.56
1:A:362:GLU:HG3	1:B:667:LYS:NZ	2.21	0.56
1:A:260:SER:HB2	1:A:318:THR:HB	1.87	0.56
1:D:496:ASN:HB2	1:D:500:GLN:NE2	2.20	0.56
1:A:648:ILE:HD12	1:A:683:LEU:HD23	1.88	0.56
1:B:140:SER:C	1:B:142:TYR:N	2.58	0.56
1:B:585:LEU:HD22	1:B:631:PRO:HD3	1.87	0.56
1:D:183:THR:CG2	1:D:185:LYS:H	2.13	0.56
1:B:103:ASP:OD1	1:B:155:LYS:HE2	2.06	0.56
1:B:541:THR:O	1:B:541:THR:HG22	2.05	0.56
1:C:533:TYR:HE2	1:C:603:ILE:HD13	1.70	0.56
1:D:591:LEU:O	1:D:595:ILE:HG13	2.06	0.56
1:A:269:PHE:CZ	1:A:352:LEU:HD11	2.40	0.55
1:D:411:ASP:O	1:D:412:PHE:O	2.24	0.55
1:D:483:LEU:O	1:D:487:VAL:HG23	2.06	0.55
1:A:412:PHE:CE1	1:A:414:LEU:HD12	2.41	0.55
1:C:367:TYR:CE1	1:C:371:MSE:HE3	2.41	0.55
1:C:442:ASP:CG	1:C:448:ARG:HH12	2.09	0.55
1:B:357:SER:OG	1:B:360:VAL:HG23	2.06	0.55
1:C:651:LEU:HD21	1:C:660:PHE:HB2	1.86	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:662:ASN:OD1	1:D:665:TYR:N	2.35	0.55
1:B:55:VAL:O	1:B:57:ALA:N	2.39	0.55
1:C:42:VAL:O	1:C:42:VAL:HG12	2.07	0.55
1:D:573:LYS:O	1:D:577:MSE:HG2	2.06	0.55
1:D:491:GLU:O	1:D:493:LYS:HD2	2.06	0.55
1:B:113:PHE:CB	1:B:164:LEU:HD11	2.37	0.55
1:D:538:THR:HG22	1:D:542:LEU:HB3	1.87	0.55
1:B:261:SER:HB3	1:B:264:LYS:HG3	1.89	0.55
1:C:555:VAL:HG13	1:C:556:PRO:HD2	1.87	0.55
1:D:55:VAL:HG11	1:D:61:GLY:HA3	1.89	0.55
1:C:542:LEU:O	1:C:542:LEU:HD12	2.07	0.55
1:B:160:ILE:O	1:B:164:LEU:HD23	2.07	0.55
1:B:382:ASN:HB3	1:B:384:GLU:CD	2.27	0.55
1:B:649:LEU:HD22	1:B:700:ILE:CD1	2.36	0.55
1:C:165:ALA:HB1	1:C:239:TRP:CG	2.42	0.55
1:D:510:MSE:HB3	1:D:583:ILE:CD1	2.36	0.55
1:B:559:GLU:CD	1:B:559:GLU:H	2.11	0.54
1:C:140:SER:HB2	1:C:142:TYR:HB2	1.89	0.54
1:D:487:VAL:CA	1:D:490:THR:HG22	2.37	0.54
1:D:59:VAL:O	1:D:63:GLU:HG2	2.07	0.54
1:A:648:ILE:HD11	1:A:680:ILE:CD1	2.37	0.54
1:B:168:TRP:CE3	1:B:203:LYS:HE3	2.42	0.54
1:B:538:THR:CG2	1:B:542:LEU:HB3	2.30	0.54
1:C:434:TYR:CE2	1:C:467:VAL:HG21	2.42	0.54
1:D:544:MSE:N	1:D:612:ASN:HD22	2.01	0.54
1:A:408:TYR:CE2	1:A:422:THR:HG21	2.42	0.54
1:D:422:THR:O	1:D:426:ILE:HB	2.07	0.54
1:B:338:ASP:OD1	1:B:351:GLY:HA3	2.07	0.54
1:B:658:GLN:HG3	1:B:661:LEU:CD1	2.35	0.54
1:D:666:ILE:HD12	1:D:696:ILE:HD12	1.88	0.54
1:B:490:THR:O	1:B:490:THR:HG22	2.07	0.54
1:C:435:LEU:HB2	1:C:506:TYR:CE1	2.42	0.54
1:B:83:VAL:O	1:B:87:GLN:HG3	2.07	0.54
1:D:345:PHE:O	1:D:347:TYR:N	2.40	0.54
1:A:316:ARG:HH12	1:A:357:SER:CB	2.20	0.54
1:D:84:GLN:HG3	1:D:135:ILE:HD12	1.90	0.54
1:C:160:ILE:O	1:C:164:LEU:HG	2.08	0.54
1:C:491:GLU:O	1:C:493:LYS:HG3	2.07	0.54
1:C:510:MSE:HB3	1:C:583:ILE:CD1	2.37	0.54
1:A:330:LEU:O	1:A:334:ILE:HG13	2.08	0.53
1:A:359:GLU:HG3	1:B:667:LYS:HE3	1.89	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:659:GLN:HG3	1:A:660:PHE:N	2.23	0.53
1:B:189:THR:HG22	1:B:189:THR:O	2.08	0.53
1:B:611:GLN:HB2	1:B:653:TYR:CE2	2.44	0.53
1:C:382:ASN:HB3	1:C:384:GLU:OE2	2.08	0.53
1:A:179:ALA:O	1:A:180:GLN:C	2.45	0.53
1:B:520:HIS:O	1:B:524:LYS:HG3	2.09	0.53
1:C:261:SER:HB3	1:C:264:LYS:CD	2.38	0.53
1:D:536:ILE:CD1	1:D:559:GLU:HG3	2.39	0.53
1:D:657:ASN:C	1:D:659:GLN:H	2.11	0.53
1:A:538:THR:CG2	1:A:542:LEU:HD23	2.38	0.53
1:B:66:ARG:HH21	1:B:76:ASN:HA	1.73	0.53
1:A:140:SER:HB2	1:A:142:TYR:HB2	1.89	0.53
1:A:610:ASN:O	1:A:613:GLY:N	2.40	0.53
1:A:438:ILE:HD13	1:A:464:VAL:HG23	1.91	0.53
1:B:422:THR:CG2	1:B:423:CYS:N	2.71	0.53
1:B:666:ILE:HD13	1:B:692:LEU:HB3	1.91	0.53
1:D:660:PHE:HD2	1:D:665:TYR:HE2	1.55	0.53
1:A:137:ASN:N	1:A:137:ASN:HD22	2.06	0.53
1:A:383:PRO:HG2	1:A:384:GLU:OE1	2.09	0.53
1:A:441:VAL:HG22	1:A:442:ASP:N	2.22	0.53
1:A:475:SER:HB3	1:A:499:PHE:HD2	1.74	0.53
1:A:695:ILE:HG12	1:A:700:ILE:HD12	1.91	0.53
1:B:84:GLN:HG2	1:B:135:ILE:CD1	2.37	0.53
1:C:694:ARG:O	1:C:699:ASN:HB2	2.09	0.53
1:D:540:SER:HA	1:D:610:ASN:ND2	2.23	0.53
1:A:315:VAL:HG11	1:A:355:LEU:HD21	1.90	0.53
1:C:542:LEU:HD12	1:C:542:LEU:C	2.28	0.53
1:A:697:TYR:CE2	1:B:363:LYS:HD3	2.44	0.53
1:A:359:GLU:HG3	1:B:667:LYS:CE	2.39	0.53
1:C:431:THR:HG23	1:C:471:ILE:HD11	1.90	0.53
1:D:121:LEU:HD13	1:D:160:ILE:CD1	2.39	0.53
1:B:55:VAL:HG23	1:B:56:GLY:N	2.24	0.53
1:D:183:THR:HG23	1:D:184:GLN:N	2.24	0.53
1:A:542:LEU:HD11	1:A:613:GLY:HA2	1.92	0.52
1:A:66:ARG:HD3	1:A:71:ASP:OD1	2.08	0.52
1:D:602:SER:C	1:D:603:ILE:HD12	2.29	0.52
1:A:455:TYR:CD1	1:A:458:MSE:HE3	2.44	0.52
1:D:106:ALA:HA	1:D:163:ARG:NH1	2.24	0.52
1:D:195:LYS:O	1:D:199:GLU:HG3	2.09	0.52
1:D:694:ARG:O	1:D:699:ASN:HB2	2.10	0.52
