



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:48 PM BST

PDB ID : 3IZH
EMDB ID: : EMD-5244
Title : Mm-cpn D386A with ATP
Authors : Douglas, N.R.; Reissmann, S.; Zhang, J.; Chen, B.; Jakana, J.; Kumar, R.;
Chiu, W.; Frydman, J.
Deposited on : 2010-10-29
Resolution : 11.00 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

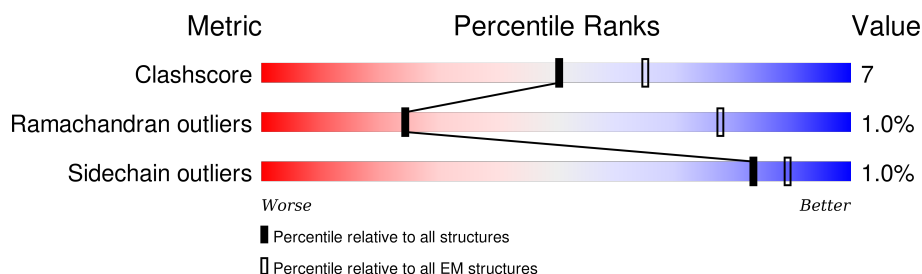
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 11.00 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	513	87% 12% .
1	B	513	88% 11% .
1	C	513	88% 11% .
1	D	513	88% 11% .
1	E	513	88% 11% .
1	F	513	88% 11% .
1	G	513	88% 11% .
1	H	513	88% 11% .
1	I	513	88% 11% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	J	513	<div><div></div><div>88%</div><div>11%</div><div></div></div>
1	K	513	<div><div></div><div>87%</div><div>12%</div><div></div></div>
1	L	513	<div><div></div><div>88%</div><div>11%</div><div></div></div>
1	M	513	<div><div></div><div>88%</div><div>11%</div><div></div></div>
1	N	513	<div><div></div><div>88%</div><div>11%</div><div></div></div>
1	O	513	<div><div></div><div>88%</div><div>10%</div><div></div></div>
1	P	513	<div><div></div><div>88%</div><div>11%</div><div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 61632 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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.

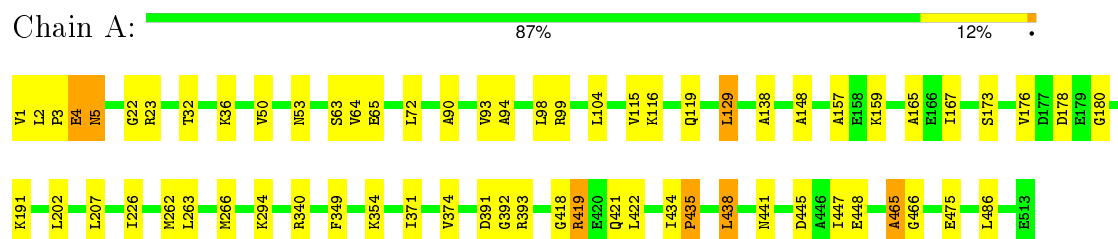
- Molecule 1 is a protein called Chaperonin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	B	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	C	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	D	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	E	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	F	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	G	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	H	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	I	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	J	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	K	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	L	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	M	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	N	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	O	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	P	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		

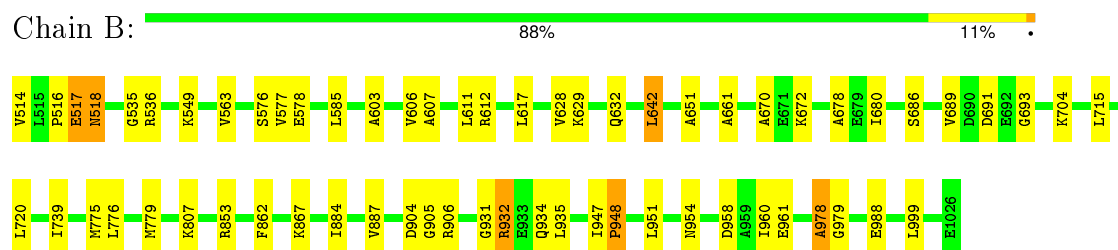
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

