



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:04 AM UTC

PDB ID : 2I03 / pdb_00002i03
Title : Crystal structure of human dipeptidyl peptidase 4 (DPP IV) with potent alkynyl cyanopyrrolidine (ABT-279)
Authors : Longenecker, K.L.; Madar, D.J.
Deposited on : 2006-08-09
Resolution : 2.40 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

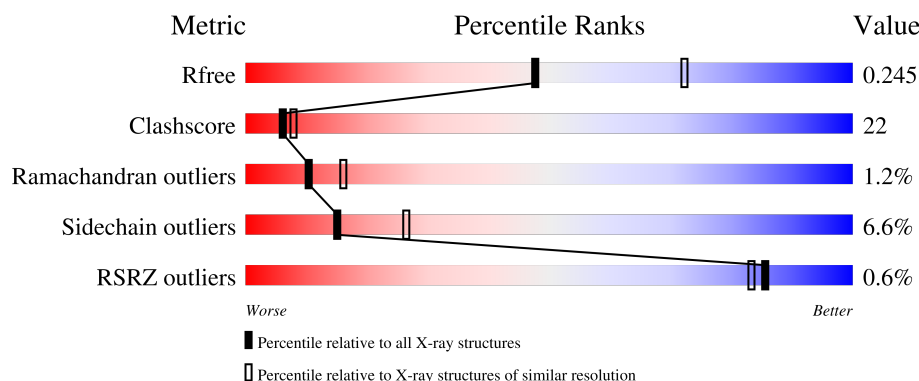
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	726	% 63% 31% 5% •
1	B	726	% 60% 36% •
1	C	726	57% 38% 5%
1	D	726	61% 33% 6%

2 Entry composition [i](#)

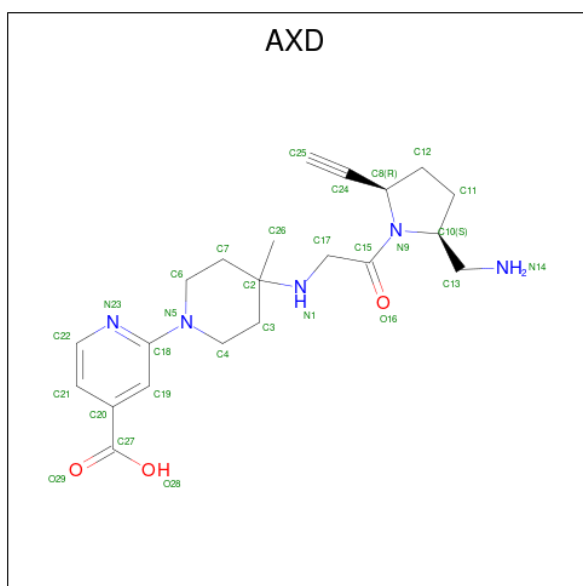
There are 3 unique types of molecules in this entry. The entry contains 26782 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	726	Total	C	N	O	S	0	0	0
			5949	3816	980	1127	26			
1	B	726	Total	C	N	O	S	0	0	0
			5949	3816	980	1127	26			
1	C	726	Total	C	N	O	S	0	0	0
			5949	3816	980	1127	26			
1	D	726	Total	C	N	O	S	0	0	0
			5949	3816	980	1127	26			

- Molecule 2 is 2-[4-({2-[(2S,5R)-2-(AMINOMETHYL)-5-ETHYNYLPYRROLIDIN-1-YL]-2-EXOETHYL}AMINO)-4-METHYLPYPERIDIN-1-YL]ISONICOTINIC ACID (CCD ID: AXD) (formula: C₂₁H₂₉N₅O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			29	21	5	3		

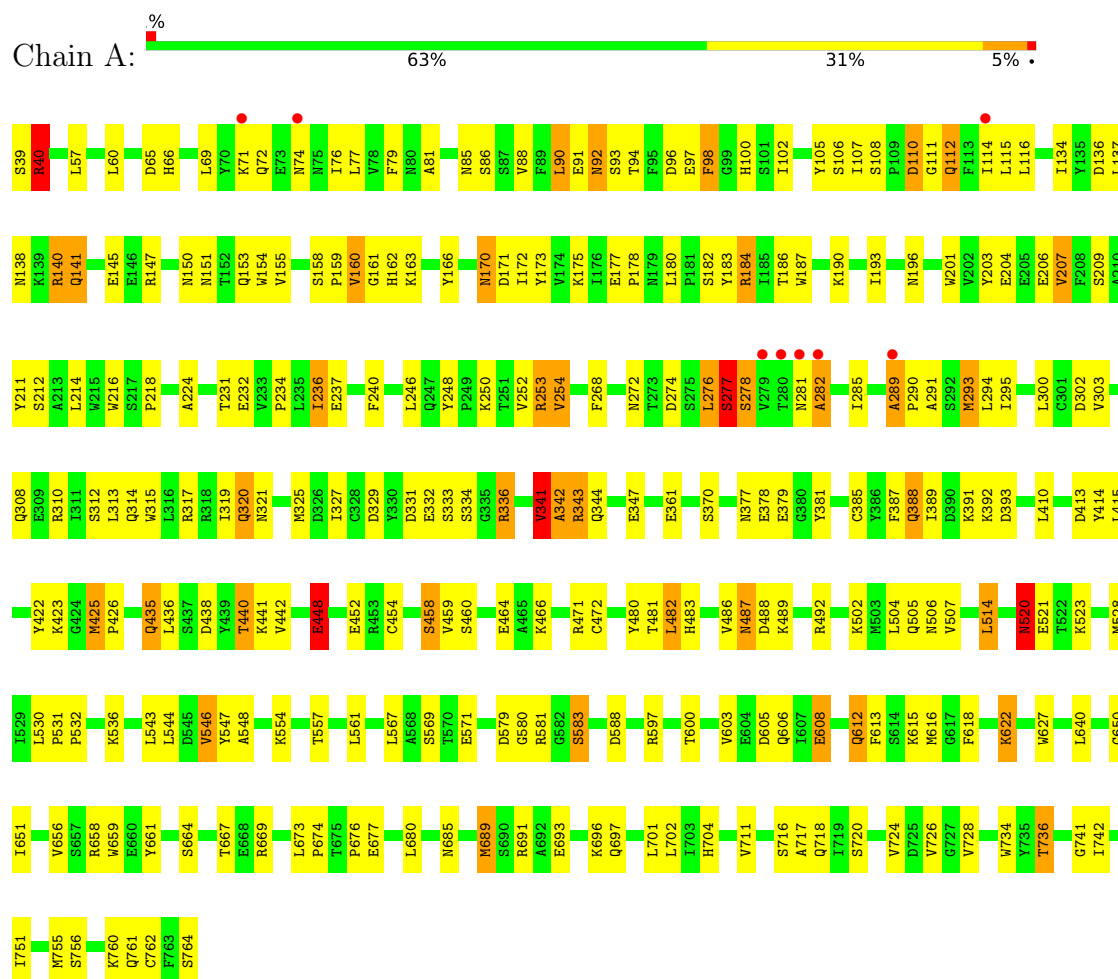
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	827	Total 827	O 827	0	0
3	B	763	Total 763	O 763	0	0
3	C	685	Total 685	O 685	0	0
3	D	682	Total 682	O 682	0	0

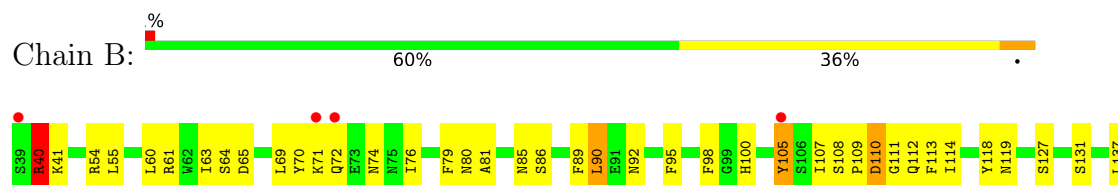
3 Residue-property plots

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: Dipeptidyl peptidase 4



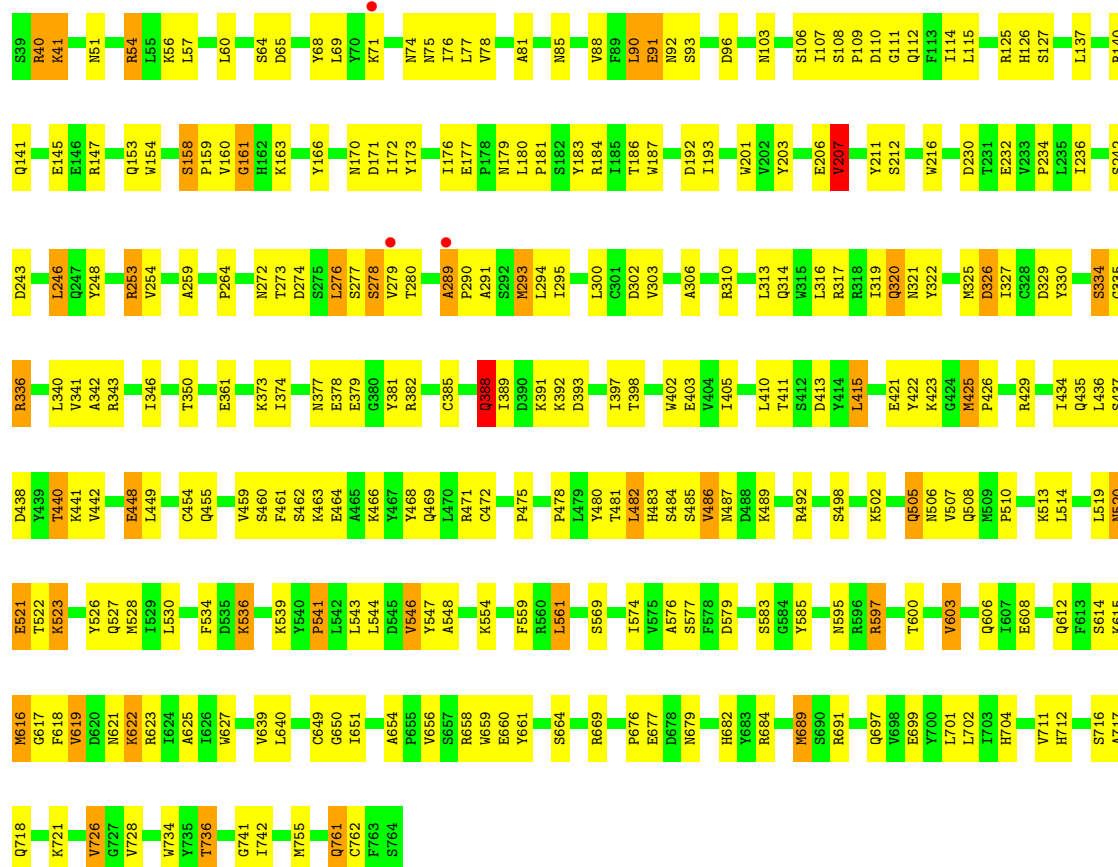
• Molecule 1: Dipeptidyl peptidase 4





• Molecule 1: Dipeptidyl peptidase 4

Chain D: 61% 33% 6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	120.25Å 126.99Å 127.26Å 90.00° 96.56° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40 20.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.9 (20.00-2.40) 96.7 (20.00-2.40)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.41Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.179 , 0.245 0.180 , 0.245	Depositor DCC
R_{free} test set	7166 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtriage
Anisotropy	0.547	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 76.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	26782	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	1/6120 (0.0%)	0.98	29/8321 (0.3%)
1	B	0.46	1/6120 (0.0%)	0.94	22/8321 (0.3%)
1	C	0.39	0/6120	0.94	22/8321 (0.3%)
1	D	0.39	0/6120	0.93	21/8321 (0.3%)
All	All	0.42	2/24480 (0.0%)	0.95	94/33284 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	630	SER	C-O	15.89	1.39	1.24
1	A	293	MET	SD-CE	-5.74	1.65	1.79

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	341	VAL	N-CA-C	-10.60	94.36	109.63
1	A	160	VAL	N-CA-C	10.49	119.90	111.62
1	C	160	VAL	N-CA-C	10.09	119.59	111.62
1	D	378	GLU	N-CA-C	-9.80	101.08	113.23
1	C	111	GLY	N-CA-C	-8.97	102.94	115.32
1	C	664	SER	N-CA-C	8.69	120.37	111.07
1	A	111	GLY	N-CA-C	-8.58	104.87	115.08
1	B	341	VAL	N-CA-C	-8.00	98.09	110.09
1	A	388	GLN	N-CA-C	-7.94	96.30	109.24
1	C	378	GLU	N-CA-C	-7.91	102.53	112.90
1	B	111	GLY	N-CA-C	-7.71	104.58	115.30
1	B	378	GLU	N-CA-C	-7.66	103.39	112.89
1	C	300	LEU	N-CA-C	-7.34	97.28	108.96
1	B	206	GLU	N-CA-C	7.33	122.52	113.50
1	A	378	GLU	N-CA-C	-7.31	103.83	112.89