1:A:509:ALA:O	1:A:514:MSE:HE3	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:GLU:HG2	1:A:79:GLU:OE2	2.09	0.52
1:B:326:THR:O	1:B:330:LEU:HG	2.10	0.52
1:B:388:LYS:HD3	1:B:391:GLN:NE2	2.25	0.52
1:B:509:ALA:O	1:B:514:MSE:HE3	2.10	0.52
1:D:330:LEU:O	1:D:334:ILE:HG13	2.10	0.52
1:B:510:MSE:HE1	1:B:580:PRO:CD	2.39	0.52
1:A:261:SER:HB3	1:A:264:LYS:CG	2.38	0.52
1:A:382:ASN:HA	1:B:531:ARG:HH21	1.75	0.52
1:D:461:LEU:HD23	1:D:579:ILE:HD13	1.92	0.52
1:D:490:THR:HG23	1:D:491:GLU:N	2.25	0.52
1:A:261:SER:H	1:A:264:LYS:HB2	1.74	0.52
1:A:342:LEU:O	1:A:346:HIS:HA	2.09	0.52
1:B:602:SER:C	1:B:603:ILE:HD12	2.30	0.52
1:D:103:ASP:OD1	1:D:155:LYS:HE2	2.10	0.52
1:A:538:THR:CG2	1:A:542:LEU:HB3	2.40	0.52
1:C:411:ASP:O	1:C:413:ASP:N	2.43	0.52
1:A:530:LEU:HD23	1:A:563:SER:OG	2.10	0.52
1:B:509:ALA:HB1	1:B:514:MSE:CE	2.40	0.52
1:C:510:MSE:HE1	1:C:580:PRO:CD	2.40	0.52
1:D:568:ARG:O	1:D:572:ASN:HB2	2.09	0.52
1:C:329:VAL:O	1:C:333:GLN:HG3	2.10	0.51
1:A:101:GLN:O	1:A:105:LEU:HG	2.10	0.51
1:A:190:SER:C	1:A:192:GLY:H	2.13	0.51
1:B:148:LEU:O	1:B:152:VAL:HG23	2.10	0.51
1:D:464:VAL:HG21	1:D:514:MSE:SE	2.61	0.51
1:A:335:LEU:CD2	1:A:410:LEU:HD21	2.40	0.51
1:C:165:ALA:HB1	1:C:239:TRP:CD1	2.46	0.51
1:D:177:LEU:HD23	1:D:247:ASN:OD1	2.10	0.51
1:B:531:ARG:NH1	1:B:531:ARG:HB2	2.19	0.51
1:C:45:SER:OG	1:C:48:ILE:HG13	2.10	0.51
1:C:592:LEU:O	1:C:596:VAL:HG23	2.11	0.51
1:D:284:ILE:CG2	1:D:296:LYS:HG2	2.41	0.51
1:A:477:ASN:HB3	1:A:480:PHE:HD1	1.76	0.51
1:A:555:VAL:CG2	1:A:556:PRO:HD2	2.40	0.51
1:B:637:TYR:CE2	1:B:682:TYR:HB3	2.45	0.51
1:C:696:ILE:HG22	1:C:697:TYR:HD2	1.73	0.51
1:A:66:ARG:NH2	1:A:76:ASN:OD1	2.43	0.51
1:C:454:LEU:HA	1:C:521:ARG:HD3	1.93	0.51
1:D:27:LYS:HB2	1:D:27:LYS:NZ	2.26	0.51
1:A:165:ALA:HB1	1:A:239:TRP:CG	2.45	0.51
1:B:657:ASN:HB3	1:B:660:PHE:CE1	2.45	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:536:ILE:HD11	1:C:559:GLU:CG	2.41	0.51
1:B:106:ALA:HB2	1:B:159:VAL:HG11	1.92	0.51
1:C:190:SER:O	1:C:192:GLY:N	2.37	0.51
1:C:414:LEU:O	1:C:414:LEU:HD23	2.11	0.51
1:C:510:MSE:HB3	1:C:583:ILE:HD11	1.92	0.51
1:D:649:LEU:HB3	1:D:700:ILE:CD1	2.40	0.51
1:A:543:GLU:OE2	1:A:543:GLU:N	2.44	0.51
1:B:48:ILE:HG12	1:B:69:TYR:CD2	2.46	0.51
1:A:352:LEU:HB3	1:A:355:LEU:HD23	1.94	0.50
1:A:77:LYS:CE	1:D:7:LEU:HB3	2.41	0.50
1:D:635:THR:O	1:D:635:THR:HG22	2.11	0.50
1:C:261:SER:HB3	1:C:264:LYS:CG	2.40	0.50
1:D:428:MSE:HE2	1:D:502:VAL:HB	1.92	0.50
1:A:364:TRP:HE1	1:A:403:TYR:HH	1.59	0.50
1:C:284:ILE:O	1:C:288:HIS:HB3	2.11	0.50
1:C:653:TYR:N	1:C:653:TYR:CD1	2.79	0.50
1:D:592:LEU:CD1	1:D:625:SER:HB2	2.41	0.50
1:A:113:PHE:CB	1:A:164:LEU:HD11	2.41	0.50
1:A:371:MSE:HA	1:A:371:MSE:HE2	1.92	0.50
1:B:536:ILE:HD11	1:B:559:GLU:CG	2.42	0.50
1:C:386:PHE:N	1:C:387:PRO:HD2	2.27	0.50
1:C:450:LYS:HD2	1:C:525:LEU:CD2	2.39	0.50
1:B:88:MSE:HE1	1:B:141:GLN:C	2.31	0.50
1:C:649:LEU:CD2	1:C:700:ILE:HD11	2.33	0.50
1:D:657:ASN:O	1:D:659:GLN:N	2.44	0.50
1:A:248:PHE:CD2	1:A:307:VAL:HG13	2.47	0.50
1:B:622:LYS:HE2	1:B:643:HIS:HE1	1.76	0.50
1:C:590:GLU:O	1:C:594:VAL:HG23	2.12	0.50
1:D:690:ASP:O	1:D:694:ARG:HG3	2.12	0.50
1:A:618:LEU:HD23	1:A:622:LYS:NZ	2.27	0.50
1:A:694:ARG:HG3	1:A:699:ASN:HB2	1.94	0.50
1:B:442:ASP:OD2	1:B:448:ARG:NH1	2.39	0.50
1:D:181:TRP:HA	1:D:186:PHE:HB2	1.92	0.50
1:D:471:ILE:HG23	1:D:499:PHE:HD2	1.76	0.50
1:A:296:LYS:HB2	1:A:297:PRO:HD3	1.94	0.50
1:A:539:TRP:O	1:A:609:PHE:HA	2.12	0.50
1:D:172:PHE:CE1	1:D:200:ASN:HB3	2.46	0.50
1:D:183:THR:HG21	1:D:185:LYS:HB2	1.94	0.50
1:D:256:PHE:CD2	1:D:268:TYR:HE2	2.30	0.50
1:D:475:SER:HB2	1:D:497:SER:OG	2.12	0.50
1:D:682:TYR:CD1	1:D:682:TYR:N	2.80	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:586:LYS:O	1:B:590:GLU:HG2	2.11	0.49
1:B:611:GLN:N	1:B:653:TYR:OH	2.45	0.49
1:C:510:MSE:HE1	1:C:580:PRO:HD3	1.94	0.49
1:D:295:THR:CG2	1:D:297:PRO:HD2	2.42	0.49
1:A:408:TYR:OH	1:A:422:THR:HG21	2.12	0.49
1:C:685:ASP:HA	1:C:688:ILE:CD1	2.42	0.49
1:A:170:ASN:O	1:A:174:GLN:HG3	2.12	0.49
1:A:324:LEU:CD2	1:A:363:LYS:HE2	2.42	0.49
1:A:262:SER:O	1:A:333:GLN:OE1	2.30	0.49
1:B:215:GLU:O	1:B:216:GLU:HB2	2.12	0.49
1:C:571:ILE:HG12	1:C:628:LEU:HD23	1.93	0.49
1:D:139:ASP:C	1:D:140:SER:O	2.49	0.49
1:D:331:ILE:HG23	1:D:410:LEU:HD11	1.94	0.49
1:D:411:ASP:O	1:D:412:PHE:C	2.50	0.49
1:A:579:ILE:HG23	1:A:580:PRO:HD2	1.95	0.49
1:B:422:THR:O	1:B:426:ILE:HB	2.13	0.49