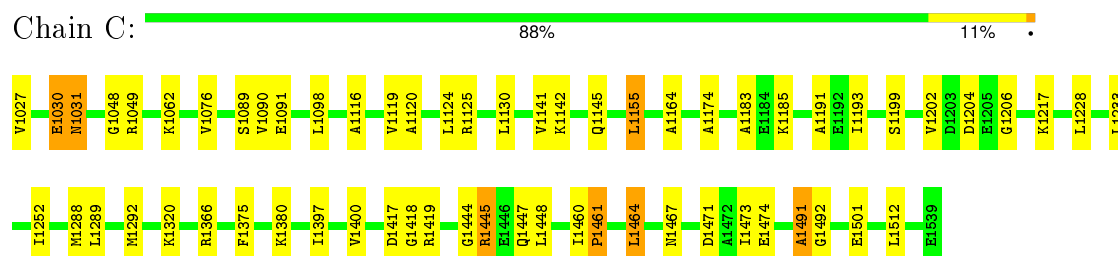
- Molecule 1: Chaperonin



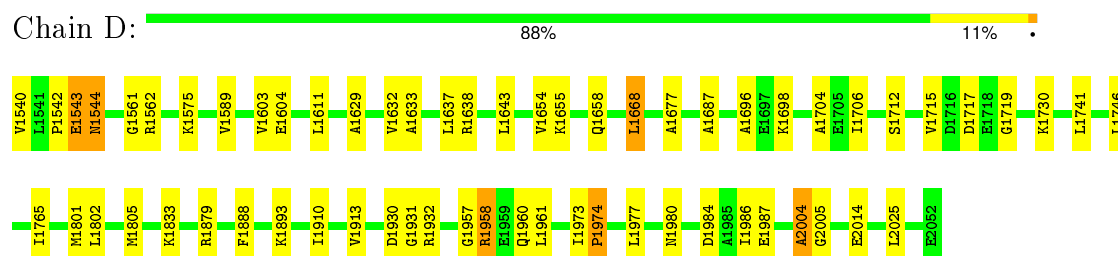
- Molecule 1: Chaperonin



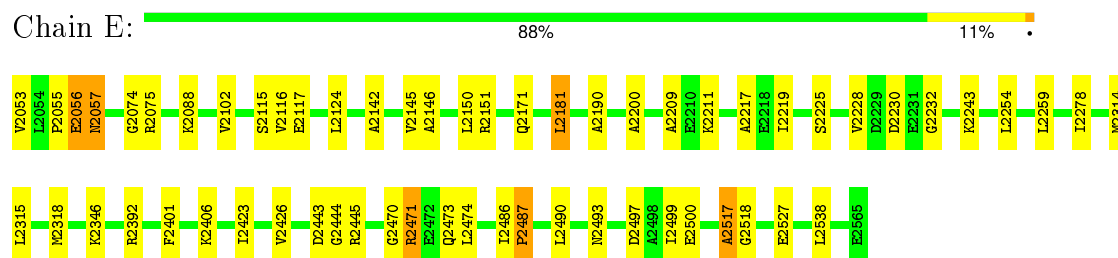
- Molecule 1: Chaperonin



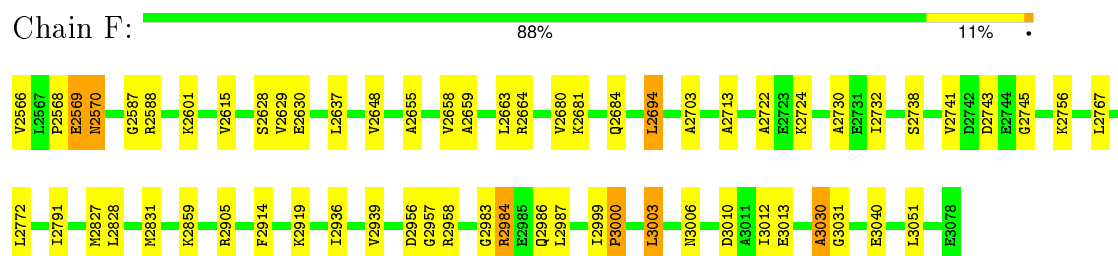
- Molecule 1: Chaperonin