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	207	VAL	N-CA-C	7.20	117.75	111.56
1	C	206	GLU	N-CA-C	7.10	122.11	113.38
1	A	659	TRP	N-CA-C	6.81	119.54	111.71
1	B	656	VAL	N-CA-C	-6.72	100.07	109.21
1	A	206	GLU	N-CA-C	6.68	121.51	113.23
1	B	546	VAL	N-CA-C	6.63	119.06	108.85
1	A	454	CYS	N-CA-C	6.60	119.16	108.41
1	C	546	VAL	N-CA-C	6.44	119.04	108.99
1	A	546	VAL	N-CA-C	6.41	118.72	108.85
1	A	300	LEU	N-CA-C	-6.39	98.11	108.52
1	D	425	MET	CA-C-N	6.32	127.74	119.84
1	D	425	MET	C-N-CA	6.32	127.74	119.84
1	A	206	GLU	CA-C-N	-6.30	116.49	123.16
1	A	206	GLU	C-N-CA	-6.30	116.49	123.16
1	A	548	ALA	N-CA-C	6.28	120.52	112.86
1	B	388	GLN	N-CA-C	-6.24	98.35	108.52
1	D	656	VAL	N-CA-C	-6.24	100.94	109.55
1	A	343	ARG	N-CA-C	-6.21	105.64	113.72
1	C	343	ARG	N-CA-C	-6.20	105.76	113.38
1	D	206	GLU	N-CA-C	6.18	121.00	112.90
1	C	365	THR	N-CA-C	-6.18	102.21	110.55
1	D	300	LEU	N-CA-C	-6.14	98.72	108.73
1	B	485	SER	N-CA-C	6.12	118.75	111.71
1	B	541	PRO	N-CA-C	-6.12	102.27	111.57
1	A	112	GLN	N-CA-C	6.07	118.86	111.82
1	D	454	CYS	N-CA-C	6.07	118.30	108.41
1	C	425	MET	CA-C-N	6.05	125.73	119.56
1	C	425	MET	C-N-CA	6.05	125.73	119.56
1	B	454	CYS	N-CA-C	6.04	118.25	108.41
1	D	546	VAL	N-CA-C	5.99	118.08	108.85
1	B	588	ASP	N-CA-C	5.99	118.77	111.82
1	A	319	ILE	N-CA-C	-5.98	98.00	107.15
1	C	388	GLN	N-CA-C	-5.98	98.67	108.41
1	A	656	VAL	N-CA-C	-5.91	99.89	108.87
1	D	541	PRO	N-CA-C	-5.90	101.83	111.68
1	A	448	GLU	N-CA-C	5.85	120.41	113.16
1	B	664	SER	N-CA-C	5.80	117.28	111.07
1	A	110	ASP	N-CA-C	-5.77	106.78	113.88
1	D	388	GLN	N-CA-C	-5.72	99.57	108.90
1	B	288	THR	CB-CA-C	-5.68	107.30	114.40
1	D	158	SER	N-CA-C	-5.65	102.07	110.20
1	A	425	MET	CA-C-N	5.64	126.89	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	425	MET	C-N-CA	5.64	126.89	119.84
1	D	206	GLU	CA-C-N	-5.64	117.38	123.08
1	D	206	GLU	C-N-CA	-5.64	117.38	123.08
1	A	458	SER	N-CA-C	-5.58	100.82	109.24
1	D	201	TRP	N-CA-C	5.56	117.03	110.97
1	B	548	ALA	N-CA-C	5.55	119.34	112.24
1	D	619	VAL	N-CA-C	5.51	115.80	107.75
1	D	616	MET	N-CA-C	-5.47	106.66	113.38
1	B	150	ASN	N-CA-C	-5.46	103.17	110.55
1	A	588	ASP	N-CA-C	5.44	118.13	111.82
1	C	659	TRP	N-CA-C	5.44	119.02	112.38
1	A	664	SER	N-CA-C	5.43	116.89	110.97
1	C	357	PHE	N-CA-C	-5.42	107.68	114.56
1	D	548	ALA	N-CA-C	5.39	119.81	113.23
1	B	698	VAL	N-CA-C	5.39	116.67	108.80
1	B	547	TYR	N-CA-C	-5.38	99.33	110.80
1	C	541	PRO	N-CA-C	-5.33	102.77	111.68
1	A	667	THR	N-CA-C	5.33	116.77	111.07
1	D	664	SER	N-CA-C	5.26	116.70	110.97
1	C	529	ILE	N-CA-C	-5.25	99.68	107.51
1	B	287	ILE	N-CA-C	-5.23	100.85	108.17
1	A	98	PHE	N-CA-C	-5.19	105.80	111.82
1	B	647	PHE	N-CA-C	5.13	117.61	109.24
1	A	236	ILE	N-CA-C	-5.12	101.08	108.71
1	D	111	GLY	N-CA-C	-5.12	108.56	115.21
1	A	201	TRP	N-CA-C	5.09	117.23	111.02
1	C	646	VAL	N-CA-C	5.09	115.86	110.72
1	C	412	SER	N-CA-C	-5.09	106.90	113.01
1	D	659	TRP	N-CA-C	5.09	118.95	112.34
1	A	211	TYR	N-CA-C	-5.07	105.40	112.45
1	B	678	ASP	N-CA-C	5.07	116.84	108.48
1	C	617	GLY	N-CA-C	5.06	120.83	114.25
1	B	659	TRP	N-CA-C	5.02	118.51	112.38
1	C	454	CYS	N-CA-C	5.01	116.56	108.34
1	B	343	ARG	N-CA-C	-5.00	106.86	113.17
1	C	530	LEU	CA-C-N	5.00	123.31	119.66
1	C	530	LEU	C-N-CA	5.00	123.31	119.66

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5949	0	5667	258	0
1	B	5949	0	5666	244	0
1	C	5949	0	5667	277	0
1	D	5949	0	5667	285	0
2	B	29	0	26	0	0
3	A	827	0	0	48	0
3	B	763	0	0	40	0
3	C	685	0	0	43	0
3	D	682	0	0	49	0
All	All	26782	0	22693	1046	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 22.