1:D:98:PHE:CE2	1:D:125:LEU:HD22	2.48	0.49
1:A:657:ASN:O	1:A:659:GLN:N	2.46	0.49
1:B:181:TRP:O	1:B:282:LYS:HE2	2.12	0.49
1:B:439:LEU:HD21	1:B:514:MSE:HE2	1.94	0.49
1:C:177:LEU:HD23	1:C:247:ASN:OD1	2.12	0.49
1:D:106:ALA:HB2	1:D:159:VAL:HG11	1.94	0.49
1:A:205:TYR:CG	1:A:294:LEU:HD21	2.48	0.49
1:A:380:THR:HB	1:A:437:TYR:CE2	2.47	0.49
1:D:320:PHE:O	1:D:320:PHE:CD1	2.66	0.49
1:D:469:ARG:HH11	1:D:469:ARG:HG2	1.78	0.49
1:D:666:ILE:HG12	1:D:692:LEU:HD13	1.94	0.49
1:A:359:GLU:OE2	1:B:667:LYS:HE3	2.12	0.49
1:B:694:ARG:O	1:B:699:ASN:HB2	2.12	0.49
1:C:109:PRO:HG2	1:C:112:GLN:CG	2.42	0.49
1:C:5:ASP:C	1:C:7:LEU:H	2.15	0.49
1:A:352:LEU:N	1:A:352:LEU:HD23	2.27	0.49
1:B:105:LEU:HD13	1:B:121:LEU:HD11	1.93	0.49
1:B:45:SER:OG	1:B:48:ILE:HG13	2.13	0.49
1:C:543:GLU:HA	1:C:612:ASN:ND2	2.28	0.49
1:C:648:ILE:HD12	1:C:683:LEU:HD23	1.94	0.49
1:A:424:SER:HA	1:A:428:MSE:HB2	1.94	0.49
1:B:122:HIS:HB2	1:B:156:TYR:OH	2.12	0.49
1:B:413:ASP:O	1:B:416:VAL:HG12	2.13	0.49
1:C:26:SER:O	1:C:30:ASN:ND2	2.45	0.49
1:C:630:LEU:HB3	1:C:631:PRO:CD	2.38	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:580:PRO:CG	1:D:583:ILE:HD12	2.43	0.49
1:A:491:GLU:O	1:A:493:LYS:HG3	2.13	0.49
1:D:109:PRO:HA	1:D:110:PRO:HD3	1.72	0.49
1:D:471:ILE:HG23	1:D:499:PHE:CD2	2.47	0.49
1:D:506:TYR:O	1:D:510:MSE:HG3	2.13	0.49
1:D:579:ILE:CG2	1:D:580:PRO:HD2	2.42	0.49
1:B:630:LEU:O	1:B:631:PRO:C	2.51	0.48
1:C:555:VAL:HG12	1:C:556:PRO:CD	2.43	0.48
1:C:573:LYS:O	1:C:577:MSE:HG2	2.13	0.48
1:D:84:GLN:HE21	1:D:135:ILE:HD13	1.78	0.48
1:D:490:THR:HG23	1:D:491:GLU:CD	2.33	0.48
1:D:540:SER:C	1:D:610:ASN:ND2	2.66	0.48
1:A:269:PHE:HE1	1:A:352:LEU:HD11	1.78	0.48
1:A:610:ASN:O	1:A:612:ASN:N	2.46	0.48
1:D:128:VAL:O	1:D:131:THR:HB	2.13	0.48
1:A:260:SER:HB2	1:A:318:THR:CB	2.43	0.48
1:C:458:MSE:HE2	1:C:574:LEU:CD1	2.40	0.48
1:D:115:LEU:O	1:D:119:LYS:HG3	2.12	0.48
1:A:42:VAL:HG12	1:A:42:VAL:O	2.13	0.48
1:B:195:LYS:O	1:B:199:GLU:HG3	2.13	0.48
1:B:408:TYR:OH	1:B:422:THR:CG2	2.61	0.48
1:C:183:THR:HG21	1:C:185:LYS:HG2	1.96	0.48
1:A:450:LYS:HE3	1:B:448:ARG:HH22	1.78	0.48
1:A:441:VAL:CG1	1:A:460:LYS:HE2	2.43	0.48
1:C:158:ASP:HA	1:C:162:GLN:HB2	1.95	0.48
1:C:235:GLU:HB2	1:C:236:PRO:HD3	1.94	0.48
1:D:166:THR:HG22	1:D:167:ASN:N	2.29	0.48
1:D:644:GLU:OE2	1:D:682:TYR:CD1	2.66	0.48
1:A:205:TYR:CE2	1:A:209:LEU:HD11	2.49	0.48
1:C:648:ILE:HD11	1:C:680:ILE:CD1	2.37	0.48
1:D:288:HIS:HA	1:D:299:ILE:HD12	1.95	0.48
1:A:129:PHE:CD2	1:A:149:LYS:HE3	2.49	0.48
1:A:438:ILE:HD11	1:A:463:HIS:HB3	1.96	0.48
1:C:284:ILE:CG2	1:C:296:LYS:HG2	2.43	0.48
1:C:496:ASN:N	1:C:500:GLN:OE1	2.35	0.48
1:A:383:PRO:HD3	1:B:531:ARG:NH2	2.29	0.48
1:B:137:ASN:O	1:B:139:ASP:N	2.47	0.48
1:B:261:SER:H	1:B:264:LYS:HD2	1.78	0.48
1:A:88:MSE:SE	1:A:142:TYR:HD1	2.47	0.48
1:A:649:LEU:CG	1:A:700:ILE:HD11	2.41	0.48
1:D:496:ASN:HB2	1:D:500:GLN:CD	2.35	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:690:ASP:HA	1:D:693:TYR:HB2	1.95	0.48
1:A:407:PHE:O	1:A:409:ASP:N	2.37	0.48
1:A:538:THR:HG22	1:A:542:LEU:HB3	1.95	0.48
1:A:454:LEU:HD23	1:A:570:LEU:HD22	1.96	0.48
1:A:645:LEU:O	1:A:649:LEU:HD13	2.14	0.48
1:B:468:TYR:CE1	1:B:507:GLU:HG3	2.49	0.48
1:A:106:ALA:HB2	1:A:159:VAL:HG11	1.96	0.47
1:A:417:ARG:O	1:A:421:MSE:HG3	2.14	0.47
1:A:441:VAL:HG12	1:A:460:LYS:HE2	1.95	0.47
1:A:47:VAL:HG13	1:A:48:ILE:N	2.29	0.47
1:A:604:LEU:HG	1:A:694:ARG:HH22	1.79	0.47
1:B:88:MSE:HE1	1:B:141:GLN:CB	2.44	0.47
1:A:610:ASN:O	1:A:611:GLN:C	2.53	0.47
1:D:328:ILE:HG13	1:D:403:TYR:CZ	2.49	0.47
1:D:536:ILE:HG12	1:D:559:GLU:HG3	1.96	0.47
1:A:39:ASP:HB2	1:A:74:ILE:HD12	1.95	0.47
1:B:450:LYS:CB	1:B:450:LYS:NZ	2.74	0.47
1:B:651:LEU:O	1:B:661:LEU:HD11	2.14	0.47
1:C:476:SER:HA	1:C:481:ILE:HD11	1.96	0.47
1:C:542:LEU:HD11	1:C:613:GLY:HA2	1.95	0.47
1:D:442:ASP:CG	1:D:448:ARG:HH12	2.16	0.47
1:B:109:PRO:O	1:B:111:ASP:N	2.48	0.47
1:B:544:MSE:H	1:B:612:ASN:HB3	1.79	0.47
1:C:540:SER:HB3	1:C:608:LYS:O	2.14	0.47
1:D:686:THR:O	1:D:690:ASP:OD1	2.32	0.47
1:B:303:PHE:O	1:B:307:VAL:HG23	2.14	0.47
1:D:259:THR:CG2	1:D:260:SER:H	2.26	0.47
1:A:422:THR:CG2	1:A:423:CYS:N	2.77	0.47
1:A:48:ILE:HG12	1:A:69:TYR:CD2	2.50	0.47
1:C:384:GLU:O	1:C:387:PRO:HD2	2.15	0.47
1:D:663:PRO:HG2	1:D:664:GLU:OE1	2.15	0.47
1:A:347:TYR:HE2	1:A:350:LEU:O	1.98	0.47
1:A:688:ILE:O	1:A:691:ALA:HB3	2.15	0.47
1:B:258:ALA:HB3	1:B:264:LYS:HZ3	1.79	0.47
1:B:386:PHE:N	1:B:387:PRO:HD2	2.30	0.47
1:A:137:ASN:HB2	1:A:140:SER:HG	1.78	0.47
1:A:559:GLU:CD	1:A:559:GLU:H	2.17	0.47
1:B:515:GLN:O	1:B:519:VAL:HG23	2.15	0.47
1:B:539:TRP:HB3	1:B:609:PHE:CD2	2.50	0.47
1:C:362:GLU:OE2	1:C:417:ARG:NH1	2.47	0.47
1:A:122:HIS:O	1:A:126:THR:HG23	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:LEU:HD22	1:A:352:LEU:HD21	1.97	0.47
1:A:422:THR:O	1:A:426:ILE:HB	2.14	0.47
1:A:694:ARG:HD2	1:A:699:ASN:OD1	2.15	0.47
1:C:122:HIS:NE2	1:C:212:LEU:HD21	2.29	0.47
1:C:153:THR:HB	1:C:214:LEU:CD2	2.45	0.47
1:C:335:LEU:HD22	1:C:410:LEU:HD11	1.96	0.47
1:C:365:ILE:HD11	1:C:418:TYR:CB	2.33	0.47
1:D:295:THR:HB	1:D:298:VAL:HG23	1.95	0.47
1:D:657:ASN:HB3	1:D:660:PHE:CE1	2.50	0.47
1:A:195:LYS:HZ3	1:A:198:ARG:HH21	1.63	0.47
1:B:204:LEU:HD12	1:B:239:TRP:HB2	1.96	0.47
1:B:258:ALA:HB1	1:B:264:LYS:HZ3	1.80	0.47
1:B:527:LYS:NZ	1:B:598:TYR:HB2	2.30	0.47
1:A:190:SER:O	1:A:192:GLY:N	2.44	0.47
1:A:660:PHE:CD1	1:A:674:LEU:HD13	2.50	0.47
1:D:662:ASN:ND2	1:D:665:TYR:HB2	2.30	0.47
1:B:84:GLN:HE21	1:B:135:ILE:HD13	1.80	0.46
1:C:290:ASP:C	1:C:292:ASN:H	2.18	0.46
1:A:157:ASN:ND2	1:A:211:TYR:CE1	2.83	0.46
1:A:319:LEU:HD21	1:A:360:VAL:HG11	1.98	0.46
1:A:462:GLN:HG3	1:A:578:ASP:H	1.79	0.46
1:B:478:PHE:H	1:B:478:PHE:HD2	1.60	0.46
1:C:390:SER:HB2	1:C:466:PHE:HD2	1.79	0.46
1:D:420:LEU:CD2	1:D:483:LEU:HD22	2.44	0.46
1:A:408:TYR:OH	1:A:422:THR:CG2	2.63	0.46
1:B:559:GLU:CD	1:B:559:GLU:N	2.69	0.46
1:D:431:THR:HB	1:D:502:VAL:HG11	1.97	0.46
1:A:108:GLN:HG3	1:A:112:GLN:HE21	1.78	0.46
1:B:180:GLN:O	1:B:183:THR:HB	2.15	0.46
1:C:281:TYR:HA	1:C:284:ILE:HD12	1.98	0.46
1:A:355:LEU:HD12	1:A:355:LEU:C	2.36	0.46
1:C:210:LEU:HA	1:C:210:LEU:HD23	1.72	0.46
1:D:261:SER:O	1:D:265:ILE:HG13	2.16	0.46
1:D:510:MSE:HB3	1:D:583:ILE:HD11	1.98	0.46
1:A:240:ASN:OD1	1:A:241:PHE:CD1	2.68	0.46
1:A:592:LEU:HD13	1:A:628:LEU:HD12	1.98	0.46
1:C:648:ILE:HD12	1:C:683:LEU:CD2	2.45	0.46
1:D:671:PHE:HE2	1:D:692:LEU:CD1	2.29	0.46
1:D:700:ILE:O	1:D:700:ILE:HG22	2.15	0.46
1:A:390:SER:OG	1:A:463:HIS:CG	2.68	0.46
1:B:140:SER:HB2	1:B:142:TYR:HB2	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:TRP:CZ3	1:B:203:LYS:HE3	2.50	0.46
1:B:284:ILE:HA	1:B:299:ILE:HG21	1.96	0.46
1:B:296:LYS:CB	1:B:297:PRO:HD3	2.45	0.46
1:C:499:PHE:O	1:C:502:VAL:HG23	2.16	0.46
1:D:61:GLY:O	1:D:64:GLN:HB2	2.15	0.46
1:B:259:THR:CG2	1:B:260:SER:H	2.20	0.46
1:C:165:ALA:HB1	1:C:239:TRP:CD2	2.51	0.46
1:D:205:TYR:CG	1:D:294:LEU:HD21	2.51	0.46
1:A:137:ASN:N	1:A:137:ASN:ND2	2.64	0.46
1:A:438:ILE:HG22	1:A:439:LEU:HD23	1.97	0.46
1:B:451:GLU:OE2	1:B:569:ARG:NH1	2.49	0.46
1:B:693:TYR:HD2	1:B:697:TYR:CE1	2.34	0.46
1:C:371:MSE:HE1	1:C:374:ARG:NH2	2.23	0.46
1:C:658:GLN:HG3	1:C:661:LEU:CD1	2.46	0.46
1:B:543:GLU:OE2	1:B:543:GLU:N	2.48	0.45
1:B:684:LYS:O	1:B:688:ILE:HG13	2.15	0.45
1:D:259:THR:CG2	1:D:260:SER:N	2.78	0.45
1:A:308:LEU:HD22	1:A:352:LEU:CD2	2.46	0.45
1:A:331:ILE:HD12	1:A:364:TRP:CD1	2.52	0.45
1:A:604:LEU:HD12	1:A:609:PHE:CE1	2.50	0.45
1:B:109:PRO:HD2	1:B:112:GLN:OE1	2.16	0.45
1:B:490:THR:O	1:B:491:GLU:HG3	2.17	0.45
1:B:55:VAL:HG22	1:B:56:GLY:H	1.81	0.45
1:B:622:LYS:HE2	1:B:643:HIS:CE1	2.51	0.45
1:C:307:VAL:O	1:C:307:VAL:HG12	2.16	0.45
1:A:205:TYR:O	1:A:208:SER:HB2	2.16	0.45
1:A:592:LEU:HD22	1:A:630:LEU:HD12	1.98	0.45
1:A:640:MSE:HE2	1:A:640:MSE:HA	1.98	0.45
1:C:490:THR:O	1:C:490:THR:HG22	2.16	0.45
1:D:102:LEU:C	1:D:104:GLU:H	2.20	0.45
1:D:41:GLU:HG2	1:D:73:GLN:NE2	2.32	0.45
1:A:454:LEU:CG	1:A:458:MSE:HE2	2.43	0.45
1:A:531:ARG:HH21	1:B:383:PRO:CD	2.04	0.45
1:A:666:ILE:HG21	1:A:693:TYR:CE2	2.51	0.45
1:B:512:THR:OG1	1:B:513:ASP:N	2.49	0.45
1:C:585:LEU:CD2	1:C:631:PRO:HD3	2.45	0.45
1:D:106:ALA:HA	1:D:163:ARG:HH12	1.81	0.45
1:A:38:ASN:HD21	1:D:6:ASP:CB	2.29	0.45
1:B:95:LEU:HD13	1:B:149:LYS:HA	1.99	0.45
1:C:658:GLN:CG	1:C:661:LEU:HD12	2.45	0.45
1:D:431:THR:CG2	1:D:471:ILE:HD11	2.46	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:ARG:HH12	1:B:450:LYS:HG3	1.81	0.45
1:A:481:ILE:HG13	1:A:482:GLN:N	2.30	0.45
1:A:694:ARG:O	1:A:699:ASN:HB2	2.16	0.45
1:D:42:VAL:HG12	1:D:42:VAL:O	2.17	0.45
1:A:116:ASP:O	1:A:119:LYS:N	2.50	0.45
1:C:543:GLU:HA	1:C:612:ASN:HD22	1.81	0.45
1:D:461:LEU:HD21	1:D:583:ILE:HG21	1.99	0.45
1:A:644:GLU:O	1:A:648:ILE:HG13	2.16	0.45
1:C:259:THR:CG2	1:C:260:SER:H	2.26	0.45
1:C:44:LEU:HD11	1:C:74:ILE:HD13	1.98	0.45