All (1046) 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:D:289:ALA:HB1	1:D:290:PRO:HA	1.29	1.15
1:B:193:ILE:HG22	1:B:194:ILE:HD12	1.34	1.09
1:C:289:ALA:HB1	1:C:290:PRO:HA	1.29	1.09
1:D:334:SER:HB3	1:D:336:ARG:HE	1.14	1.08
1:B:289:ALA:HB1	1:B:290:PRO:HA	1.36	1.07
1:A:651:ILE:HG21	1:A:755:MET:HE3	1.38	1.04
1:D:114:ILE:HD11	1:D:137:LEU:HD21	1.40	1.00
1:C:293:MET:HE2	1:C:317:ARG:HG3	1.43	0.97
1:A:289:ALA:HB1	1:A:290:PRO:HA	1.43	0.97
1:C:651:ILE:HG21	1:C:755:MET:HE3	1.49	0.94
1:A:253:ARG:HH22	1:B:253:ARG:HH22	1.01	0.93
1:A:289:ALA:HB1	1:A:290:PRO:CA	1.98	0.93
1:A:505:GLN:HB3	3:A:1227:HOH:O	1.69	0.92
1:A:293:MET:HE1	1:A:317:ARG:HG3	1.49	0.92
1:A:172:ILE:H	1:A:186:THR:HG22	1.35	0.92
1:A:76:ILE:HD12	1:A:90:LEU:HD11	1.53	0.91
1:A:762:CYS:HB2	3:A:880:HOH:O	1.71	0.90
1:B:334:SER:HB3	1:B:336:ARG:HE	1.36	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:334:SER:HB3	1:D:336:ARG:NE	1.86	0.88
1:B:289:ALA:HB1	1:B:290:PRO:CA	2.03	0.88
1:D:172:ILE:H	1:D:186:THR:HG22	1.36	0.88
1:B:76:ILE:HD12	1:B:90:LEU:HD11	1.56	0.88
1:D:621:ASN:HB3	3:D:912:HOH:O	1.75	0.87
1:A:276:LEU:HB3	3:A:1062:HOH:O	1.74	0.86
1:C:102:ILE:HD13	1:C:116:LEU:HD22	1.58	0.86
1:C:111:GLY:O	1:C:137:LEU:HD12	1.76	0.85
1:A:253:ARG:NH2	1:B:253:ARG:HH22	1.75	0.84
1:B:138:ASN:HA	3:B:2063:HOH:O	1.76	0.84
1:C:717:ALA:O	1:D:736:THR:HG21	1.77	0.84
1:D:289:ALA:HB1	1:D:290:PRO:CA	2.07	0.84
1:C:172:ILE:H	1:C:186:THR:HG22	1.41	0.84
1:D:614:SER:HB2	3:D:912:HOH:O	1.77	0.83
1:D:40:ARG:HA	3:D:850:HOH:O	1.77	0.83
1:A:438:ASP:OD1	1:A:440:THR:HB	1.79	0.82
1:A:253:ARG:HH22	1:B:253:ARG:NH2	1.75	0.82
1:C:105:TYR:HB2	3:C:861:HOH:O	1.79	0.82
1:B:60:LEU:HB3	3:B:2373:HOH:O	1.78	0.82
1:C:171:ASP:OD1	1:C:186:THR:HG23	1.79	0.82
1:D:276:LEU:H	1:D:276:LEU:HD22	1.45	0.82
1:D:397:ILE:HD12	1:D:434:ILE:HD13	1.63	0.81
1:D:69:LEU:HD11	1:D:107:ILE:HD12	1.63	0.81
1:D:293:MET:HE2	1:D:317:ARG:HG3	1.61	0.80
1:A:717:ALA:O	1:B:736:THR:HG21	1.80	0.80
1:C:289:ALA:HB1	1:C:290:PRO:CA	2.09	0.80
1:B:176:ILE:HD11	1:B:276:LEU:HD21	1.62	0.80
1:A:361:GLU:HB3	3:A:820:HOH:O	1.80	0.80
1:C:293:MET:CE	1:C:317:ARG:HG3	2.12	0.80
1:D:528:MET:HE2	1:D:530:LEU:HD21	1.65	0.79
1:D:160:VAL:HG23	1:D:161:GLY:H	1.47	0.79
1:C:736:THR:HG21	1:D:717:ALA:O	1.83	0.79
1:D:528:MET:HE3	1:D:574:ILE:HG21	1.65	0.79
1:B:410:LEU:HD13	1:B:415:LEU:HD23	1.65	0.79
1:A:177:GLU:HB2	1:A:180:LEU:HD22	1.65	0.79
1:B:172:ILE:H	1:B:186:THR:HG22	1.47	0.78
1:A:276:LEU:H	1:A:276:LEU:HD23	1.47	0.78
1:B:171:ASP:OD1	1:B:186:THR:HG23	1.84	0.78
1:A:392:LYS:HB3	3:A:1077:HOH:O	1.84	0.78
1:A:697:GLN:HG3	3:A:1250:HOH:O	1.81	0.78
1:B:160:VAL:HG23	1:B:161:GLY:H	1.47	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:762:CYS:HB2	3:B:1776:HOH:O	1.84	0.78
1:B:334:SER:HB3	1:B:336:ARG:NE	1.99	0.77
1:A:153:GLN:HE22	1:A:170:ASN:ND2	1.83	0.77
1:D:289:ALA:HB2	3:D:1388:HOH:O	1.85	0.77
1:C:410:LEU:HD13	1:C:415:LEU:HD23	1.65	0.76
1:D:676:PRO:HG2	1:D:677:GLU:OE2	1.85	0.76
1:A:487:ASN:HB2	3:A:1369:HOH:O	1.84	0.76
1:A:347:GLU:HG2	3:A:1566:HOH:O	1.83	0.76
1:A:140:ARG:HG2	1:A:140:ARG:HH11	1.50	0.75
1:D:272:ASN:ND2	1:D:274:ASP:H	1.84	0.75
1:A:334:SER:HB3	1:A:336:ARG:NE	2.02	0.74
1:A:502:LYS:O	1:A:505:GLN:HG2	1.87	0.74
1:C:334:SER:HB3	1:C:336:ARG:HE	1.50	0.74
1:D:114:ILE:CD1	1:D:137:LEU:HD21	2.17	0.74
1:C:184:ARG:NH1	1:C:187:TRP:HA	2.03	0.73
1:C:293:MET:HE2	1:C:317:ARG:CG	2.18	0.73
1:D:289:ALA:HA	1:D:294:LEU:HD11	1.68	0.73
1:A:71:LYS:NZ	1:A:105:TYR:HB2	2.03	0.73
1:A:289:ALA:CB	1:A:290:PRO:HA	2.18	0.73
1:C:486:VAL:HG13	3:C:787:HOH:O	1.88	0.73
1:D:77:LEU:HD23	1:D:88:VAL:HA	1.71	0.73
1:A:341:VAL:O	1:A:342:ALA:CB	2.36	0.73
1:B:320:GLN:OE1	1:B:669:ARG:HD3	1.88	0.73
1:D:184:ARG:NH1	1:D:187:TRP:HA	2.04	0.73
1:A:108:SER:C	1:A:110:ASP:H	1.94	0.73
1:B:528:MET:HE3	1:B:530:LEU:HD21	1.70	0.72
1:C:597:ARG:HG3	1:C:600:THR:HG21	1.70	0.72
1:A:140:ARG:HD2	3:A:1042:HOH:O	1.87	0.72
1:B:341:VAL:O	1:B:342:ALA:HB3	1.89	0.72
1:C:106:SER:HB3	1:C:115:LEU:HB3	1.71	0.72
1:A:410:LEU:HD13	1:A:415:LEU:HD23	1.72	0.72
1:A:293:MET:HE1	1:A:317:ARG:CG	2.20	0.71
1:C:272:ASN:ND2	1:C:274:ASP:H	1.89	0.71
1:A:171:ASP:OD1	1:A:186:THR:HG23	1.90	0.71
1:A:203:TYR:HA	1:A:207:VAL:HG13	1.73	0.71
1:A:597:ARG:HG3	1:A:600:THR:HG21	1.74	0.70
1:A:71:LYS:HG2	1:A:76:ILE:HG12	1.73	0.70
1:B:596:ARG:O	1:B:597:ARG:HD3	1.92	0.70
1:D:158:SER:HB3	1:D:163:LYS:HB2	1.74	0.70
1:D:489:LYS:NZ	1:D:489:LYS:HB3	2.06	0.70
1:B:640:LEU:HD11	1:B:650:GLY:HA3	1.74	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ILE:HD13	1:A:116:LEU:HD22	1.73	0.69
1:B:289:ALA:CB	1:B:290:PRO:HA	2.18	0.69
1:C:184:ARG:HH11	1:C:187:TRP:HA	1.56	0.69
1:B:114:ILE:HD11	1:B:137:LEU:HD21	1.75	0.69
1:D:177:GLU:HB2	1:D:180:LEU:HD22	1.74	0.69
1:A:448:GLU:HG3	3:A:1524:HOH:O	1.92	0.69
1:C:88:VAL:HG11	1:C:91:GLU:OE2	1.93	0.69
1:D:320:GLN:OE1	1:D:669:ARG:HD3	1.93	0.69
1:C:71:LYS:HE2	3:C:1167:HOH:O	1.92	0.69
1:C:314:GLN:HE22	1:C:373:LYS:HZ1	1.39	0.68
1:B:697:GLN:HG3	3:B:2070:HOH:O	1.94	0.68
1:B:160:VAL:HG23	1:B:161:GLY:N	2.09	0.68
1:D:471:ARG:HG2	1:D:480:TYR:CD2	2.28	0.68
1:D:640:LEU:HD11	1:D:650:GLY:HA3	1.74	0.68
1:A:334:SER:HB3	1:A:336:ARG:HE	1.57	0.68
1:C:289:ALA:CB	1:C:290:PRO:HA	2.16	0.68
1:C:621:ASN:HB3	3:C:1063:HOH:O	1.92	0.68
1:D:615:LYS:HB2	3:D:1373:HOH:O	1.93	0.68
1:A:92:ASN:HD22	1:A:93:SER:N	1.92	0.68
1:C:147:ARG:HB2	3:C:1398:HOH:O	1.93	0.67
1:A:334:SER:HB3	1:A:336:ARG:CD	2.24	0.67
1:C:331:ASP:HB3	1:C:334:SER:HB2	1.76	0.67
1:A:289:ALA:HB1	1:A:290:PRO:C	2.19	0.67
1:C:224:ALA:HB1	1:C:268:PHE:CZ	2.30	0.67
1:D:153:GLN:HE22	1:D:170:ASN:ND2	1.92	0.67
1:C:76:ILE:HD12	1:C:90:LEU:HD11	1.75	0.67
1:A:190:LYS:HG2	1:A:193:ILE:HB	1.77	0.66
1:A:651:ILE:CG2	1:A:755:MET:HE3	2.22	0.66
1:A:170:ASN:N	1:A:170:ASN:HD22	1.94	0.66
1:D:410:LEU:HD13	1:D:415:LEU:HD23	1.77	0.66
1:B:291:ALA:O	1:B:295:ILE:HG23	1.96	0.66
1:B:272:ASN:HD22	1:B:274:ASP:H	1.41	0.66
1:C:627:TRP:CE3	1:C:755:MET:HE1	2.29	0.66
1:B:627:TRP:CZ3	1:B:755:MET:HE1	2.31	0.66
1:C:77:LEU:HD23	1:C:88:VAL:HA	1.78	0.66
1:C:487:ASN:HB2	3:C:787:HOH:O	1.95	0.66
1:C:697:GLN:HG3	3:C:1253:HOH:O	1.96	0.66
1:D:56:LYS:HD2	3:D:870:HOH:O	1.96	0.66
1:D:486:VAL:HG13	1:D:487:ASN:H	1.59	0.66
1:B:544:LEU:HD21	1:B:606:GLN:HG3	1.78	0.66
1:A:579:ASP:HB3	1:A:583:SER:OG	1.97	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:203:TYR:HA	1:D:207:VAL:HG13	1.77	0.65
1:C:217:SER:HB3	1:C:222:PHE:HB2	1.78	0.65
1:C:377:ASN:HB2	1:C:381:TYR:O	1.97	0.65
1:A:289:ALA:HB2	3:A:1403:HOH:O	1.96	0.65
1:B:487:ASN:HB2	3:B:1728:HOH:O	1.95	0.65
1:C:219:ASN:ND2	3:C:870:HOH:O	2.28	0.65
1:D:290:PRO:HG3	1:D:326:ASP:OD2	1.97	0.65
1:C:502:LYS:O	1:C:505:GLN:HG2	1.96	0.65
1:A:472:CYS:SG	3:A:905:HOH:O	2.55	0.65
1:C:176:ILE:HG22	1:C:177:GLU:HG2	1.79	0.65
1:B:502:LYS:O	1:B:505:GLN:HG2	1.97	0.65
1:C:141:GLN:HA	3:C:1325:HOH:O	1.95	0.65
1:D:160:VAL:HG23	1:D:161:GLY:N	2.11	0.65
1:A:489:LYS:NZ	1:A:489:LYS:HB3	2.11	0.65
1:C:243:ASP:HB3	3:C:906:HOH:O	1.97	0.65
1:A:281:ASN:HB2	3:A:1529:HOH:O	1.95	0.65
1:D:505:GLN:HB3	3:D:1281:HOH:O	1.97	0.65
1:B:89:PHE:CE1	1:B:107:ILE:HD13	2.32	0.65
1:C:183:TYR:HE1	1:C:277:SER:O	1.80	0.65
1:C:203:TYR:HA	1:C:207:VAL:HG13	1.78	0.65
1:C:334:SER:HB3	1:C:336:ARG:NE	2.12	0.65
1:C:57:LEU:HD21	3:C:1295:HOH:O	1.96	0.64
1:B:76:ILE:HB	1:B:90:LEU:CD1	2.26	0.64
1:B:726:VAL:CG1	1:B:728:VAL:HG23	2.28	0.64
1:C:272:ASN:HD22	1:C:274:ASP:H	1.45	0.64
1:B:272:ASN:ND2	1:B:274:ASP:H	1.95	0.64
1:B:627:TRP:CE3	1:B:755:MET:HE1	2.32	0.64
1:C:361:GLU:HB3	3:C:1133:HOH:O	1.97	0.64
1:D:704:HIS:HD2	1:D:716:SER:OG	1.80	0.64
1:C:178:PRO:HG3	3:C:1425:HOH:O	1.97	0.63
1:C:290:PRO:HG3	1:C:326:ASP:OD2	1.98	0.63
1:D:361:GLU:HB3	3:D:836:HOH:O	1.97	0.63
1:A:184:ARG:HD3	1:A:186:THR:O	1.97	0.63
1:B:140:ARG:HH11	1:B:140:ARG:HG2	1.62	0.63
1:A:736:THR:HG21	1:B:717:ALA:O	1.97	0.63
1:B:108:SER:C	1:B:110:ASP:H	2.05	0.63
1:B:177:GLU:HB2	1:B:180:LEU:HD13	1.80	0.63
1:D:71:LYS:HE2	3:D:963:HOH:O	1.97	0.63
1:B:452:GLU:HG2	3:B:2056:HOH:O	1.97	0.63
1:B:336:ARG:HB2	3:B:2390:HOH:O	1.97	0.63
1:D:183:TYR:CD2	1:D:276:LEU:HG	2.34	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:340:LEU:O	1:D:343:ARG:HB3	1.98	0.63
1:C:314:GLN:HE22	1:C:373:LYS:NZ	1.97	0.63
1:D:377:ASN:HB3	1:D:379:GLU:H	1.64	0.63
1:D:614:SER:HA	1:D:619:VAL:HB	1.81	0.63
1:D:173:TYR:CE2	1:D:184:ARG:HG3	2.34	0.62
1:A:293:MET:HE3	1:A:293:MET:HA	1.81	0.62
1:B:184:ARG:HD3	1:B:186:THR:O	1.99	0.62
1:A:704:HIS:HD2	1:A:716:SER:OG	1.83	0.62
1:D:272:ASN:HD22	1:D:272:ASN:C	2.07	0.62
1:A:71:LYS:HZ1	1:A:105:TYR:HB2	1.65	0.62
1:B:554:LYS:HG2	3:B:1985:HOH:O	2.00	0.62
1:B:218:PRO:HB2	1:B:308:GLN:NE2	2.15	0.62
1:A:726:VAL:HG13	1:A:728:VAL:HG23	1.82	0.61
1:B:535:ASP:OD1	1:B:537:SER:HB3	1.98	0.61
1:D:69:LEU:CD1	1:D:107:ILE:HD12	2.29	0.61
1:A:234:PRO:HB2	1:B:248:TYR:CZ	2.35	0.61
1:B:676:PRO:HG2	1:B:677:GLU:OE2	2.01	0.61
1:C:286:GLN:NE2	1:C:288:THR:HG22	2.15	0.61
1:C:431:LEU:HG	1:C:445:LEU:HD12	1.82	0.61
1:A:331:ASP:HB3	1:A:334:SER:HB2	1.82	0.61
1:A:175:LYS:NZ	1:A:182:SER:HB2	2.15	0.61
1:A:289:ALA:CB	1:A:290:PRO:CA	2.73	0.61
1:A:651:ILE:HG21	1:A:755:MET:CE	2.24	0.61
1:D:544:LEU:HD12	1:D:576:ALA:O	2.01	0.61
1:D:547:TYR:HB3	3:D:1434:HOH:O	1.99	0.61
1:B:193:ILE:HG22	1:B:194:ILE:CD1	2.22	0.61
1:C:405:ILE:HG12	1:C:419:SER:HA	1.82	0.61
1:B:61:ARG:NH2	1:B:63:ILE:HG22	2.15	0.61
1:C:113:PHE:CE2	1:C:178:PRO:HG2	2.36	0.61
1:C:658:ARG:HG2	1:C:661:TYR:CE2	2.36	0.61
1:D:279:VAL:HB	3:D:973:HOH:O	2.01	0.61
1:D:422:TYR:CE2	1:D:423:LYS:HD3	2.35	0.61
1:A:214:LEU:HG	3:A:1054:HOH:O	2.01	0.60
1:B:272:ASN:HD22	1:B:272:ASN:C	2.09	0.60
1:D:411:THR:C	1:D:413:ASP:H	2.09	0.60
1:D:489:LYS:HB3	1:D:489:LYS:HZ3	1.66	0.60
1:A:276:LEU:HD21	3:A:1022:HOH:O	2.00	0.60
1:C:651:ILE:CG2	1:C:755:MET:HE3	2.28	0.60
1:A:333:SER:HB3	3:A:962:HOH:O	2.00	0.60
1:B:158:SER:HB3	1:B:163:LYS:HB2	1.83	0.60
1:B:361:GLU:HB3	3:B:1644:HOH:O	2.00	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:ASN:HB2	1:A:381:TYR:O	2.02	0.60
1:A:435:GLN:HE22	1:A:441:LYS:NZ	1.99	0.60
1:B:81:ALA:O	1:B:492:ARG:NH2	2.33	0.60
1:D:57:LEU:HD23	3:D:1427:HOH:O	2.01	0.60
1:D:108:SER:C	1:D:110:ASP:H	2.09	0.60
1:A:276:LEU:H	1:A:276:LEU:CD2	2.15	0.60
1:D:459:VAL:HG22	1:D:460:SER:N	2.17	0.60
1:D:486:VAL:HG13	1:D:487:ASN:N	2.17	0.59
1:B:114:ILE:CD1	1:B:137:LEU:HD21	2.32	0.59
1:B:392:LYS:HG3	1:B:393:ASP:H	1.67	0.59
1:C:263:ASN:ND2	1:C:318:ARG:CZ	2.65	0.59
1:C:272:ASN:HD22	1:C:272:ASN:C	2.10	0.59
1:D:438:ASP:OD2	1:D:441:LYS:HG3	2.02	0.59
1:D:597:ARG:NH1	1:D:682:HIS:HB2	2.17	0.59
1:D:697:GLN:HG3	3:D:1015:HOH:O	2.02	0.59
1:D:726:VAL:CG1	1:D:728:VAL:HG23	2.32	0.59
1:B:65:ASP:CG	1:B:464:GLU:HB2	2.27	0.59
1:A:92:ASN:ND2	1:A:93:SER:N	2.51	0.59
1:D:60:LEU:HD12	1:D:60:LEU:C	2.27	0.59
1:A:481:THR:OG1	1:A:483:HIS:HE1	1.85	0.59
1:B:74:ASN:C	1:B:92:ASN:HB3	2.28	0.59
1:C:608:GLU:O	1:C:612:GLN:HG2	2.02	0.59
1:C:184:ARG:HD3	1:C:186:THR:O	2.02	0.59
1:C:341:VAL:C	1:C:343:ARG:H	2.09	0.58
1:A:640:LEU:HD11	1:A:650:GLY:HA3	1.84	0.58
1:D:388:GLN:HB2	1:D:391:LYS:HB2	1.85	0.58
1:A:76:ILE:HB	1:A:90:LEU:CD1	2.33	0.58
1:A:544:LEU:HD21	1:A:606:GLN:HG3	1.85	0.58
1:D:510:PRO:HD3	1:D:569:SER:HB2	1.83	0.58
1:A:77:LEU:HD23	1:A:88:VAL:HA	1.85	0.58
1:A:506:ASN:HB2	3:A:1012:HOH:O	2.04	0.58
1:C:114:ILE:HG13	1:C:137:LEU:HD21	1.84	0.58
1:B:693:GLU:OE1	1:B:696:LYS:HE2	2.04	0.58
1:C:81:ALA:O	1:C:492:ARG:NH2	2.37	0.58
1:C:614:SER:HB2	3:C:1063:HOH:O	2.03	0.58
1:D:498:SER:O	1:D:502:LYS:HG2	2.04	0.58
1:A:140:ARG:HG2	1:A:140:ARG:NH1	2.18	0.58
1:D:147:ARG:HB2	3:D:851:HOH:O	2.04	0.58
1:C:65:ASP:OD2	1:C:466:LYS:HB2	2.04	0.58
1:D:691:ARG:NE	3:D:1422:HOH:O	2.23	0.58
1:C:158:SER:HB3	1:C:163:LYS:HB2	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:422:TYR:CE2	1:C:423:LYS:HD3	2.39	0.58
1:C:600:THR:O	1:C:603:VAL:HG13	2.04	0.58
1:D:172:ILE:H	1:D:186:THR:CG2	2.13	0.58
1:A:676:PRO:HG2	1:A:677:GLU:OE2	2.04	0.57
1:C:244:GLU:CD	1:D:689:MET:HG3	2.29	0.57
1:D:106:SER:HB3	1:D:115:LEU:HB3	1.86	0.57
1:B:177:GLU:CB	1:B:180:LEU:HD13	2.34	0.57
1:B:528:MET:HE1	1:B:618:PHE:CE1	2.39	0.57
1:B:704:HIS:HD2	1:B:716:SER:OG	1.87	0.57
1:D:761:GLN:HE21	1:D:762:CYS:N	2.03	0.57
1:D:392:LYS:HE3	1:D:393:ASP:OD2	2.04	0.57
1:A:147:ARG:HD3	3:A:1158:HOH:O	2.03	0.57
1:A:734:TRP:CD1	1:A:736:THR:HG22	2.40	0.57
1:C:651:ILE:HG21	1:C:755:MET:CE	2.29	0.57
1:D:184:ARG:HH11	1:D:187:TRP:HA	1.69	0.57
1:D:293:MET:CE	1:D:317:ARG:HG3	2.33	0.57
1:D:429:ARG:NE	3:D:1140:HOH:O	2.33	0.57
1:D:627:TRP:CE3	1:D:755:MET:HE1	2.40	0.57
1:A:97:GLU:HB3	3:A:938:HOH:O	2.05	0.57
1:B:285:ILE:HD12	1:B:285:ILE:N	2.20	0.57
1:C:69:LEU:CD1	1:C:107:ILE:HD12	2.34	0.57
1:D:289:ALA:HA	1:D:294:LEU:CD1	2.35	0.57
1:D:361:GLU:HB3	3:D:1154:HOH:O	2.04	0.57
1:C:114:ILE:CD1	1:C:137:LEU:HD21	2.34	0.57
1:C:272:ASN:HD22	1:C:273:THR:N	2.03	0.57
1:C:285:ILE:N	1:C:285:ILE:HD12	2.19	0.57
1:D:272:ASN:HD22	1:D:274:ASP:H	1.50	0.57
1:B:334:SER:HB3	1:B:336:ARG:CD	2.35	0.57
1:C:156:THR:HG21	1:C:214:LEU:HD11	1.86	0.57
1:C:361:GLU:HB3	3:C:821:HOH:O	2.04	0.57
1:C:76:ILE:HB	1:C:90:LEU:CD1	2.35	0.56
1:D:402:TRP:CD2	1:D:421:GLU:HB2	2.39	0.56
1:A:177:GLU:CB	1:A:180:LEU:HD22	2.33	0.56
1:C:71:LYS:HG2	3:C:1167:HOH:O	2.06	0.56
1:C:90:LEU:HD13	1:C:90:LEU:O	2.04	0.56
1:B:302:ASP:HB3	1:B:314:GLN:HB2	1.87	0.56
1:C:317:ARG:HD2	1:C:322:TYR:HB3	1.85	0.56
1:C:542:LEU:C	1:C:542:LEU:HD23	2.30	0.56
1:A:173:TYR:CE2	1:A:184:ARG:HG3	2.40	0.56
1:B:483:HIS:HD2	3:B:2039:HOH:O	1.87	0.56
1:B:536:LYS:NZ	1:B:536:LYS:HB3	2.21	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:341:VAL:O	1:D:342:ALA:HB3	2.05	0.56
1:D:415:LEU:HB3	1:D:434:ILE:HG23	1.87	0.56
1:C:197:GLY:C	1:C:213:ALA:HB3	2.30	0.56
1:A:272:ASN:C	1:A:272:ASN:HD22	2.13	0.56
1:A:276:LEU:HD23	1:A:276:LEU:N	2.20	0.56
1:C:435:GLN:HG2	1:C:438:ASP:H	1.69	0.56
1:D:90:LEU:HD22	1:D:90:LEU:O	2.06	0.56
1:B:528:MET:CE	1:B:530:LEU:HD21	2.36	0.56
1:B:691:ARG:NH1	3:B:2362:HOH:O	2.26	0.56
1:A:341:VAL:O	1:A:342:ALA:HB3	2.04	0.56
1:A:528:MET:CE	1:A:530:LEU:HD21	2.35	0.56
1:B:726:VAL:HG12	1:B:728:VAL:HG23	1.87	0.56
1:C:354:VAL:HG12	1:C:359:PRO:HG3	1.87	0.56
1:C:506:ASN:HB3	3:C:1321:HOH:O	2.05	0.56
1:A:487:ASN:O	1:A:488:ASP:HB2	2.05	0.56
1:B:180:LEU:HD23	3:B:1823:HOH:O	2.05	0.56
1:B:504:LEU:HA	1:B:507:VAL:CG1	2.35	0.56
1:B:214:LEU:HD12	1:B:214:LEU:O	2.06	0.55
1:C:253:ARG:HH12	1:D:253:ARG:HH22	1.54	0.55
1:D:74:ASN:C	1:D:92:ASN:HB3	2.31	0.55
1:A:514:LEU:HD12	1:A:557:THR:HG22	1.88	0.55
1:B:69:LEU:CD1	1:B:107:ILE:HD12	2.36	0.55
1:D:627:TRP:CZ3	1:D:755:MET:HE1	2.41	0.55
1:B:269:PHE:CE2	1:B:286:GLN:HB2	2.41	0.55
1:B:377:ASN:HB3	1:B:379:GLU:H	1.71	0.55
1:B:481:THR:OG1	1:B:483:HIS:HE1	1.89	0.55
1:C:74:ASN:HB3	1:C:92:ASN:HB3	1.88	0.55
1:C:704:HIS:HD2	1:C:716:SER:OG	1.90	0.55
1:D:697:GLN:HG3	3:D:1141:HOH:O	2.04	0.55
1:A:72:GLN:HB3	3:A:957:HOH:O	2.05	0.55
1:D:277:SER:O	1:D:278:SER:HB3	2.06	0.55
1:B:764:SER:HA	3:B:1895:HOH:O	2.06	0.55
1:C:340:LEU:O	1:C:343:ARG:HB3	2.07	0.55
1:C:546:VAL:HG22	1:C:547:TYR:N	2.22	0.55
1:D:243:ASP:HB3	3:D:1061:HOH:O	2.07	0.55
1:D:472:CYS:O	1:D:478:PRO:HA	2.07	0.55
1:C:377:ASN:HB2	1:C:381:TYR:H	1.72	0.55
1:A:39:SER:HB3	1:A:40:ARG:HE	1.72	0.55
1:B:319:ILE:HG22	1:B:321:ASN:HB2	1.88	0.55
1:A:248:TYR:CZ	1:B:234:PRO:HB2	2.42	0.54
1:A:272:ASN:HD22	1:A:274:ASP:H	1.55	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:TYR:CE2	1:B:184:ARG:HG3	2.42	0.54
1:C:140:ARG:HG2	1:C:140:ARG:HH11	1.72	0.54