1:D:187:ALA:C	1:D:189:THR:H	2.20	0.45
1:D:415:LEU:HD13	1:D:419:LYS:HE3	1.99	0.45
1:D:365:ILE:HD12	1:D:418:TYR:HD2	1.81	0.45
1:D:468:TYR:CZ	1:D:472:LYS:HE3	2.52	0.45
1:D:644:GLU:OE2	1:D:682:TYR:HD1	1.99	0.45
1:C:438:ILE:HD11	1:C:463:HIS:HB2	1.99	0.45
1:D:377:ILE:HA	1:D:380:THR:CG2	2.47	0.45
1:D:428:MSE:HA	1:D:428:MSE:CE	2.47	0.45
1:D:438:ILE:CD1	1:D:463:HIS:HB3	2.46	0.45
1:D:5:ASP:N	1:D:7:LEU:HD21	2.31	0.45
1:D:600:THR:HG22	1:D:601:GLU:OE2	2.16	0.45
1:A:622:LYS:HE2	1:A:643:HIS:NE2	2.32	0.45
1:B:159:VAL:O	1:B:163:ARG:HD3	2.17	0.45
1:C:536:ILE:HD11	1:C:559:GLU:HG2	1.98	0.45
1:D:41:GLU:O	1:D:42:VAL:C	2.54	0.45
1:D:493:LYS:HG2	1:D:495:TYR:HE1	1.81	0.45
1:D:567:LEU:O	1:D:571:ILE:HB	2.15	0.45
1:B:666:ILE:HG22	1:B:693:TYR:CE1	2.52	0.44
1:C:135:ILE:HG22	1:C:136:ASN:N	2.32	0.44
1:A:335:LEU:HA	1:A:335:LEU:HD23	1.78	0.44
1:C:637:TYR:CD1	1:C:682:TYR:HD2	2.35	0.44
1:A:488:ASN:HD21	1:A:495:TYR:H	1.64	0.44
1:D:580:PRO:HG2	1:D:583:ILE:HD12	2.00	0.44
1:D:647:LYS:HE3	1:D:647:LYS:HB2	1.83	0.44
1:C:320:PHE:CD1	1:C:321:GLN:N	2.85	0.44
1:D:491:GLU:HB3	1:D:493:LYS:HZ3	1.82	0.44
1:A:321:GLN:O	1:A:321:GLN:HG3	2.18	0.44
1:A:597:ASN:HD21	1:A:638:LYS:HE2	1.83	0.44
1:D:365:ILE:O	1:D:369:VAL:HG23	2.18	0.44
1:D:536:ILE:CG1	1:D:559:GLU:HG3	2.48	0.44
1:D:5:ASP:N	1:D:7:LEU:CD2	2.80	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:ILE:O	1:A:14:ILE:HG13	2.17	0.44
1:A:538:THR:O	1:A:540:SER:N	2.50	0.44
1:B:249:ASN:ND2	1:B:310:PRO:HB3	2.32	0.44
1:C:468:TYR:CE1	1:C:507:GLU:HG2	2.53	0.44
1:C:451:GLU:CD	1:C:569:ARG:HH12	2.19	0.44
1:C:539:TRP:O	1:C:609:PHE:HA	2.17	0.44
1:D:592:LEU:HD13	1:D:628:LEU:HD12	1.97	0.44
1:A:116:ASP:O	1:A:117:ASP:C	2.56	0.44
1:A:265:ILE:HA	1:A:268:TYR:CD1	2.53	0.44
1:A:328:ILE:HG23	1:A:329:VAL:N	2.33	0.44
1:A:363:LYS:HA	1:B:697:TYR:CE2	2.50	0.44
1:B:338:ASP:OD2	1:B:352:LEU:N	2.51	0.44
1:A:377:ILE:CD1	1:B:534:PHE:HZ	2.20	0.44
1:B:637:TYR:HE2	1:B:682:TYR:HB3	1.80	0.44
1:B:665:TYR:O	1:B:668:THR:HB	2.18	0.44
1:D:181:TRP:HA	1:D:186:PHE:CG	2.52	0.44
1:D:523:GLN:NE2	1:D:594:VAL:HG13	2.32	0.44
1:A:37:SER:C	1:A:39:ASP:H	2.21	0.44
1:A:521:ARG:CG	1:A:521:ARG:HH11	2.07	0.44
1:A:632:SER:O	1:A:633:HIS:C	2.55	0.44
1:D:293:GLY:O	1:D:298:VAL:HG21	2.17	0.44
1:D:365:ILE:HG21	1:D:421:MSE:HE2	1.98	0.44
1:A:542:LEU:HD12	1:A:542:LEU:O	2.17	0.44
1:A:659:GLN:HG3	1:A:660:PHE:H	1.81	0.44
1:D:338:ASP:O	1:D:342:LEU:HB2	2.18	0.44
1:D:350:LEU:HD21	1:D:354:SER:CB	2.47	0.44
1:D:386:PHE:N	1:D:387:PRO:HD2	2.33	0.44
1:A:179:ALA:O	1:A:181:TRP:N	2.51	0.43
1:B:240:ASN:OD1	1:B:241:PHE:N	2.51	0.43
1:B:284:ILE:HG21	1:B:296:LYS:HG3	2.00	0.43
1:B:55:VAL:CG2	1:B:56:GLY:H	2.31	0.43
1:B:657:ASN:HB3	1:B:660:PHE:HE1	1.83	0.43
1:A:362:GLU:HG3	1:B:667:LYS:HZ1	1.82	0.43
1:A:540:SER:C	1:A:610:ASN:ND2	2.72	0.43
1:A:597:ASN:ND2	1:A:638:LYS:HE2	2.33	0.43
1:B:422:THR:HG22	1:B:423:CYS:N	2.33	0.43
1:C:109:PRO:HG2	1:C:112:GLN:CD	2.38	0.43
1:D:535:LYS:O	1:D:535:LYS:HG2	2.19	0.43
1:A:114:THR:HG22	1:A:115:LEU:N	2.33	0.43
1:C:338:ASP:CG	1:C:352:LEU:H	2.20	0.43
1:C:533:TYR:CD1	1:C:560:LEU:HB2	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:257:HIS:ND1	1:D:258:ALA:N	2.66	0.43
1:D:577:MSE:HB3	1:D:579:ILE:HG13	1.99	0.43
1:A:648:ILE:HG12	1:A:680:ILE:HD11	2.01	0.43
1:A:7:LEU:HD11	1:D:77:LYS:HB3	1.99	0.43
1:B:657:ASN:O	1:B:659:GLN:N	2.50	0.43
1:C:259:THR:CG2	1:C:260:SER:N	2.79	0.43
1:A:27:LYS:HD2	1:D:20:GLU:OE2	2.19	0.43
1:D:321:GLN:HG2	1:D:321:GLN:O	2.18	0.43
1:D:662:ASN:HD21	1:D:665:TYR:CB	2.30	0.43
1:B:362:GLU:HG2	1:B:418:TYR:CE2	2.44	0.43
1:B:408:TYR:OH	1:B:422:THR:HG21	2.17	0.43
1:B:542:LEU:HD12	1:B:542:LEU:C	2.38	0.43
1:C:169:SER:HA	1:C:204:LEU:HD21	2.01	0.43
1:C:461:LEU:HD23	1:C:579:ILE:HD13	2.01	0.43
1:B:382:ASN:HB3	1:B:384:GLU:OE1	2.19	0.43
1:B:478:PHE:N	1:B:478:PHE:CD2	2.86	0.43
1:C:295:THR:OG1	1:C:297:PRO:HD2	2.18	0.43
1:D:510:MSE:HE2	1:D:583:ILE:HD12	2.01	0.43
1:A:156:TYR:O	1:A:160:ILE:HB	2.18	0.43
1:B:109:PRO:C	1:B:111:ASP:H	2.21	0.43
1:B:41:GLU:OE1	1:B:73:GLN:HB3	2.18	0.43
1:B:424:SER:CA	1:B:428:MSE:HE3	2.46	0.43
1:A:448:ARG:NH1	1:B:450:LYS:HG3	2.33	0.43
1:B:660:PHE:HE2	1:B:673:SER:HB2	1.83	0.43
1:B:88:MSE:HE1	1:B:141:GLN:HB2	2.01	0.43
1:C:320:PHE:CZ	1:C:321:GLN:NE2	2.87	0.43
1:C:405:GLU:HB3	1:C:406:PRO:CD	2.48	0.43
1:D:377:ILE:HA	1:D:380:THR:HG22	2.01	0.43
1:A:256:PHE:O	1:A:314:LYS:NZ	2.48	0.43
1:A:365:ILE:HD11	1:A:418:TYR:HB3	1.99	0.43
1:B:66:ARG:NH2	1:B:76:ASN:HA	2.33	0.43
1:C:319:LEU:HD12	1:C:319:LEU:HA	1.77	0.43
1:D:568:ARG:HA	1:D:627:ILE:HG21	2.00	0.43
1:D:598:TYR:O	1:D:602:SER:HB2	2.18	0.43
1:D:603:ILE:N	1:D:603:ILE:HD12	2.34	0.43
1:D:630:LEU:HD22	1:D:632:SER:H	1.84	0.43
1:A:632:SER:O	1:A:634:ALA:N	2.52	0.43
1:A:80:LYS:O	1:A:83:VAL:HG12	2.19	0.43
1:B:183:THR:HG22	1:B:185:LYS:N	2.07	0.43
1:B:449:THR:HG22	1:B:452:GLN:NE2	2.34	0.43
1:B:31:LEU:HD23	1:B:53:ILE:HG12	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:PRO:O	1:A:301:GLU:HB2	2.19	0.43
1:A:249:ASN:OD1	1:A:310:PRO:HB3	2.19	0.43
1:A:644:GLU:OE2	1:A:682:TYR:HD1	2.01	0.43
1:B:176:LEU:HD22	1:B:181:TRP:CD1	2.53	0.43
1:B:260:SER:HB2	1:B:318:THR:OG1	2.19	0.43
1:B:324:LEU:O	1:B:328:ILE:HG12	2.19	0.43
1:D:295:THR:HG22	1:D:297:PRO:HD2	2.00	0.43
1:D:355:LEU:HD12	1:D:356:ILE:N	2.34	0.43
1:A:431:THR:CG2	1:A:502:VAL:HG11	2.49	0.42
1:A:542:LEU:HD12	1:A:542:LEU:C	2.39	0.42
1:C:474:LEU:HD22	1:C:480:PHE:HE1	1.84	0.42
1:C:560:LEU:CD2	1:C:620:ASP:HB3	2.49	0.42
1:D:571:ILE:HA	1:D:571:ILE:HD12	1.79	0.42
1:A:657:ASN:C	1:A:659:GLN:N	2.72	0.42
1:C:510:MSE:CA	1:C:514:MSE:HE3	2.48	0.42
1:C:538:THR:O	1:C:538:THR:HG22	2.18	0.42
1:D:348:HIS:O	1:D:348:HIS:ND1	2.52	0.42
1:A:315:VAL:O	1:A:318:THR:HG22	2.19	0.42
1:B:319:LEU:O	1:B:322:ASN:HB2	2.19	0.42
1:B:365:ILE:CD1	1:B:421:MSE:SE	3.17	0.42
1:B:591:LEU:HD23	1:B:591:LEU:HA	1.79	0.42
1:C:265:ILE:HG21	1:C:330:LEU:CD2	2.48	0.42
1:C:27:LYS:HA	1:C:27:LYS:HD2	1.79	0.42
1:A:240:ASN:OD1	1:A:241:PHE:HD1	2.03	0.42
1:A:269:PHE:HA	1:A:272:LEU:HB3	2.00	0.42
1:A:28:LEU:HG	1:A:32:LYS:NZ	2.34	0.42
1:B:183:THR:CG2	1:B:184:GLN:N	2.82	0.42
1:B:320:PHE:CG	1:B:321:GLN:N	2.87	0.42
1:B:592:LEU:HD11	1:B:639:CYS:SG	2.59	0.42
1:B:60:GLU:O	1:B:64:GLN:HG3	2.20	0.42
1:C:177:LEU:HD23	1:C:177:LEU:HA	1.88	0.42
1:C:533:TYR:CE2	1:C:603:ILE:HD13	2.52	0.42
1:D:519:VAL:HG21	1:D:590:GLU:HB3	2.02	0.42
1:D:84:GLN:HG3	1:D:135:ILE:CD1	2.49	0.42
1:A:19:ASN:O	1:A:22:ASN:N	2.52	0.42
1:A:259:THR:HG22	1:A:260:SER:N	2.35	0.42
1:A:309:GLN:HB3	1:A:310:PRO:CD	2.50	0.42
1:A:377:ILE:HD11	1:B:606:LEU:CD1	2.49	0.42
1:A:488:ASN:ND2	1:A:495:TYR:H	2.18	0.42
1:A:521:ARG:CG	1:A:521:ARG:NH1	2.67	0.42
1:B:99:GLU:OE2	1:B:151:LYS:HE3	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:362:GLU:O	1:B:366:ASN:HB2	2.20	0.42
1:C:115:LEU:O	1:C:115:LEU:HD12	2.19	0.42
1:C:39:ASP:HB2	1:C:74:ILE:HD12	2.01	0.42
1:D:180:GLN:O	1:D:183:THR:HG22	2.19	0.42
1:D:380:THR:OG1	1:D:437:TYR:CE2	2.72	0.42
1:A:74:ILE:HG23	1:A:75:LEU:HD12	2.01	0.42
1:B:284:ILE:CG2	1:B:296:LYS:HG3	2.49	0.42
1:D:109:PRO:HG2	1:D:112:GLN:CD	2.39	0.42
1:D:137:ASN:CB	1:D:140:SER:HB2	2.50	0.42
1:D:295:THR:HG22	1:D:297:PRO:CD	2.49	0.42
1:D:590:GLU:HA	1:D:590:GLU:OE1	2.18	0.42
1:A:428:MSE:HE3	1:A:502:VAL:CG2	2.49	0.42
1:D:357:SER:HB3	1:D:360:VAL:HG23	2.02	0.42
1:B:651:LEU:HD11	1:B:674:LEU:HD11	2.01	0.42
1:B:98:PHE:CD2	1:B:125:LEU:HD13	2.55	0.42
1:D:295:THR:HB	1:D:297:PRO:HD2	2.00	0.42
1:B:417:ARG:HG3	1:B:418:TYR:N	2.34	0.42
1:B:581:LEU:O	1:B:585:LEU:HG	2.20	0.42
1:B:659:GLN:HG3	1:B:660:PHE:N	2.34	0.42
1:D:158:ASP:C	1:D:158:ASP:OD1	2.58	0.42
1:D:460:LYS:O	1:D:464:VAL:HG23	2.19	0.42
1:D:95:LEU:O	1:D:98:PHE:N	2.51	0.42
1:B:88:MSE:HE1	1:B:141:GLN:O	2.20	0.42
1:B:204:LEU:HB3	1:B:240:ASN:HB3	2.01	0.42
1:B:302:GLN:OE1	1:B:302:GLN:HA	2.19	0.42
1:C:62:LEU:HD23	1:C:62:LEU:HA	1.85	0.42
1:D:10:ILE:O	1:D:14:ILE:HG13	2.19	0.42
1:D:195:LYS:HB2	1:D:195:LYS:NZ	2.35	0.42
1:A:631:PRO:HG2	1:A:634:ALA:CB	2.49	0.41
1:B:63:GLU:HG2	1:B:79:GLU:OE1	2.19	0.41
1:C:614:LEU:HA	1:C:614:LEU:HD12	1.92	0.41
1:D:102:LEU:C	1:D:104:GLU:N	2.73	0.41
1:A:195:LYS:O	1:A:199:GLU:HG3	2.19	0.41
1:B:121:LEU:HD23	1:B:121:LEU:HA	1.91	0.41
1:B:542:LEU:HD11	1:B:613:GLY:N	2.34	0.41
1:B:683:LEU:HD12	1:B:683:LEU:HA	1.88	0.41
1:C:338:ASP:HA	1:C:341:LEU:HD12	2.02	0.41
1:C:431:THR:HG22	1:C:432:SER:N	2.34	0.41
1:A:302:GLN:O	1:A:305:ASN:HB3	2.21	0.41
1:A:660:PHE:CZ	1:A:673:SER:HB3	2.55	0.41
1:B:164:LEU:O	1:B:165:ALA:C	2.57	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:592:LEU:HD11	1:D:625:SER:HB2	2.01	0.41
1:A:205:TYR:CD1	1:A:294:LEU:HD21	2.55	0.41
1:A:318:THR:O	1:A:322:ASN:HB2	2.20	0.41
1:A:450:LYS:HE3	1:B:448:ARG:NH2	2.35	0.41
1:A:462:GLN:HG3	1:A:578:ASP:N	2.35	0.41