1:C:489:LYS:NZ	1:C:489:LYS:HB3	2.22	0.54
1:A:177:GLU:CG	1:A:180:LEU:HD22	2.37	0.54
1:A:627:TRP:CE3	1:A:755:MET:HE1	2.41	0.54
1:A:751:ILE:O	1:A:755:MET:HG3	2.06	0.54
1:C:146:GLU:OE2	1:C:181:PRO:HG3	2.08	0.54
1:D:76:ILE:HB	1:D:90:LEU:CD1	2.36	0.54
1:D:306:ALA:CB	1:D:310:ARG:HD2	2.37	0.54
1:A:153:GLN:HE22	1:A:170:ASN:HD21	1.52	0.54
1:A:669:ARG:HD2	3:A:1572:HOH:O	2.07	0.54
1:C:78:VAL:HG12	1:C:87:SER:O	2.07	0.54
1:A:74:ASN:C	1:A:92:ASN:HB3	2.31	0.54
1:A:291:ALA:O	1:A:295:ILE:HG23	2.06	0.54
1:C:354:VAL:CG1	1:C:359:PRO:HG3	2.37	0.54
3:C:792:HOH:O	1:D:736:THR:HG23	2.07	0.54
1:D:40:ARG:HB2	1:D:506:ASN:O	2.07	0.54
1:A:321:ASN:ND2	3:A:863:HOH:O	2.40	0.54
1:B:147:ARG:HD3	3:B:2363:HOH:O	2.07	0.54
1:B:341:VAL:O	1:B:342:ALA:CB	2.52	0.54
1:B:597:ARG:NH1	1:B:679:ASN:HD21	2.05	0.54
1:D:76:ILE:HD12	1:D:90:LEU:HD11	1.88	0.54
1:D:543:LEU:HD11	1:D:627:TRP:CD1	2.43	0.54
1:C:387:PHE:CD2	1:C:394:CYS:HB3	2.43	0.54
1:A:187:TRP:N	1:A:187:TRP:CD1	2.75	0.54
1:D:492:ARG:HA	3:D:1076:HOH:O	2.08	0.54
1:A:171:ASP:HA	1:A:186:THR:CG2	2.38	0.54
1:A:285:ILE:N	1:A:285:ILE:HD12	2.23	0.54
1:A:580:GLY:O	1:A:583:SER:HB2	2.07	0.54
1:C:234:PRO:HB2	1:D:248:TYR:CZ	2.43	0.54
1:D:600:THR:O	1:D:603:VAL:HG13	2.07	0.54
1:D:622:LYS:HB2	1:D:622:LYS:NZ	2.22	0.54
1:D:242:SER:HB3	1:D:246:LEU:HD12	1.89	0.54
1:A:160:VAL:HG23	1:A:161:GLY:N	2.23	0.53
1:A:172:ILE:N	1:A:186:THR:HG22	2.15	0.53
1:C:341:VAL:HG22	1:C:342:ALA:N	2.23	0.53
1:C:535:ASP:C	1:C:537:SER:H	2.16	0.53
1:A:158:SER:HB3	1:A:163:LYS:HB2	1.90	0.53
1:C:85:ASN:ND2	3:C:871:HOH:O	2.41	0.53
1:C:172:ILE:H	1:C:186:THR:CG2	2.17	0.53
1:D:93:SER:HA	1:D:96:ASP:OD1	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:293:MET:HE2	1:D:317:ARG:CG	2.36	0.53
1:C:60:LEU:C	1:C:60:LEU:HD12	2.34	0.53
1:A:106:SER:HB3	1:A:115:LEU:HB3	1.90	0.53
1:C:438:ASP:OD2	1:C:441:LYS:HG3	2.09	0.53
1:D:74:ASN:HB3	1:D:92:ASN:HB3	1.89	0.53
1:C:74:ASN:C	1:C:92:ASN:HB3	2.33	0.53
1:D:41:LYS:H	1:D:41:LYS:HD3	1.73	0.53
1:D:513:LYS:HD3	3:D:1177:HOH:O	2.07	0.53
1:A:40:ARG:CD	1:A:40:ARG:H	2.19	0.53
1:C:277:SER:O	1:C:278:SER:HB3	2.07	0.53
1:C:481:THR:OG1	1:C:483:HIS:HE1	1.91	0.53
1:A:276:LEU:CD2	1:A:276:LEU:N	2.71	0.53
1:A:310:ARG:NH1	1:A:329:ASP:OD1	2.42	0.53
1:C:177:GLU:HB2	1:C:180:LEU:HD13	1.90	0.53
1:C:486:VAL:HG13	1:C:487:ASN:H	1.73	0.53
1:C:764:SER:HB3	3:C:1066:HOH:O	2.08	0.53
1:D:170:ASN:N	1:D:170:ASN:HD22	2.04	0.53
1:D:40:ARG:H	1:D:40:ARG:CD	2.21	0.53
1:B:40:ARG:HD2	1:B:40:ARG:N	2.24	0.53
1:D:541:PRO:HG3	1:D:623:ARG:CZ	2.38	0.53
1:B:41:LYS:HG3	3:B:1682:HOH:O	2.07	0.53
1:D:125:ARG:HG2	1:D:126:HIS:NE2	2.23	0.53
1:D:183:TYR:HE1	1:D:277:SER:O	1.92	0.53
1:D:528:MET:HE1	1:D:618:PHE:CE1	2.44	0.52
1:A:627:TRP:HB2	1:A:651:ILE:HB	1.91	0.52
1:B:71:LYS:NZ	1:B:105:TYR:HB2	2.24	0.52
1:B:512:LYS:HD3	3:B:2185:HOH:O	2.08	0.52
1:B:513:LYS:HE3	1:B:530:LEU:HD11	1.90	0.52
1:B:597:ARG:HH12	1:B:679:ASN:HD21	1.56	0.52
1:C:177:GLU:CB	1:C:180:LEU:HD13	2.39	0.52
1:C:253:ARG:HH22	1:D:253:ARG:HH22	1.56	0.52
1:D:51:ASN:OD1	1:D:54:ARG:HD3	2.09	0.52
1:C:382:ARG:NH2	3:C:766:HOH:O	2.42	0.52
1:B:184:ARG:HD2	1:B:187:TRP:CD2	2.43	0.52
1:B:654:ALA:HA	1:B:704:HIS:CD2	2.43	0.52
1:D:109:PRO:HG2	1:D:160:VAL:O	2.08	0.52
1:D:704:HIS:CD2	1:D:716:SER:OG	2.62	0.52
1:C:536:LYS:HE3	3:C:1007:HOH:O	2.09	0.52
1:A:98:PHE:CE2	1:A:100:HIS:HB2	2.44	0.52
1:A:471:ARG:HG2	1:A:480:TYR:CD2	2.44	0.52
1:C:341:VAL:HG12	3:C:1142:HOH:O	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:411:THR:C	1:D:413:ASP:N	2.65	0.52
1:A:162:HIS:HD2	1:A:178:PRO:HD3	1.75	0.52
1:B:546:VAL:HG22	1:B:547:TYR:N	2.24	0.52
1:B:629:TRP:HB3	3:B:2210:HOH:O	2.09	0.52
1:C:144:THR:HA	1:C:147:ARG:NH2	2.24	0.52
1:C:242:SER:HB3	1:C:246:LEU:HD12	1.91	0.52
1:C:649:CYS:HB3	1:C:699:GLU:HB2	1.92	0.52
1:D:522:THR:HG22	1:D:523:LYS:N	2.25	0.52
1:B:579:ASP:HB3	1:B:583:SER:OG	2.10	0.52
1:C:286:GLN:HE21	1:C:288:THR:HG22	1.75	0.52
1:C:422:TYR:CD2	1:C:423:LYS:HD3	2.45	0.52
1:B:293:MET:HG2	1:B:315:TRP:HB3	1.90	0.52
1:D:289:ALA:CB	1:D:290:PRO:HA	2.19	0.52
1:A:40:ARG:NH1	1:A:505:GLN:O	2.43	0.52
1:A:310:ARG:HG3	1:A:329:ASP:OD1	2.09	0.52
1:A:320:GLN:OE1	1:A:669:ARG:HD3	2.10	0.52
1:B:98:PHE:CD2	1:B:100:HIS:HB2	2.45	0.52
1:B:322:TYR:CD2	1:B:348:MET:HE2	2.45	0.52
1:B:429:ARG:NH2	3:B:2361:HOH:O	2.42	0.51
1:C:85:ASN:HB2	3:C:1196:HOH:O	2.09	0.51
1:B:413:ASP:HB2	3:B:2372:HOH:O	2.10	0.51
1:B:451:PRO:HG2	3:B:2056:HOH:O	2.09	0.51
1:C:510:PRO:HD3	1:C:569:SER:HB2	1.93	0.51
1:A:107:ILE:HG12	1:A:114:ILE:HG12	1.92	0.51
1:A:313:LEU:N	1:A:313:LEU:HD22	2.25	0.51
1:A:392:LYS:HG3	1:A:393:ASP:H	1.76	0.51
1:A:567:LEU:O	1:A:571:GLU:HB2	2.10	0.51
1:B:377:ASN:HB2	1:B:381:TYR:H	1.75	0.51
1:B:614:SER:HA	1:B:619:VAL:HB	1.91	0.51
1:C:458:SER:OG	1:C:471:ARG:HB2	2.10	0.51
1:D:41:LYS:NZ	1:D:507:VAL:HB	2.26	0.51
1:A:487:ASN:HB3	1:A:489:LYS:HG3	1.92	0.51
1:C:172:ILE:N	1:C:186:THR:HG22	2.19	0.51
1:A:741:GLY:O	1:A:742:ILE:C	2.53	0.51
1:C:74:ASN:HB2	3:C:904:HOH:O	2.11	0.51
1:C:305:TRP:CE2	1:C:311:ILE:HD12	2.46	0.51
1:D:147:ARG:HH11	1:D:147:ARG:HG2	1.75	0.51
1:D:171:ASP:OD1	1:D:186:THR:HG23	2.11	0.51
1:A:608:GLU:HA	1:A:608:GLU:OE1	2.09	0.51
1:D:718:GLN:HA	1:D:718:GLN:HE21	1.75	0.51
1:A:528:MET:HE1	1:A:618:PHE:HE1	1.76	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:334:SER:HB3	1:B:336:ARG:HD2	1.92	0.51
1:C:330:TYR:HE1	1:C:335:GLY:O	1.94	0.51
1:C:612:GLN:O	1:C:616:MET:HG3	2.10	0.51
1:D:403:GLU:OE1	1:D:585:TYR:HA	2.10	0.51
1:D:435:GLN:HG2	1:D:437:SER:H	1.76	0.51
1:D:485:SER:O	1:D:486:VAL:C	2.54	0.51
1:D:543:LEU:HD23	1:D:625:ALA:HB3	1.93	0.51
1:A:520:ASN:ND2	3:A:1188:HOH:O	2.43	0.51
1:A:658:ARG:HG2	1:A:661:TYR:CE2	2.46	0.51
1:B:140:ARG:HG2	1:B:140:ARG:NH1	2.26	0.51
1:C:108:SER:C	1:C:110:ASP:H	2.19	0.51
1:C:146:GLU:O	1:C:175:LYS:HE2	2.11	0.51
1:C:336:ARG:HG2	1:C:336:ARG:HH11	1.76	0.51
1:A:466:LYS:HB2	3:A:1332:HOH:O	2.10	0.50
1:B:489:LYS:HB3	1:B:489:LYS:HZ3	1.76	0.50
1:C:302:ASP:HB3	1:C:314:GLN:HB2	1.93	0.50
1:D:177:GLU:HB2	1:D:180:LEU:HD13	1.93	0.50
1:B:392:LYS:HG3	1:B:393:ASP:N	2.26	0.50
1:B:544:LEU:CD2	1:B:606:GLN:HG3	2.42	0.50
1:C:153:GLN:HE22	1:C:170:ASN:ND2	2.09	0.50
1:C:276:LEU:HD13	1:C:276:LEU:H	1.76	0.50
1:D:40:ARG:HH11	1:D:40:ARG:HG2	1.76	0.50
1:A:60:LEU:HD12	1:A:60:LEU:C	2.36	0.50
1:A:92:ASN:ND2	1:A:93:SER:H	2.08	0.50
1:B:489:LYS:HB3	1:B:489:LYS:NZ	2.25	0.50
1:C:320:GLN:OE1	1:C:669:ARG:HD3	2.11	0.50
1:D:65:ASP:OD2	1:D:466:LYS:HB2	2.10	0.50
1:D:108:SER:C	1:D:110:ASP:N	2.69	0.50
1:D:176:ILE:HD13	1:D:183:TYR:CE2	2.46	0.50
1:D:276:LEU:H	1:D:276:LEU:CD2	2.21	0.50
1:D:539:LYS:NZ	1:D:617:GLY:O	2.44	0.50
1:A:74:ASN:HB3	1:A:92:ASN:OD1	2.12	0.50
1:A:413:ASP:HB3	1:A:414:TYR:CD1	2.47	0.50
1:B:153:GLN:HE22	1:B:170:ASN:ND2	2.10	0.50
1:A:39:SER:CB	1:A:40:ARG:HE	2.25	0.50
1:B:76:ILE:HB	1:B:90:LEU:HD13	1.92	0.50
1:C:214:LEU:HD12	1:C:214:LEU:O	2.11	0.50
1:D:520:ASN:O	1:D:521:GLU:HB2	2.10	0.50
1:B:325:MET:HE1	1:B:371:PHE:CE2	2.47	0.50
1:A:528:MET:HE1	1:A:618:PHE:CE1	2.46	0.50
1:C:387:PHE:CE2	1:C:394:CYS:HB3	2.46	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:726:VAL:HG12	1:C:728:VAL:HG23	1.93	0.50
1:B:760:LYS:HE3	3:B:2134:HOH:O	2.10	0.50
1:C:41:LYS:H	1:C:41:LYS:HD3	1.77	0.50
1:D:85:ASN:ND2	3:D:845:HOH:O	2.45	0.50
1:D:597:ARG:HG2	3:D:1165:HOH:O	2.11	0.50
1:A:90:LEU:C	1:A:90:LEU:HD22	2.37	0.50
1:B:596:ARG:C	1:B:597:ARG:HD3	2.36	0.50
1:C:402:TRP:CD2	1:C:421:GLU:HB2	2.47	0.50
1:D:276:LEU:HD23	1:D:276:LEU:O	2.11	0.50
1:D:534:PHE:HZ	1:D:618:PHE:CG	2.30	0.50
1:A:489:LYS:HB3	1:A:489:LYS:HZ3	1.75	0.49
1:B:108:SER:C	1:B:110:ASP:N	2.70	0.49
1:B:510:PRO:HD3	1:B:569:SER:HB2	1.92	0.49
1:D:64:SER:O	1:D:463:LYS:HG2	2.12	0.49
1:D:319:ILE:HB	3:D:925:HOH:O	2.12	0.49
1:D:435:GLN:NE2	1:D:441:LYS:HD2	2.27	0.49
1:D:651:ILE:HG21	1:D:755:MET:HE3	1.94	0.49
1:A:232:GLU:N	3:A:1546:HOH:O	2.37	0.49
1:D:291:ALA:O	1:D:295:ILE:HG23	2.12	0.49
1:D:536:LYS:HG2	3:D:873:HOH:O	2.12	0.49
1:B:60:LEU:HD12	1:B:60:LEU:O	2.12	0.49
1:D:334:SER:HB3	1:D:336:ARG:CD	2.43	0.49
1:D:526:TYR:CD1	1:D:526:TYR:C	2.90	0.49
1:B:276:LEU:HD23	1:B:276:LEU:O	2.12	0.49
1:C:115:LEU:HD21	1:C:155:VAL:HG11	1.95	0.49
1:A:272:ASN:ND2	1:A:274:ASP:H	2.09	0.49
1:C:341:VAL:HG22	1:C:342:ALA:H	1.77	0.49
1:C:388:GLN:HB3	1:C:391:LYS:HD3	1.94	0.49
1:C:654:ALA:HA	1:C:704:HIS:CD2	2.47	0.49
1:D:179:ASN:OD1	1:D:180:LEU:HD12	2.11	0.49
1:B:471:ARG:NH2	3:B:2160:HOH:O	2.46	0.49
1:C:289:ALA:HB3	3:C:1431:HOH:O	2.12	0.49
1:D:280:THR:HB	3:D:1024:HOH:O	2.11	0.49
1:D:612:GLN:O	1:D:616:MET:HG3	2.12	0.49
1:D:734:TRP:HE1	1:D:736:THR:HG22	1.78	0.49
1:A:332:GLU:HB2	3:A:903:HOH:O	2.12	0.49
1:C:160:VAL:HG22	3:C:1376:HOH:O	2.13	0.49
1:C:170:ASN:N	1:C:170:ASN:HD22	2.10	0.49
1:D:181:PRO:HD2	3:D:1356:HOH:O	2.12	0.49
1:A:622:LYS:HB2	1:A:622:LYS:NZ	2.28	0.49
1:B:276:LEU:CD2	1:B:276:LEU:H	2.26	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:615:LYS:HE2	3:B:2019:HOH:O	2.12	0.49
1:B:71:LYS:HZ1	1:B:105:TYR:HB2	1.78	0.49
1:B:336:ARG:HG2	1:B:336:ARG:HH11	1.76	0.49
1:B:516:PHE:CE2	1:B:523:LYS:HE2	2.47	0.49
1:C:76:ILE:CD1	1:C:90:LEU:HD11	2.43	0.49
1:D:313:LEU:N	3:D:1433:HOH:O	2.45	0.49
1:D:546:VAL:HG22	1:D:547:TYR:N	2.27	0.49
1:A:147:ARG:HB2	3:A:828:HOH:O	2.13	0.49
1:C:273:THR:HA	1:C:276:LEU:CD1	2.43	0.49
1:C:273:THR:HA	1:C:276:LEU:HD11	1.94	0.49
1:A:613:PHE:C	1:A:615:LYS:H	2.19	0.48
1:C:388:GLN:CB	1:C:391:LYS:HD3	2.43	0.48
1:D:484:SER:OG	1:D:489:LYS:HB2	2.12	0.48
1:A:40:ARG:HD2	1:A:40:ARG:N	2.28	0.48
1:D:654:ALA:HA	1:D:704:HIS:CD2	2.49	0.48
1:B:513:LYS:O	1:B:527:GLN:HA	2.13	0.48
1:C:397:ILE:HG13	1:C:398:THR:HG23	1.94	0.48
1:D:147:ARG:HD3	3:D:1136:HOH:O	2.14	0.48
1:D:341:VAL:HG12	3:D:805:HOH:O	2.13	0.48
1:D:554:LYS:HB3	1:D:577:SER:HB3	1.96	0.48
1:A:141:GLN:HG2	3:A:1372:HOH:O	2.14	0.48
1:B:98:PHE:CE2	1:B:100:HIS:HB2	2.48	0.48
1:C:60:LEU:HD12	1:C:60:LEU:O	2.13	0.48
1:C:136:ASP:O	1:C:140:ARG:HA	2.14	0.48
1:D:726:VAL:HG13	1:D:728:VAL:HG23	1.95	0.48
1:B:504:LEU:O	1:B:507:VAL:HG13	2.13	0.48
1:D:272:ASN:HD21	1:D:274:ASP:HB2	1.77	0.48
1:D:290:PRO:O	1:D:294:LEU:HG	2.14	0.48
1:A:392:LYS:HG3	1:A:393:ASP:N	2.28	0.48
1:C:377:ASN:ND2	1:C:383:HIS:HD2	2.12	0.48
1:D:438:ASP:C	1:D:440:THR:H	2.21	0.48
1:A:325:MET:HE2	1:A:327:ILE:HD11	1.96	0.48
1:A:546:VAL:HG22	1:A:547:TYR:N	2.28	0.48
1:B:74:ASN:HB3	1:B:92:ASN:HB3	1.96	0.48
1:C:58:TYR:CE2	1:C:494:LEU:HB3	2.49	0.48
1:C:145:GLU:HA	3:C:1447:HOH:O	2.13	0.48
1:C:374:ILE:HD11	1:C:406:GLY:HA2	1.95	0.48
1:C:546:VAL:CG2	1:C:547:TYR:N	2.76	0.48
1:D:64:SER:C	1:D:463:LYS:HG2	2.39	0.48
1:D:415:LEU:HD13	1:D:415:LEU:C	2.39	0.48
1:A:81:ALA:O	1:A:492:ARG:NH2	2.46	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:SER:O	1:A:278:SER:HB3	2.14	0.48
1:B:41:LYS:HB2	3:B:1948:HOH:O	2.14	0.48
1:C:159:PRO:HG2	1:C:217:SER:O	2.14	0.48
1:D:153:GLN:HE22	1:D:170:ASN:HD21	1.61	0.48
1:D:595:ASN:C	1:D:597:ARG:H	2.21	0.48
1:A:415:LEU:C	1:A:415:LEU:HD13	2.38	0.47
1:A:658:ARG:O	1:A:658:ARG:HG3	2.14	0.47
1:B:289:ALA:CB	1:B:290:PRO:CA	2.78	0.47
1:C:253:ARG:HH22	1:D:253:ARG:HH12	1.61	0.47
1:C:472:CYS:O	1:C:478:PRO:HA	2.14	0.47
1:C:486:VAL:HG13	1:C:487:ASN:N	2.29	0.47
1:C:627:TRP:CZ3	1:C:755:MET:HE1	2.49	0.47
1:A:154:TRP:CE2	1:A:212:SER:HB2	2.48	0.47
1:B:177:GLU:HB2	1:B:180:LEU:HD22	1.95	0.47
1:B:658:ARG:HG2	1:B:661:TYR:CE2	2.49	0.47
1:C:336:ARG:HG2	1:C:336:ARG:NH1	2.30	0.47
1:D:140:ARG:HG2	1:D:140:ARG:HH11	1.79	0.47
1:D:429:ARG:NH2	3:D:945:HOH:O	2.46	0.47
1:D:704:HIS:HE1	1:D:711:VAL:O	1.98	0.47
1:B:41:LYS:H	1:B:41:LYS:HD3	1.79	0.47
1:B:385:CYS:HB3	1:B:387:PHE:CE1	2.50	0.47
1:D:41:LYS:HZ2	1:D:507:VAL:HB	1.79	0.47
1:D:455:GLN:HG3	1:D:475:PRO:CD	2.44	0.47
1:C:125:ARG:HB3	3:C:1031:HOH:O	2.13	0.47
1:D:40:ARG:HD2	1:D:508:GLN:HG3	1.95	0.47
1:A:71:LYS:HZ3	1:A:105:TYR:HB2	1.75	0.47
1:B:60:LEU:HD12	1:B:60:LEU:C	2.40	0.47
1:B:105:TYR:HB2	3:B:1825:HOH:O	2.13	0.47
1:B:486:VAL:HG13	1:B:487:ASN:N	2.30	0.47
1:D:597:ARG:HH11	1:D:682:HIS:HB2	1.78	0.47
1:A:214:LEU:O	1:A:214:LEU:HD12	2.15	0.47
1:A:486:VAL:HG13	1:A:487:ASN:N	2.29	0.47
1:C:64:SER:O	1:C:463:LYS:HG2	2.14	0.47
1:C:420:ASN:HB2	1:C:426:PRO:HA	1.96	0.47
1:D:520:ASN:O	1:D:521:GLU:CB	2.62	0.47
1:B:289:ALA:HB1	1:B:290:PRO:C	2.40	0.47
1:B:458:SER:OG	1:B:471:ARG:HB2	2.14	0.47
1:C:40:ARG:HB2	1:C:506:ASN:O	2.15	0.47
1:C:676:PRO:HG2	1:C:677:GLU:OE2	2.15	0.47
1:D:85:ASN:ND2	3:D:916:HOH:O	2.47	0.47
1:D:306:ALA:HB3	1:D:310:ARG:HD2	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:513:LYS:O	1:D:527:GLN:HA	2.15	0.47
1:D:734:TRP:NE1	1:D:736:THR:HG22	2.29	0.47
1:D:741:GLY:O	1:D:742:ILE:C	2.58	0.47
1:A:39:SER:HB3	1:A:40:ARG:NE	2.29	0.47
1:A:60:LEU:HD12	1:A:60:LEU:O	2.15	0.47
1:A:110:ASP:C	1:A:112:GLN:H	2.23	0.47
1:A:140:ARG:HH11	1:A:140:ARG:CG	2.25	0.47
1:A:689:MET:HE3	1:B:244:GLU:HG3	1.96	0.47
1:B:55:LEU:HD23	1:B:500:LEU:HD22	1.96	0.47
1:C:237:GLU:HA	1:C:252:VAL:O	2.15	0.47
1:A:290:PRO:HG2	1:A:293:MET:HB2	1.97	0.47
1:D:429:ARG:NH2	3:D:1140:HOH:O	2.46	0.47
1:A:532:PRO:HD3	1:A:569:SER:HA	1.97	0.47
1:B:79:PHE:CE1	1:B:86:SER:HB3	2.50	0.47
1:B:107:ILE:HG12	1:B:114:ILE:HG12	1.96	0.47
1:B:528:MET:HE1	1:B:618:PHE:CZ	2.49	0.47
1:C:103:ASN:HB2	3:C:1239:HOH:O	2.14	0.47
1:D:93:SER:HB2	1:D:96:ASP:OD2	2.14	0.47
1:D:302:ASP:HB3	1:D:314:GLN:HB2	1.97	0.47
1:A:691:ARG:NH2	3:A:1556:HOH:O	2.40	0.46
1:A:734:TRP:NE1	1:A:736:THR:HG22	2.30	0.46
1:D:608:GLU:O	1:D:612:GLN:HG2	2.15	0.46
1:A:93:SER:HB2	1:A:96:ASP:OD2	2.16	0.46
1:A:704:HIS:HE1	1:A:711:VAL:O	1.98	0.46
1:C:90:LEU:C	1:C:90:LEU:HD22	2.40	0.46
1:C:358:ARG:HB3	3:C:909:HOH:O	2.15	0.46
1:C:701:LEU:HD22	1:C:703:ILE:HG13	1.96	0.46
1:A:108:SER:C	1:A:110:ASP:N	2.64	0.46
1:C:58:TYR:CD2	1:C:494:LEU:HB3	2.51	0.46
1:C:114:ILE:CG1	1:C:137:LEU:HD21	2.45	0.46
1:C:183:TYR:CE1	1:C:277:SER:O	2.65	0.46
1:D:74:ASN:HB3	1:D:92:ASN:CB	2.45	0.46
1:D:461:PHE:CD2	1:D:468:TYR:HB3	2.50	0.46
1:D:577:SER:HA	3:D:894:HOH:O	2.14	0.46
1:D:649:CYS:HB3	1:D:699:GLU:HB2	1.96	0.46
1:A:240:PHE:HB3	1:A:250:LYS:HG3	1.97	0.46
1:B:118:TYR:HB2	3:B:1772:HOH:O	2.15	0.46
1:B:272:ASN:HD22	1:B:273:THR:N	2.13	0.46
1:B:293:MET:HE2	1:B:293:MET:CA	2.45	0.46
1:C:136:ASP:CG	1:C:139:LYS:HG2	2.40	0.46
1:D:350:THR:HG22	3:D:1142:HOH:O	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:734:TRP:CD1	1:D:736:THR:HG22	2.50	0.46
1:A:154:TRP:CD1	3:A:1054:HOH:O	2.68	0.46
1:A:377:ASN:HB3	1:A:379:GLU:H	1.80	0.46
1:B:203:TYR:HA	1:B:207:VAL:HG13	1.96	0.46
1:B:612:GLN:HE21	1:B:612:GLN:HB3	1.54	0.46
1:C:77:LEU:CD2	1:C:88:VAL:HA	2.45	0.46
1:D:127:SER:HB3	1:D:211:TYR:CG	2.50	0.46
1:A:370:SER:HB2	1:A:387:PHE:O	2.15	0.46
1:A:691:ARG:NH1	3:A:862:HOH:O	2.48	0.46
1:B:127:SER:HB3	1:B:211:TYR:CD1	2.50	0.46
1:A:186:THR:HG21	1:A:196:ASN:CB	2.45	0.46
1:A:422:TYR:CE2	1:A:423:LYS:HD3	2.49	0.46
1:B:554:LYS:HB3	1:B:577:SER:HB3	1.98	0.46
1:C:175:LYS:NZ	1:C:182:SER:HB2	2.30	0.46
1:A:57:LEU:HD23	3:A:939:HOH:O	2.16	0.46
1:A:136:ASP:OD1	1:A:138:ASN:HB2	2.16	0.46
1:A:459:VAL:HG22	1:A:460:SER:N	2.30	0.46
1:A:720:SER:O	1:A:724:VAL:HG23	2.16	0.46
1:B:231:THR:HG22	1:B:232:GLU:HG3	1.96	0.46
1:C:248:TYR:CZ	1:D:234:PRO:HB2	2.50	0.46
1:C:276:LEU:N	1:C:276:LEU:HD22	2.31	0.46
1:C:693:GLU:HA	1:C:726:VAL:HG11	1.97	0.46
1:C:696:LYS:CG	1:C:728:VAL:HG22	2.46	0.46
1:D:154:TRP:O	1:D:166:TYR:HA	2.16	0.46
1:D:176:ILE:HD13	1:D:183:TYR:HE2	1.81	0.46
1:A:172:ILE:H	1:A:186:THR:CG2	2.15	0.46
1:A:293:MET:CE	1:A:317:ARG:CG	2.91	0.46