1:B:238:LEU:HD23	1:B:238:LEU:HA	1.82	0.41
1:B:474:LEU:HD22	1:B:480:PHE:CE1	2.56	0.41
1:D:657:ASN:HB3	1:D:660:PHE:HE1	1.85	0.41
1:D:671:PHE:O	1:D:675:LYS:HB2	2.20	0.41
1:A:448:ARG:CD	1:A:453:GLU:OE1	2.68	0.41
1:A:683:LEU:HA	1:A:683:LEU:HD12	1.90	0.41
1:C:645:LEU:O	1:C:649:LEU:HG	2.21	0.41
1:D:390:SER:HB3	1:D:466:PHE:CD2	2.52	0.41
1:A:31:LEU:HG	1:A:35:LEU:HD11	2.01	0.41
1:A:358:ASP:OD1	1:A:418:TYR:OH	2.38	0.41
1:A:431:THR:HG21	1:A:471:ILE:CD1	2.51	0.41
1:A:431:THR:HG21	1:A:471:ILE:HD11	2.03	0.41
1:A:648:ILE:HD13	1:A:688:ILE:HG23	2.02	0.41
1:A:649:LEU:HG	1:A:700:ILE:CD1	2.47	0.41
1:B:377:ILE:HA	1:B:380:THR:HG22	2.02	0.41
1:C:650:LYS:C	1:C:652:LYS:H	2.23	0.41
1:D:256:PHE:CD2	1:D:268:TYR:CE2	3.08	0.41
1:D:330:LEU:HG	1:D:334:ILE:HD11	2.03	0.41
1:A:172:PHE:CE1	1:A:200:ASN:HB3	2.56	0.41
1:A:542:LEU:HD12	1:A:612:ASN:HB2	2.02	0.41
1:A:693:TYR:O	1:A:697:TYR:HD1	2.04	0.41
1:A:79:GLU:HA	1:A:82:ALA:HB3	2.03	0.41
1:B:114:THR:HG22	1:B:115:LEU:N	2.36	0.41
1:B:165:ALA:HB1	1:B:239:TRP:CG	2.56	0.41
1:B:416:VAL:HG22	1:B:416:VAL:O	2.21	0.41
1:C:172:PHE:CE2	1:C:176:LEU:HD11	2.55	0.41
1:D:657:ASN:C	1:D:659:GLN:N	2.73	0.41
1:A:571:ILE:HD11	1:A:628:LEU:HD23	2.03	0.41
1:A:638:LYS:HB3	1:A:638:LYS:HE3	1.81	0.41
1:B:308:LEU:HD22	1:B:352:LEU:HD21	2.03	0.41
1:D:512:THR:O	1:D:513:ASP:C	2.59	0.41
1:D:541:THR:HG22	1:D:541:THR:O	2.21	0.41
1:A:630:LEU:HB3	1:A:631:PRO:HD2	2.02	0.41
1:A:660:PHE:HD1	1:A:674:LEU:HD13	1.85	0.41
1:B:181:TRP:HA	1:B:186:PHE:CD1	2.56	0.41
1:B:562:ASN:O	1:B:566:VAL:HG23	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:320:PHE:CG	1:C:321:GLN:N	2.89	0.41
1:C:675:LYS:HE3	1:C:675:LYS:HB2	1.86	0.41
1:D:281:TYR:CD1	1:D:282:LYS:N	2.89	0.41
1:D:490:THR:HG23	1:D:491:GLU:H	1.86	0.41
1:D:543:GLU:HG2	1:D:543:GLU:O	2.20	0.41
1:D:608:LYS:HA	1:D:699:ASN:O	2.20	0.41
1:A:22:ASN:O	1:A:25:ALA:HB3	2.21	0.41
1:A:371:MSE:HA	1:A:371:MSE:CE	2.49	0.41
1:A:478:PHE:CD1	1:A:481:ILE:HD11	2.55	0.41
1:B:668:THR:HG22	1:B:670:ASN:H	1.84	0.41
1:C:422:THR:CG2	1:C:423:CYS:N	2.84	0.41
1:C:610:ASN:O	1:C:611:GLN:C	2.59	0.41
1:D:431:THR:HG23	1:D:471:ILE:HD11	2.02	0.41
1:A:165:ALA:HB1	1:A:239:TRP:CD2	2.56	0.41
1:A:699:ASN:HD22	1:A:699:ASN:HA	1.55	0.41
1:C:204:LEU:HA	1:C:204:LEU:HD12	1.87	0.41
1:D:114:THR:HG22	1:D:115:LEU:N	2.36	0.41
1:D:477:ASN:O	1:D:481:ILE:HG13	2.21	0.41
1:A:602:SER:C	1:A:603:ILE:HD12	2.41	0.40
1:B:345:PHE:O	1:B:346:HIS:HB2	2.21	0.40
1:B:393:PHE:O	1:B:396:LEU:HB3	2.21	0.40
1:B:602:SER:O	1:B:603:ILE:HD12	2.21	0.40
1:C:432:SER:HB3	1:C:502:VAL:CG1	2.46	0.40
1:D:208:SER:OG	1:D:239:TRP:HD1	2.04	0.40
1:D:329:VAL:O	1:D:333:GLN:HG3	2.20	0.40
1:D:439:LEU:HD21	1:D:514:MSE:CE	2.35	0.40
1:D:638:LYS:HB3	1:D:638:LYS:HE3	1.88	0.40
1:A:169:SER:HA	1:A:204:LEU:HD21	2.02	0.40
1:B:84:GLN:CG	1:B:135:ILE:HD13	2.45	0.40
1:A:299:ILE:O	1:A:300:HIS:C	2.58	0.40
1:A:379:ILE:HG13	1:A:380:THR:HG23	2.02	0.40
1:A:588:LYS:CB	1:A:630:LEU:HD21	2.51	0.40
1:B:281:TYR:HB2	1:C:481:ILE:HD12	2.03	0.40
1:B:649:LEU:HB3	1:B:700:ILE:HD13	2.03	0.40
1:D:671:PHE:HE2	1:D:692:LEU:HD12	1.86	0.40
1:A:407:PHE:C	1:A:409:ASP:H	2.23	0.40
1:A:540:SER:HB2	1:A:701:LEU:HD12	2.03	0.40
1:A:7:LEU:HB2	1:D:81:VAL:HG21	2.04	0.40
1:B:658:GLN:HG2	1:B:658:GLN:O	2.21	0.40
1:C:666:ILE:HD12	1:C:696:ILE:HD11	1.99	0.40
1:D:106:ALA:HB2	1:D:159:VAL:CG1	2.51	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:TRP:O	1:A:364:TRP:HB3	2.22	0.40
1:C:19:ASN:O	1:C:22:ASN:HB2	2.21	0.40
1:C:172:PHE:CD1	1:C:200:ASN:HB3	2.56	0.40
1:C:294:LEU:HA	1:C:294:LEU:HD23	1.90	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	667/706 (94%)	589 (88%)	64 (10%)	14 (2%)	8	38
1	B	667/706 (94%)	610 (92%)	43 (6%)	14 (2%)	8	38
1	C	667/706 (94%)	606 (91%)	49 (7%)	12 (2%)	10	43
1	D	667/706 (94%)	592 (89%)	59 (9%)	16 (2%)	7	34
All	All	2668/2824 (94%)	2397 (90%)	215 (8%)	56 (2%)	8	38

All (56) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	539	TRP
1	A	611	GLN
1	A	633	HIS
1	B	56	GLY
1	B	138	ILE
1	B	631	PRO
1	C	138	ILE
1	C	412	PHE
1	C	631	PRO
1	D	56	GLY
1	D	412	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	512	THR
1	D	633	HIS
1	A	138	ILE
1	A	140	SER
1	A	180	GLN
1	A	191	VAL
1	A	544	MSE
1	B	544	MSE
1	C	492	SER
1	D	138	ILE
1	D	141	GLN
1	D	658	GLN
1	A	258	ALA
1	A	658	GLN
1	B	110	PRO
1	C	259	THR
1	C	685	ASP
1	D	158	ASP
1	D	321	GLN
1	D	411	ASP
1	B	258	ALA
1	B	259	THR