1:B:55:LEU:HD23	1:B:500:LEU:CD2	2.45	0.46
1:B:79:PHE:CD1	1:B:86:SER:HB3	2.51	0.46
1:D:259:ALA:HB3	1:D:660:GLU:HA	1.98	0.46
1:D:377:ASN:HB2	1:D:381:TYR:O	2.16	0.46
1:A:334:SER:HB3	1:A:336:ARG:HD2	1.98	0.45
1:A:435:GLN:HE22	1:A:441:LYS:HZ2	1.64	0.45
1:B:193:ILE:CG2	1:B:194:ILE:HD12	2.25	0.45
1:B:310:ARG:HG3	1:B:329:ASP:OD1	2.15	0.45
1:C:333:SER:HB2	3:C:945:HOH:O	2.15	0.45
1:C:334:SER:HB3	1:C:336:ARG:CD	2.46	0.45
1:C:736:THR:OG1	1:D:721:LYS:HD3	2.15	0.45
1:D:232:GLU:HG3	3:D:1026:HOH:O	2.16	0.45
1:A:285:ILE:N	1:A:285:ILE:CD1	2.78	0.45
1:A:291:ALA:C	1:A:293:MET:H	2.24	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:195:TYR:HB3	1:C:198:ILE:HG13	1.98	0.45
1:C:325:MET:O	1:C:344:GLN:HB2	2.17	0.45
1:A:155:VAL:HG13	1:A:166:TYR:HB3	1.99	0.45
1:A:691:ARG:NE	3:A:1556:HOH:O	2.34	0.45
1:B:127:SER:HB3	1:B:211:TYR:CG	2.51	0.45
1:B:221:THR:HG23	1:B:274:ASP:OD2	2.17	0.45
1:D:192:ASP:O	1:D:193:ILE:HD13	2.16	0.45
1:C:65:ASP:CG	1:C:464:GLU:HB2	2.42	0.45
1:C:244:GLU:HG3	1:D:689:MET:HE3	1.99	0.45
1:A:281:ASN:O	1:A:282:ALA:C	2.59	0.45
1:A:458:SER:OG	1:A:471:ARG:HB2	2.15	0.45
1:B:741:GLY:O	1:B:742:ILE:C	2.58	0.45
1:D:520:ASN:HB2	3:D:1354:HOH:O	2.16	0.45
1:A:40:ARG:CD	1:A:40:ARG:N	2.79	0.45
1:A:302:ASP:HB2	3:A:1560:HOH:O	2.16	0.45
1:A:425:MET:HA	1:A:426:PRO:HD3	1.77	0.45
1:C:140:ARG:HG2	1:C:140:ARG:NH1	2.31	0.45
1:D:528:MET:HE2	1:D:530:LEU:CD2	2.43	0.45
1:B:377:ASN:ND2	1:B:383:HIS:HD2	2.15	0.45
1:C:147:ARG:HG2	1:C:147:ARG:HH11	1.82	0.45
1:D:78:VAL:HG13	1:D:78:VAL:O	2.15	0.45
1:A:237:GLU:HA	1:A:252:VAL:O	2.17	0.45
1:A:504:LEU:HA	1:A:507:VAL:HG12	1.98	0.45
1:A:616:MET:HB3	1:A:618:PHE:CE2	2.52	0.45
1:C:60:LEU:HB2	1:C:68:TYR:CD1	2.51	0.45
1:C:331:ASP:O	1:C:332:GLU:C	2.59	0.45
1:C:520:ASN:C	1:C:521:GLU:HG2	2.42	0.45
1:D:184:ARG:HD2	1:D:187:TRP:CZ2	2.51	0.45
1:D:272:ASN:ND2	1:D:272:ASN:C	2.73	0.45
1:D:388:GLN:CB	1:D:391:LYS:HB2	2.45	0.45
1:A:65:ASP:CG	1:A:464:GLU:HB2	2.42	0.45
1:A:471:ARG:HG2	1:A:480:TYR:HD2	1.80	0.45
1:A:756:SER:O	1:A:760:LYS:HG3	2.17	0.45
1:C:154:TRP:O	1:C:166:TYR:HA	2.17	0.45
1:C:415:LEU:HB3	1:C:434:ILE:HG22	1.99	0.45
1:C:658:ARG:HD2	1:C:661:TYR:CE1	2.51	0.45
1:D:81:ALA:O	1:D:492:ARG:NH2	2.49	0.45
1:A:69:LEU:HD13	1:A:107:ILE:HD12	1.98	0.45
1:A:392:LYS:HG2	3:A:1151:HOH:O	2.16	0.45
1:C:123:GLN:HG2	1:C:124:TRP:CD2	2.52	0.45
1:C:614:SER:HA	1:C:619:VAL:HB	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:736:THR:HG23	3:D:854:HOH:O	2.17	0.45
1:A:183:TYR:HE1	1:A:278:SER:HA	1.82	0.44
1:B:407:ILE:HG23	1:B:415:LEU:HD21	1.99	0.44
1:D:651:ILE:HG21	1:D:755:MET:CE	2.47	0.44
1:A:90:LEU:HD22	1:A:90:LEU:O	2.16	0.44
1:B:319:ILE:C	1:B:321:ASN:H	2.24	0.44
1:C:322:TYR:HE1	1:C:324:VAL:CG2	2.30	0.44
1:A:293:MET:CE	1:A:317:ARG:HG3	2.35	0.44
1:C:82:GLU:HG3	1:C:83:TYR:CE1	2.53	0.44
1:C:175:LYS:HZ3	1:C:182:SER:HB2	1.81	0.44
1:C:596:ARG:N	1:C:670:TYR:O	2.50	0.44
1:C:741:GLY:O	1:C:742:ILE:C	2.59	0.44
1:D:377:ASN:HB2	1:D:381:TYR:H	1.83	0.44
1:B:65:ASP:OD2	1:B:466:LYS:HB2	2.18	0.44
1:B:107:ILE:HG22	3:B:1872:HOH:O	2.16	0.44
1:B:317:ARG:HG2	3:B:1755:HOH:O	2.18	0.44
1:C:474:GLY:HA3	1:C:557:THR:O	2.17	0.44
1:C:551:CYS:O	1:C:551:CYS:SG	2.76	0.44
1:D:330:TYR:HE1	1:D:335:GLY:O	2.01	0.44
1:B:712:HIS:O	1:B:713:PHE:C	2.60	0.44
1:C:648:LYS:HE3	3:C:989:HOH:O	2.18	0.44
1:D:322:TYR:OH	1:D:346:ILE:HD13	2.18	0.44
1:D:471:ARG:HG2	1:D:480:TYR:HD2	1.79	0.44
1:A:764:SER:HB3	3:A:1321:HOH:O	2.18	0.44
1:C:415:LEU:C	1:C:415:LEU:HD13	2.43	0.44
1:C:512:LYS:HD3	3:C:954:HOH:O	2.16	0.44
1:D:481:THR:OG1	1:D:483:HIS:HE1	2.00	0.44
1:D:608:GLU:HB2	3:D:966:HOH:O	2.16	0.44
1:B:160:VAL:CG2	1:B:161:GLY:H	2.25	0.44
1:B:254:VAL:HA	1:B:255:PRO:HD3	1.86	0.44
1:B:438:ASP:HA	3:B:1773:HOH:O	2.16	0.44
1:B:429:ARG:NE	3:B:2330:HOH:O	2.33	0.44
1:C:250:LYS:NZ	3:C:1194:HOH:O	2.50	0.44
1:D:277:SER:O	1:D:278:SER:CB	2.66	0.44
1:D:442:VAL:HG13	1:D:442:VAL:O	2.18	0.44
1:A:184:ARG:HD2	1:A:187:TRP:CD2	2.53	0.44
1:B:546:VAL:CG2	1:B:547:TYR:N	2.81	0.44
1:C:341:VAL:C	1:C:343:ARG:N	2.73	0.44
1:C:761:GLN:HE21	1:C:762:CYS:N	2.16	0.44
1:D:141:GLN:HG2	3:D:1016:HOH:O	2.18	0.44
1:D:435:GLN:OE1	1:D:437:SER:HB2	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:ASN:ND2	3:A:795:HOH:O	2.45	0.43
1:A:159:PRO:HD3	1:A:216:TRP:HB3	1.99	0.43
1:A:184:ARG:HD2	1:A:187:TRP:CE2	2.53	0.43
1:B:85:ASN:ND2	3:B:1802:HOH:O	2.50	0.43
1:B:392:LYS:HE3	1:B:393:ASP:OD2	2.17	0.43
1:B:633:GLY:HA3	1:B:655:PRO:HB3	2.00	0.43
1:C:358:ARG:HD2	3:C:895:HOH:O	2.17	0.43
1:A:325:MET:HE2	1:A:327:ILE:CG1	2.49	0.43
1:A:379:GLU:HG2	1:A:381:TYR:CD1	2.53	0.43
1:B:95:PHE:HB3	1:B:98:PHE:HB2	2.00	0.43
1:B:142:LEU:O	1:B:144:THR:HG23	2.18	0.43
1:B:195:TYR:O	1:B:227:GLN:HA	2.18	0.43
1:B:726:VAL:O	1:B:726:VAL:HG13	2.17	0.43
1:D:40:ARG:NH1	3:D:1222:HOH:O	2.51	0.43
1:D:127:SER:HB3	1:D:211:TYR:CD1	2.54	0.43
1:D:276:LEU:HD22	1:D:276:LEU:N	2.23	0.43
1:D:528:MET:HE3	1:D:574:ILE:CG2	2.41	0.43
1:A:76:ILE:HB	1:A:90:LEU:HD13	2.01	0.43
1:B:80:ASN:HB3	1:B:85:ASN:OD1	2.18	0.43
1:B:218:PRO:HB2	1:B:308:GLN:CD	2.43	0.43
1:C:103:ASN:OD1	1:C:117:GLU:HG2	2.19	0.43
1:C:358:ARG:HG2	1:C:358:ARG:HH11	1.83	0.43
1:C:668:GLU:HG2	1:C:673:LEU:HD12	1.99	0.43
1:D:316:LEU:HD21	1:D:320:GLN:HG2	2.00	0.43
1:D:595:ASN:C	1:D:597:ARG:N	2.76	0.43
1:B:90:LEU:C	1:B:90:LEU:HD22	2.43	0.43
1:B:397:ILE:HG13	1:B:398:THR:HG23	2.00	0.43
1:B:489:LYS:NZ	1:B:489:LYS:CB	2.81	0.43
1:B:542:LEU:C	1:B:542:LEU:HD23	2.43	0.43
1:C:63:ILE:HG21	1:C:69:LEU:HG	2.00	0.43
1:D:606:GLN:NE2	3:D:894:HOH:O	2.50	0.43
1:A:289:ALA:HA	1:A:294:LEU:HG	2.00	0.43
1:A:693:GLU:OE1	1:A:696:LYS:HE3	2.18	0.43
1:C:110:ASP:HB3	1:C:112:GLN:HB2	2.00	0.43
1:C:485:SER:O	1:C:486:VAL:C	2.61	0.43
1:C:530:LEU:HA	1:C:531:PRO:HD3	1.86	0.43
1:D:140:ARG:HG2	1:D:140:ARG:NH1	2.34	0.43
1:D:177:GLU:CB	1:D:180:LEU:HD13	2.48	0.43
1:D:273:THR:HA	1:D:276:LEU:HD13	2.00	0.43
1:D:486:VAL:HG13	3:D:1060:HOH:O	2.17	0.43
1:D:559:PHE:CZ	1:D:561:LEU:HD13	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:343:ARG:HA	1:A:389:ILE:O	2.18	0.43
1:B:113:PHE:CE2	1:B:178:PRO:HG2	2.53	0.43
1:B:224:ALA:HB1	1:B:268:PHE:CZ	2.53	0.43
1:C:314:GLN:NE2	1:C:373:LYS:NZ	2.65	0.43
1:D:246:LEU:HD22	1:D:248:TYR:O	2.18	0.43
1:D:519:LEU:O	1:D:520:ASN:C	2.62	0.43
1:A:236:ILE:CG2	1:A:254:VAL:HG13	2.48	0.43
1:B:172:ILE:H	1:B:186:THR:CG2	2.26	0.43
1:C:597:ARG:HG2	3:C:1236:HOH:O	2.17	0.43
1:A:291:ALA:C	1:A:293:MET:N	2.77	0.43
1:A:554:LYS:HA	3:A:1580:HOH:O	2.18	0.43
1:B:266:VAL:HG22	1:B:267:LYS:N	2.34	0.43
1:B:684:ARG:HG3	1:B:684:ARG:HH11	1.84	0.43
1:C:341:VAL:O	1:C:342:ALA:HB3	2.19	0.43
1:C:520:ASN:O	1:C:520:ASN:ND2	2.51	0.43
1:D:68:TYR:CD1	1:D:68:TYR:C	2.97	0.43
1:D:203:TYR:HA	1:D:207:VAL:CG1	2.47	0.43
1:D:374:ILE:CG2	1:D:382:ARG:HB3	2.49	0.43
1:D:546:VAL:CG2	1:D:547:TYR:N	2.81	0.43
1:A:704:HIS:CE1	1:A:711:VAL:O	2.71	0.43
1:B:159:PRO:HG2	1:B:217:SER:O	2.19	0.43
1:C:69:LEU:HD13	1:C:107:ILE:HD12	2.00	0.43
1:C:516:PHE:CD2	1:C:523:LYS:HB2	2.53	0.43
1:C:751:ILE:O	1:C:755:MET:HG3	2.19	0.43
1:A:612:GLN:HE21	1:A:612:GLN:HB3	1.54	0.43
1:C:50:LYS:NZ	3:C:1164:HOH:O	2.52	0.43
1:C:448:GLU:O	1:C:449:LEU:C	2.62	0.43
1:D:658:ARG:HD2	1:D:661:TYR:CE1	2.54	0.43
1:A:147:ARG:HA	3:A:1160:HOH:O	2.19	0.42
1:B:72:GLN:HB2	3:B:2029:HOH:O	2.19	0.42
1:B:214:LEU:HD12	1:B:214:LEU:C	2.44	0.42
1:C:125:ARG:HG2	1:C:126:HIS:NE2	2.34	0.42
1:C:388:GLN:HG3	3:C:1105:HOH:O	2.19	0.42
1:D:425:MET:HA	1:D:426:PRO:HD2	1.81	0.42
1:D:718:GLN:HA	1:D:718:GLN:NE2	2.33	0.42
1:A:71:LYS:HB3	3:A:1164:HOH:O	2.17	0.42
1:A:231:THR:HB	3:A:1546:HOH:O	2.18	0.42
1:B:170:ASN:N	1:B:170:ASN:HD22	2.16	0.42
1:B:336:ARG:HG2	1:B:336:ARG:NH1	2.33	0.42
1:C:600:THR:OG1	1:C:601:PHE:N	2.50	0.42
1:D:622:LYS:NZ	1:D:622:LYS:CB	2.83	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:LEU:O	1:A:90:LEU:HD13	2.19	0.42
1:A:224:ALA:HB1	1:A:268:PHE:CZ	2.55	0.42
1:A:236:ILE:O	1:A:253:ARG:HA	2.19	0.42
3:A:776:HOH:O	1:B:736:THR:HG23	2.19	0.42
1:B:301:CYS:O	1:B:302:ASP:HB2	2.19	0.42
1:C:636:THR:O	1:C:640:LEU:HG	2.19	0.42
1:C:671:MET:HE1	1:C:682:HIS:CD2	2.54	0.42
1:B:70:TYR:HD1	3:B:2373:HOH:O	1.97	0.42
1:C:272:ASN:HD21	1:C:274:ASP:HB2	1.83	0.42
1:C:704:HIS:HE1	1:C:711:VAL:O	2.02	0.42
1:D:183:TYR:CE1	1:D:277:SER:O	2.71	0.42
1:D:319:ILE:C	1:D:321:ASN:H	2.27	0.42
1:D:341:VAL:HG22	1:D:342:ALA:N	2.34	0.42
1:D:448:GLU:O	1:D:449:LEU:C	2.63	0.42
1:D:482:LEU:HD23	1:D:483:HIS:H	1.84	0.42
1:B:761:GLN:HE21	1:B:761:GLN:HB3	1.61	0.42
1:C:471:ARG:HG2	1:C:480:TYR:CD2	2.54	0.42
1:D:487:ASN:HB2	3:D:1060:HOH:O	2.19	0.42
1:A:72:GLN:C	1:A:74:ASN:N	2.76	0.42
1:A:140:ARG:NH1	1:A:140:ARG:CG	2.80	0.42
1:A:581:ARG:HE	1:A:605:ASP:CG	2.27	0.42
1:A:616:MET:HE2	1:A:618:PHE:CZ	2.55	0.42
1:B:154:TRP:CE2	1:B:212:SER:HB3	2.55	0.42
1:B:203:TYR:HA	1:B:207:VAL:CG1	2.49	0.42
1:B:536:LYS:HB3	1:B:536:LYS:HZ3	1.84	0.42
1:C:79:PHE:CD1	1:C:86:SER:HB3	2.54	0.42
1:C:110:ASP:HB3	1:C:112:GLN:H	1.84	0.42
1:C:118:TYR:O	1:C:130:ALA:HB1	2.19	0.42
1:C:382:ARG:HH11	1:C:382:ARG:HG2	1.84	0.42
1:D:684:ARG:HG3	3:D:1085:HOH:O	2.19	0.42
1:A:253:ARG:NE	3:A:1408:HOH:O	2.39	0.42
1:A:530:LEU:HA	1:A:531:PRO:HD3	1.86	0.42
1:B:74:ASN:HB2	3:B:2029:HOH:O	2.20	0.42
1:B:305:TRP:CE2	1:B:311:ILE:HD12	2.54	0.42
1:B:520:ASN:O	1:B:521:GLU:HB2	2.20	0.42
1:A:183:TYR:CE1	1:A:278:SER:HA	2.54	0.42
1:B:110:ASP:HB3	1:B:112:GLN:HB2	2.01	0.42
1:B:186:THR:HG21	1:B:196:ASN:CB	2.50	0.42
1:B:402:TRP:CD2	1:B:421:GLU:HB2	2.55	0.42
1:C:93:SER:HA	1:C:96:ASP:OD1	2.20	0.42
1:C:622:LYS:HB2	1:C:622:LYS:NZ	2.34	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:230:ASP:OD1	1:D:264:PRO:HB3	2.19	0.42
1:D:310:ARG:NH1	1:D:329:ASP:OD1	2.52	0.42
1:A:212:SER:HA	3:A:1054:HOH:O	2.20	0.42
1:C:598:LEU:HD22	1:C:631:TYR:OH	2.19	0.42
1:D:325:MET:CE	1:D:327:ILE:HD11	2.50	0.42
1:A:76:ILE:HD12	1:A:90:LEU:CD1	2.35	0.42
1:A:218:PRO:HB2	1:A:308:GLN:NE2	2.35	0.42
1:A:325:MET:O	1:A:344:GLN:HA	2.19	0.42
1:A:482:LEU:HD23	1:A:482:LEU:HA	1.84	0.42
1:B:236:ILE:CG2	1:B:254:VAL:HG13	2.49	0.42
1:B:410:LEU:CD1	1:B:415:LEU:HD23	2.43	0.42
1:B:649:CYS:HB3	1:B:699:GLU:HB2	2.01	0.42
1:C:276:LEU:H	1:C:276:LEU:HD22	1.84	0.42
1:C:319:ILE:C	1:C:321:ASN:H	2.24	0.42
1:C:334:SER:HB3	1:C:336:ARG:HD2	2.01	0.42
1:C:696:LYS:HG2	1:C:728:VAL:HG22	2.02	0.42
1:D:60:LEU:HB2	1:D:68:TYR:CD1	2.55	0.42
1:D:272:ASN:HD22	1:D:273:THR:N	2.18	0.42
1:D:341:VAL:C	1:D:343:ARG:H	2.27	0.42
1:D:405:ILE:HG13	1:D:429:ARG:CD	2.50	0.42
1:D:459:VAL:HG23	1:D:469:GLN:O	2.19	0.42
1:A:546:VAL:CG2	1:A:547:TYR:N	2.83	0.41
1:A:734:TRP:HE1	1:A:736:THR:HG22	1.85	0.41
1:B:90:LEU:HD22	1:B:90:LEU:O	2.20	0.41
1:B:455:GLN:HB2	1:B:475:PRO:HD3	2.02	0.41
1:C:484:SER:O	1:C:488:ASP:HA	2.20	0.41
1:D:658:ARG:HG2	1:D:661:TYR:CE2	2.55	0.41
1:C:192:ASP:O	1:C:193:ILE:HD13	2.20	0.41
1:C:489:LYS:HB3	1:C:489:LYS:HZ3	1.86	0.41
1:C:693:GLU:HB3	3:C:1054:HOH:O	2.20	0.41
1:D:415:LEU:HB2	1:D:436:LEU:HD11	2.01	0.41
1:D:615:LYS:CB	3:D:1373:HOH:O	2.59	0.41
1:A:302:ASP:HB3	1:A:314:GLN:HB2	2.01	0.41
1:A:452:GLU:HB2	3:A:1399:HOH:O	2.20	0.41
1:A:718:GLN:HE21	1:A:718:GLN:HA	1.86	0.41
1:B:119:ASN:HD22	1:B:131:SER:CB	2.32	0.41
1:B:216:TRP:HB2	3:B:2115:HOH:O	2.20	0.41
1:B:720:SER:O	1:B:724:VAL:HG23	2.20	0.41
1:C:596:ARG:HA	1:C:670:TYR:O	2.20	0.41
1:D:327:ILE:HB	1:D:343:ARG:HG2	2.02	0.41
1:D:397:ILE:HG13	1:D:398:THR:HG23	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:448:GLU:HG3	3:B:1827:HOH:O	2.20	0.41
1:B:461:PHE:CD2	1:B:468:TYR:HB3	2.55	0.41
1:C:184:ARG:HD2	1:C:187:TRP:CE2	2.55	0.41
1:D:110:ASP:OD2	1:D:112:GLN:NE2	2.53	0.41
1:D:459:VAL:CG2	1:D:460:SER:N	2.81	0.41
1:D:579:ASP:HB3	1:D:583:SER:OG	2.21	0.41
1:A:277:SER:HB2	1:A:278:SER:H	1.64	0.41
1:A:341:VAL:O	1:A:342:ALA:HB2	2.16	0.41
1:A:520:ASN:O	1:A:521:GLU:HB2	2.20	0.41
1:A:581:ARG:NE	1:A:605:ASP:OD2	2.46	0.41
3:A:776:HOH:O	1:B:736:THR:CG2	2.67	0.41
1:B:64:SER:O	1:B:463:LYS:HG2	2.20	0.41
1:B:65:ASP:HA	1:B:462:SER:HB2	2.02	0.41
1:C:626:ILE:HG23	1:C:636:THR:HG23	2.03	0.41
1:A:134:ILE:HG21	1:A:178:PRO:HB3	2.02	0.41
1:A:150:ASN:O	1:A:151:ASN:HB2	2.20	0.41
1:A:674:PRO:O	1:A:680:LEU:HD13	2.20	0.41
1:B:54:ARG:HG2	3:B:2202:HOH:O	2.20	0.41
1:B:160:VAL:CG2	1:B:161:GLY:N	2.79	0.41
1:B:438:ASP:CG	1:B:440:THR:HG22	2.45	0.41
1:B:536:LYS:NZ	1:B:536:LYS:CB	2.83	0.41
1:B:704:HIS:CD2	1:B:716:SER:OG	2.71	0.41
1:C:176:ILE:HD13	1:C:183:TYR:CE2	2.56	0.41
1:C:734:TRP:CD1	1:C:734:TRP:C	2.99	0.41
1:D:40:ARG:HH11	1:D:40:ARG:CG	2.33	0.41
1:D:236:ILE:HG12	1:D:712:HIS:CE1	2.56	0.41
1:D:554:LYS:HG2	3:D:1434:HOH:O	2.20	0.41
1:A:204:GLU:O	1:A:209:SER:HA	2.21	0.41
1:B:109:PRO:HG2	1:B:161:GLY:O	2.21	0.41
1:C:160:VAL:HG23	1:C:161:GLY:N	2.36	0.41
1:C:289:ALA:HA	1:C:294:LEU:HD11	2.03	0.41
1:C:322:TYR:OH	1:C:346:ILE:HD13	2.21	0.41
1:B:152:THR:HG23	1:B:167:VAL:O	2.20	0.41
1:B:159:PRO:HG3	3:B:2115:HOH:O	2.21	0.41
1:B:464:GLU:O	1:B:465:ALA:HB3	2.21	0.41
1:C:123:GLN:HG2	1:C:124:TRP:N	2.35	0.41
1:D:154:TRP:CE2	1:D:212:SER:HB2	2.55	0.41
1:A:114:ILE:HG13	1:A:137:LEU:HD11	2.02	0.41
1:A:159:PRO:HD3	1:A:216:TRP:CB	2.50	0.41
1:A:312:SER:HB2	1:A:325:MET:HE3	2.01	0.41
1:B:40:ARG:HB2	1:B:506:ASN:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:377:ASN:ND2	1:B:383:HIS:CD2	2.89	0.41
1:B:526:TYR:HB3	1:B:578:PHE:HD1	1.86	0.41
1:C:235:LEU:HD13	3:C:1211:HOH:O	2.21	0.41
1:C:377:ASN:HB2	1:C:381:TYR:N	2.35	0.41
1:D:65:ASP:CG	1:D:466:LYS:HB2	2.46	0.41
1:D:436:LEU:HG	3:D:1418:HOH:O	2.20	0.41
1:D:455:GLN:HG3	1:D:475:PRO:HD2	2.03	0.41
1:A:79:PHE:CD1	1:A:86:SER:HB3	2.56	0.41
1:A:91:GLU:HG2	3:A:1505:HOH:O	2.21	0.41
1:A:93:SER:O	1:A:94:THR:C	2.63	0.41
1:A:392:LYS:HG2	3:A:1573:HOH:O	2.21	0.41
1:B:411:THR:HB	3:B:2372:HOH:O	2.20	0.41
1:C:616:MET:HE1	3:C:1361:HOH:O	2.21	0.41
1:C:658:ARG:O	1:C:658:ARG:HG3	2.19	0.41
1:D:65:ASP:HA	1:D:462:SER:HB2	2.02	0.41
1:A:613:PHE:C	1:A:615:LYS:N	2.78	0.40
1:B:148:ILE:HA	1:B:149:PRO:HD3	1.95	0.40
1:C:425:MET:HA	1:C:426:PRO:HD2	1.83	0.40
1:C:633:GLY:HA3	1:C:655:PRO:HB3	2.04	0.40
1:D:316:LEU:CD2	1:D:320:GLN:HG2	2.51	0.40
1:D:603:VAL:HG23	1:D:639:VAL:HG22	2.01	0.40
1:D:734:TRP:CD1	1:D:734:TRP:C	2.98	0.40
1:A:293:MET:HG2	1:A:315:TRP:HB3	2.04	0.40
1:C:170:ASN:O	1:C:196:ASN:HB2	2.22	0.40
1:C:176:ILE:HD13	1:C:183:TYR:HE2	1.86	0.40
1:C:514:LEU:HD23	1:C:514:LEU:HA	1.90	0.40
1:B:242:SER:HB3	1:B:246:LEU:HD12	2.02	0.40
1:B:306:ALA:HB3	1:B:310:ARG:HB3	2.03	0.40
1:B:743:ALA:O	1:B:744:SER:C	2.62	0.40
1:C:544:LEU:HD23	1:C:626:ILE:HD12	2.04	0.40
1:D:40:ARG:H	1:D:40:ARG:HD2	1.85	0.40
1:D:438:ASP:OD2	1:D:440:THR:HG22	2.22	0.40
1:D:483:HIS:HD2	3:D:1040:HOH:O	2.04	0.40
1:D:684:ARG:HA	1:D:684:ARG:HD3	1.90	0.40
1:D:718:GLN:HE21	1:D:718:GLN:CA	2.31	0.40
1:B:109:PRO:HG2	1:B:160:VAL:O	2.21	0.40
1:B:156:THR:HG21	1:B:214:LEU:HD11	2.03	0.40
1:B:331:ASP:HB3	1:B:334:SER:HB2	2.02	0.40
1:B:739:ASP:HB2	3:B:1667:HOH:O	2.22	0.40
1:C:175:LYS:NZ	3:C:1423:HOH:O	2.54	0.40
1:B:162:HIS:HD2	1:B:178:PRO:HD3	1.86	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:358:ARG:HG2	1:C:358:ARG:NH1	2.35	0.40
1:D:65:ASP:CG	1:D:464:GLU:HB2	2.47	0.40
1:D:159:PRO:HD3	1:D:216:TRP:CB	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	724/726 (100%)	666 (92%)	50 (7%)	8 (1%)	11	18
1	B	724/726 (100%)	662 (91%)	54 (8%)	8 (1%)	11	18
1	C	724/726 (100%)	665 (92%)	50 (7%)	9 (1%)	10	16
1	D	724/726 (100%)	657 (91%)	57 (8%)	10 (1%)	9	13
All	All	2896/2904 (100%)	2650 (92%)	211 (7%)	35 (1%)	10	16