1	B	513	ASP
1	B	539	TRP
1	C	140	SER
1	D	685	ASP
1	A	38	ASN
1	A	319	LEU
1	A	423	CYS
1	B	140	SER
1	B	265	ILE
1	B	658	GLN
1	C	291	CYS
1	C	544	MSE
1	D	110	PRO
1	D	186	PHE
1	D	497	SER
1	B	663	PRO
1	C	191	VAL
1	C	258	ALA
1	D	191	VAL
1	C	441	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	42	VAL
1	B	133	PRO
1	A	194	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	633/648 (98%)	601 (95%)	32 (5%)	28	66
1	B	633/648 (98%)	601 (95%)	32 (5%)	28	66
1	C	633/648 (98%)	607 (96%)	26 (4%)	35	73
1	D	633/648 (98%)	592 (94%)	41 (6%)	20	56
All	All	2532/2592 (98%)	2401 (95%)	131 (5%)	27	65

All (131) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ASP
1	A	51	ASP
1	A	60	GLU
1	A	71	ASP
1	A	83	VAL
1	A	111	ASP
1	A	146	ASN
1	A	164	LEU
1	A	242	LYS
1	A	253	THR
1	A	257	HIS
1	A	267	THR
1	A	318	THR
1	A	320	PHE
1	A	322	ASN
1	A	340	ASN
1	A	355	LEU
1	A	397	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	409	ASP
1	A	412	PHE
1	A	415	LEU
1	A	422	THR
1	A	450	LYS
1	A	463	HIS
1	A	478	PHE
1	A	521	ARG
1	A	526	LEU
1	A	531	ARG
1	A	633	HIS
1	A	693	TYR
1	A	694	ARG
1	A	699	ASN
1	B	38	ASN
1	B	54	GLU
1	B	75	LEU
1	B	84	GLN
1	B	89	GLN
1	B	127	SER
1	B	200	ASN
1	B	204	LEU
1	B	215	GLU
1	B	242	LYS
1	B	290	ASP
1	B	296	LYS
1	B	314	LYS
1	B	323	ASP
1	B	338	ASP
1	B	341	LEU
1	B	380	THR
1	B	399	LYS
1	B	411	ASP
1	B	415	LEU
1	B	422	THR
1	B	450	LYS
1	B	452	GLN
1	B	478	PHE
1	B	515	GLN
1	B	526	LEU
1	B	531	ARG
1	B	631	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	637	TYR
1	B	662	ASN
1	B	676	GLU
1	B	694	ARG
1	C	12	ASP
1	C	47	VAL
1	C	51	ASP
1	C	121	LEU
1	C	251	ARG
1	C	301	GLU
1	C	314	LYS
1	C	328	ILE
1	C	337	THR
1	C	339	LYS
1	C	368	GLU
1	C	380	THR
1	C	399	LYS
1	C	402	ASP
1	C	415	LEU
1	C	431	THR
1	C	438	ILE
1	C	440	THR
1	C	441	VAL
1	C	442	ASP
1	C	469	ARG
1	C	502	VAL
1	C	504	ASN
1	C	631	PRO
1	C	656	ASN
1	C	694	ARG
1	D	7	LEU
1	D	27	LYS
1	D	28	LEU
1	D	54	GLU
1	D	66	ARG
1	D	73	GLN
1	D	75	LEU
1	D	76	ASN
1	D	112	GLN
1	D	137	ASN
1	D	173	ASP
1	D	174	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	180	GLN
1	D	183	THR
1	D	200	ASN
1	D	273	ASN
1	D	326	THR
1	D	327	LEU
1	D	338	ASP
1	D	341	LEU
1	D	345	PHE
1	D	346	HIS
1	D	348	HIS
1	D	411	ASP
1	D	415	LEU
1	D	423	CYS
1	D	428	MSE
1	D	469	ARG
1	D	477	ASN
1	D	517	SER
1	D	518	ILE
1	D	521	ARG
1	D	538	THR
1	D	572	ASN
1	D	590	GLU
1	D	630	LEU
1	D	653	TYR
1	D	659	GLN
1	D	690	ASP
1	D	693	TYR
1	D	696	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	GLN
1	A	108	GLN
1	A	112	GLN
1	A	137	ASN
1	A	322	ASN
1	A	333	GLN
1	A	392	ASN
1	A	488	ASN
1	A	572	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	610	ASN
1	A	616	GLN
1	A	633	HIS
1	A	689	GLN
1	B	22	ASN
1	B	84	GLN
1	B	206	GLN
1	B	249	ASN
1	B	321	GLN
1	B	343	ASN
1	B	373	ASN
1	B	391	GLN
1	B	429	ASN
1	B	496	ASN
1	B	500	GLN
1	B	562	ASN
1	B	612	ASN
1	B	615	ASN
1	B	643	HIS
1	C	33	GLN
1	C	50	GLN
1	C	85	GLN
1	C	112	GLN
1	C	137	ASN
1	C	206	GLN
1	C	321	GLN
1	C	373	ASN
1	C	496	ASN
1	C	589	ASN
1	C	612	ASN
1	C	636	ASN
1	D	84	GLN
1	D	137	ASN
1	D	146	ASN
1	D	343	ASN
1	D	392	ASN
1	D	500	GLN
1	D	504	ASN
1	D	523	GLN
1	D	593	ASN
1	D	612	ASN
1	D	633	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	636	ASN
1	D	659	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	663/706 (93%)	-0.13	8 (1%)	79 53	47, 83, 125, 155	0
1	B	663/706 (93%)	-0.14	4 (0%)	89 71	44, 70, 121, 160	0
1	C	663/706 (93%)	-0.16	5 (0%)	86 64	42, 71, 127, 161	0
1	D	663/706 (93%)	-0.09	18 (2%)	55 26	52, 86, 128, 162	0
All	All	2652/2824 (93%)	-0.13	35 (1%)	77 51	42, 77, 125, 162	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	553	SER	4.9
1	D	674	LEU	4.3
1	B	141	GLN	4.0
1	D	138	ILE	3.8
1	A	260	SER	3.6
1	D	545	SER	3.5
1	D	680	ILE	3.2
1	D	135	ILE	2.9
1	D	671	PHE	2.9
1	C	552	PRO	2.7
1	B	701	LEU	2.7
1	D	137	ASN	2.6
1	C	262	SER	2.6
1	A	633	HIS	2.6
1	D	554	SER	2.5
1	D	139	ASP	2.5
1	B	260	SER	2.5
1	A	269	PHE	2.4
1	C	651	LEU	2.4
1	A	327	LEU	2.4
1	A	671	PHE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	260	SER	2.3
1	D	296	LYS	2.3
1	D	631	PRO	2.3
1	A	141	GLN	2.3
1	D	678	TYR	2.2
1	C	553	SER	2.2
1	A	139	ASP	2.2
1	A	262	SER	2.1
1	D	649	LEU	2.1
1	D	366	ASN	2.1
1	D	673	SER	2.1
1	B	216	GLU	2.0
1	D	688	ILE	2.0
1	D	555	VAL	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 carbohydrates 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.