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	278	SER
1	A	289	ALA
1	B	277	SER
1	B	278	SER
1	C	40	ARG
1	C	278	SER
1	D	278	SER
1	D	320	GLN
1	A	282	ALA
1	A	342	ALA
1	B	40	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	161	GLY
1	B	289	ALA
1	B	320	GLN
1	C	289	ALA
1	C	320	GLN
1	C	520	ASN
1	D	289	ALA
1	D	334	SER
1	D	486	VAL
1	D	520	ASN
1	D	521	GLU
1	B	334	SER
1	B	520	ASN
1	C	138	ASN
1	C	332	GLU
1	C	536	LYS
1	D	91	GLU
1	D	161	GLY
1	A	277	SER
1	A	320	GLN
1	A	520	ASN
1	D	389	ILE
1	C	486	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	651/651 (100%)	605 (93%)	46 (7%)	13	23
1	B	651/651 (100%)	607 (93%)	44 (7%)	14	25
1	C	651/651 (100%)	608 (93%)	43 (7%)	15	26
1	D	651/651 (100%)	612 (94%)	39 (6%)	17	31
All	All	2604/2604 (100%)	2432 (93%)	172 (7%)	15	26

All (172) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	66	HIS
1	A	90	LEU
1	A	92	ASN
1	A	140	ARG
1	A	141	GLN
1	A	145	GLU
1	A	170	ASN
1	A	184	ARG
1	A	207	VAL
1	A	246	LEU
1	A	253	ARG
1	A	254	VAL
1	A	276	LEU
1	A	277	SER
1	A	303	VAL
1	A	336	ARG
1	A	341	VAL
1	A	385	CYS
1	A	388	GLN
1	A	391	LYS
1	A	435	GLN
1	A	436	LEU
1	A	440	THR
1	A	442	VAL
1	A	448	GLU
1	A	482	LEU
1	A	487	ASN
1	A	514	LEU
1	A	520	ASN
1	A	523	LYS
1	A	536	LYS
1	A	543	LEU
1	A	561	LEU
1	A	583	SER
1	A	603	VAL
1	A	608	GLU
1	A	612	GLN
1	A	622	LYS
1	A	673	LEU
1	A	685	ASN
1	A	689	MET
1	A	701	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	702	LEU
1	A	736	THR
1	A	761	GLN
1	B	40	ARG
1	B	90	LEU
1	B	105	TYR
1	B	110	ASP
1	B	140	ARG
1	B	141	GLN
1	B	142	LEU
1	B	145	GLU
1	B	170	ASN
1	B	207	VAL
1	B	246	LEU
1	B	253	ARG
1	B	254	VAL
1	B	272	ASN
1	B	276	LEU
1	B	280	THR
1	B	293	MET
1	B	303	VAL
1	B	313	LEU
1	B	326	ASP
1	B	332	GLU
1	B	336	ARG
1	B	373	LYS
1	B	385	CYS
1	B	436	LEU
1	B	440	THR
1	B	442	VAL
1	B	448	GLU
1	B	482	LEU
1	B	507	VAL
1	B	514	LEU
1	B	518	ILE
1	B	536	LYS
1	B	543	LEU
1	B	561	LEU
1	B	603	VAL
1	B	658	ARG
1	B	673	LEU
1	B	689	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	701	LEU
1	B	702	LEU
1	B	726	VAL
1	B	736	THR
1	B	761	GLN
1	C	40	ARG
1	C	90	LEU
1	C	145	GLU
1	C	170	ASN
1	C	176	ILE
1	C	184	ARG
1	C	207	VAL
1	C	246	LEU
1	C	253	ARG
1	C	254	VAL
1	C	276	LEU
1	C	293	MET
1	C	303	VAL
1	C	326	ASP
1	C	336	ARG
1	C	376	SER
1	C	385	CYS
1	C	388	GLN
1	C	390	ASP
1	C	436	LEU
1	C	440	THR
1	C	448	GLU
1	C	472	CYS
1	C	482	LEU
1	C	507	VAL
1	C	514	LEU
1	C	523	LYS
1	C	536	LYS
1	C	538	LYS
1	C	543	LEU
1	C	561	LEU
1	C	589	LYS
1	C	603	VAL
1	C	655	PRO
1	C	663	ASP
1	C	679	ASN
1	C	689	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	701	LEU
1	C	702	LEU
1	C	726	VAL
1	C	736	THR
1	C	760	LYS
1	C	761	GLN
1	D	40	ARG
1	D	41	LYS
1	D	54	ARG
1	D	75	ASN
1	D	90	LEU
1	D	91	GLU
1	D	103	ASN
1	D	145	GLU
1	D	207	VAL
1	D	246	LEU
1	D	253	ARG
1	D	254	VAL
1	D	276	LEU
1	D	293	MET
1	D	303	VAL
1	D	326	ASP
1	D	336	ARG
1	D	373	LYS
1	D	385	CYS
1	D	388	GLN
1	D	415	LEU
1	D	440	THR
1	D	448	GLU
1	D	482	LEU
1	D	505	GLN
1	D	514	LEU
1	D	523	LYS
1	D	536	LYS
1	D	561	LEU
1	D	597	ARG
1	D	603	VAL
1	D	622	LYS
1	D	679	ASN
1	D	689	MET
1	D	701	LEU
1	D	702	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	726	VAL
1	D	736	THR
1	D	761	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (100) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	72	GLN
1	A	92	ASN
1	A	141	GLN
1	A	170	ASN
1	A	247	GLN
1	A	272	ASN
1	A	286	GLN
1	A	314	GLN
1	A	344	GLN
1	A	369	ASN
1	A	435	GLN
1	A	455	GLN
1	A	483	HIS
1	A	533	HIS
1	A	612	GLN
1	A	679	ASN
1	A	694	ASN
1	A	704	HIS
1	A	718	GLN
1	A	731	GLN
1	A	761	GLN
1	B	51	ASN
1	B	72	GLN
1	B	75	ASN
1	B	92	ASN
1	B	119	ASN
1	B	150	ASN
1	B	169	ASN
1	B	170	ASN
1	B	247	GLN
1	B	272	ASN
1	B	314	GLN
1	B	369	ASN
1	B	377	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	430	ASN
1	B	435	GLN
1	B	483	HIS
1	B	487	ASN
1	B	533	HIS
1	B	572	ASN
1	B	612	GLN
1	B	679	ASN
1	B	694	ASN
1	B	704	HIS
1	B	718	GLN
1	B	731	GLN
1	B	749	GLN
1	B	761	GLN
1	C	51	ASN
1	C	72	GLN
1	C	169	ASN
1	C	170	ASN
1	C	247	GLN
1	C	263	ASN
1	C	272	ASN
1	C	286	GLN
1	C	314	GLN
1	C	377	ASN
1	C	383	HIS
1	C	435	GLN
1	C	455	GLN
1	C	483	HIS
1	C	487	ASN
1	C	505	GLN
1	C	520	ASN
1	C	533	HIS
1	C	572	ASN
1	C	595	ASN
1	C	612	GLN
1	C	679	ASN
1	C	685	ASN
1	C	694	ASN
1	C	704	HIS
1	C	718	GLN
1	C	731	GLN
1	C	761	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	72	GLN
1	D	112	GLN
1	D	169	ASN
1	D	170	ASN
1	D	247	GLN
1	D	263	ASN
1	D	272	ASN
1	D	314	GLN
1	D	344	GLN
1	D	369	ASN
1	D	430	ASN
1	D	483	HIS
1	D	487	ASN
1	D	505	GLN
1	D	520	ASN
1	D	612	GLN
1	D	679	ASN
1	D	685	ASN
1	D	694	ASN
1	D	704	HIS
1	D	718	GLN
1	D	731	GLN
1	D	761	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	AXD	B	1630	1	30,31,31	1.66	9 (30%)	33,44,44	1.52	5 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AXD	B	1630	1	-	3/20/47/47	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1630	AXD	C4-N5	3.21	1.52	1.46
2	B	1630	AXD	C13-C10	2.94	1.56	1.53
2	B	1630	AXD	C13-N14	-2.81	1.34	1.48
2	B	1630	AXD	C7-C2	2.72	1.57	1.53
2	B	1630	AXD	C21-C20	2.64	1.43	1.39
2	B	1630	AXD	C18-N23	2.42	1.39	1.34
2	B	1630	AXD	C26-C2	2.23	1.57	1.53
2	B	1630	AXD	C15-N9	2.07	1.38	1.36
2	B	1630	AXD	C6-N5	2.06	1.50	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1630	AXD	C20-C19-C18	4.84	120.55	117.11
2	B	1630	AXD	C4-C3-C2	-2.53	110.57	113.15
2	B	1630	AXD	C26-C2-N1	-2.51	108.87	113.91
2	B	1630	AXD	C6-N5-C4	2.29	116.73	111.57
2	B	1630	AXD	C22-N23-C18	2.27	120.10	116.81

There are no chirality outliers.

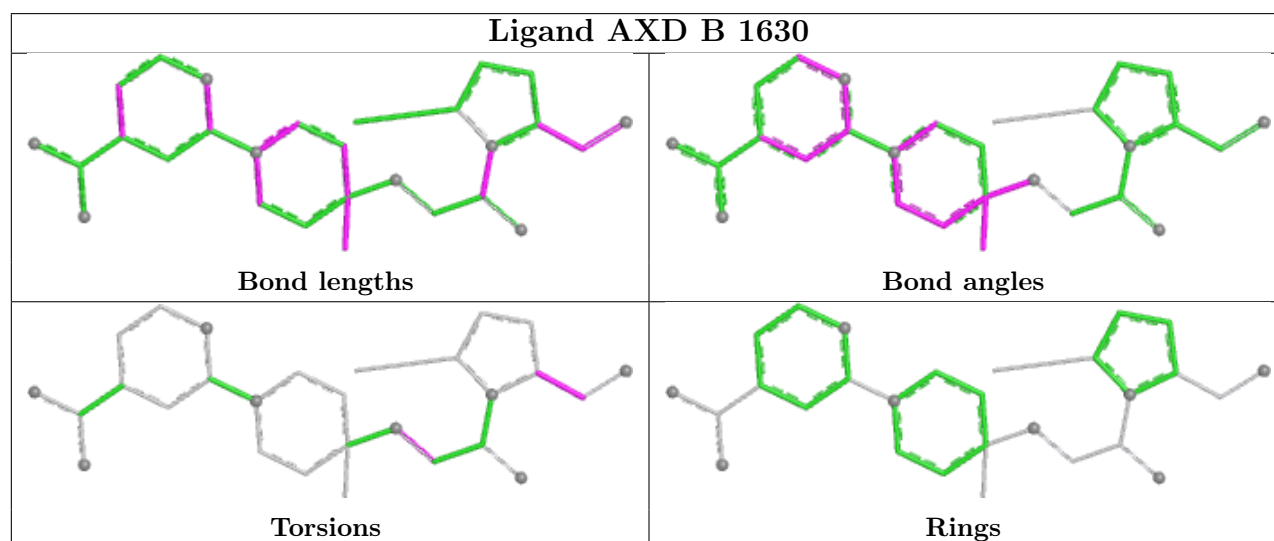
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1630	AXD	N9-C10-C13-N14
2	B	1630	AXD	C11-C10-C13-N14
2	B	1630	AXD	C15-C17-N1-C2

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	726/726 (100%)	-0.46	8 (1%) 78 74	22, 41, 81, 170	0
1	B	726/726 (100%)	-0.45	4 (0%) 85 83	23, 43, 89, 134	0
1	C	726/726 (100%)	-0.35	2 (0%) 90 88	27, 49, 93, 169	0
1	D	726/726 (100%)	-0.34	3 (0%) 88 86	26, 48, 94, 144	0
All	All	2904/2904 (100%)	-0.40	17 (0%) 85 83	22, 45, 90, 170	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	280	THR	4.8
1	A	279	VAL	3.9
1	A	281	ASN	3.6
1	B	71	LYS	3.3
1	D	289	ALA	2.8
1	D	71	LYS	2.7
1	B	105	TYR	2.6
1	A	114	ILE	2.5
1	B	39	SER	2.5
1	C	289	ALA	2.5
1	A	71	LYS	2.4
1	A	74	ASN	2.3
1	A	282	ALA	2.3
1	B	72	GLN	2.3
1	C	71	LYS	2.2
1	D	279	VAL	2.1
1	A	289	ALA	2.1

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

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

6.3 Carbohydrates [i](#)

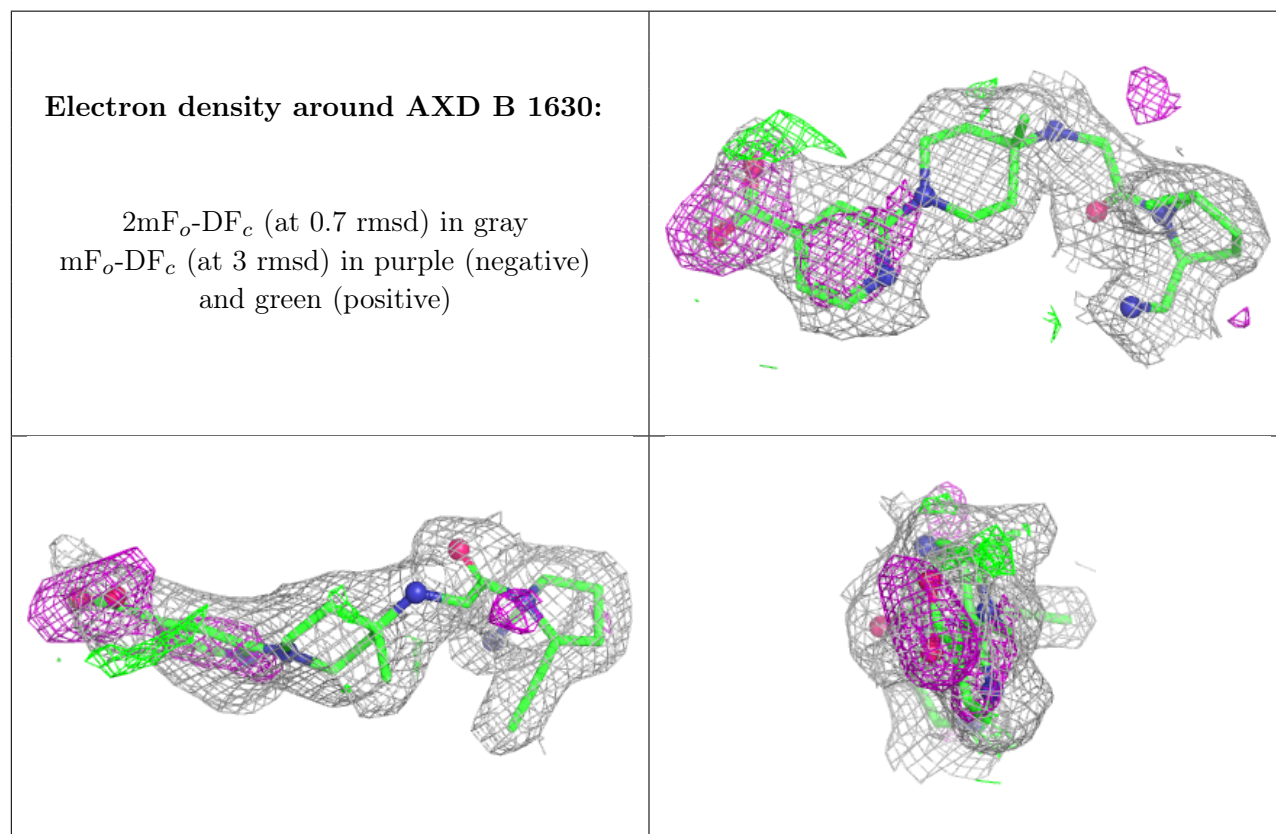
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
2	AXD	B	1630	29/29	0.84	0.11	31,31,31,31	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.