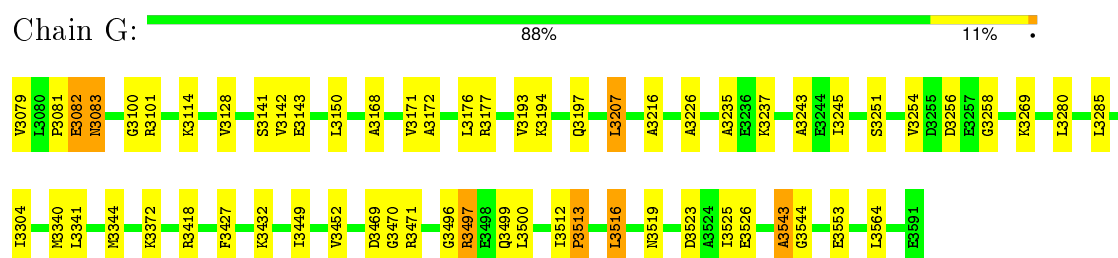
- Molecule 1: Chaperonin



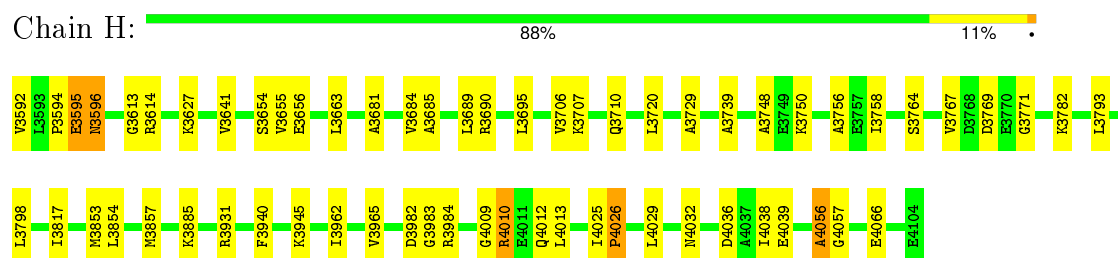
- Molecule 1: Chaperonin



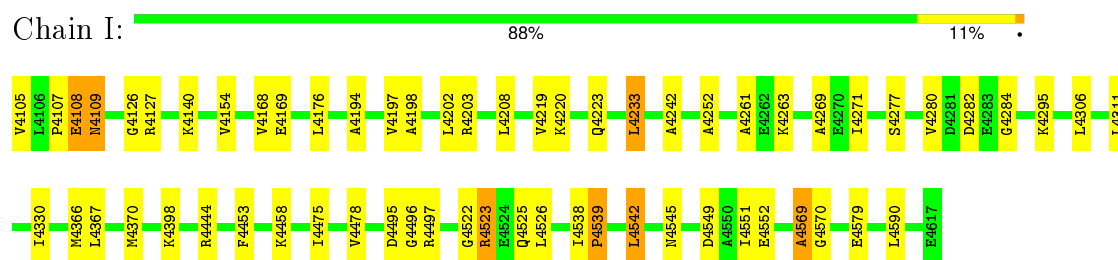
- Molecule 1: Chaperonin



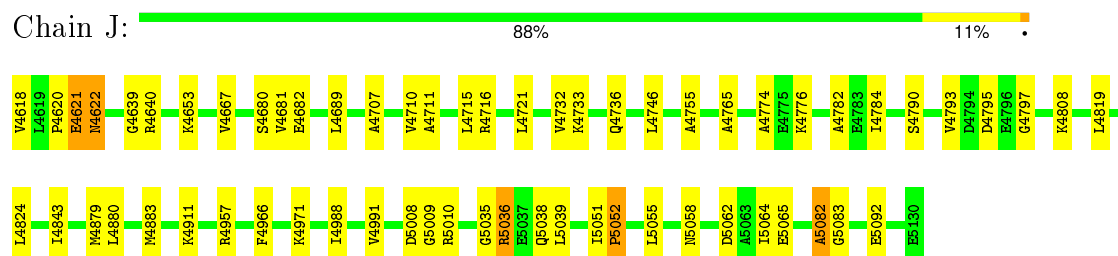
- Molecule 1: Chaperonin



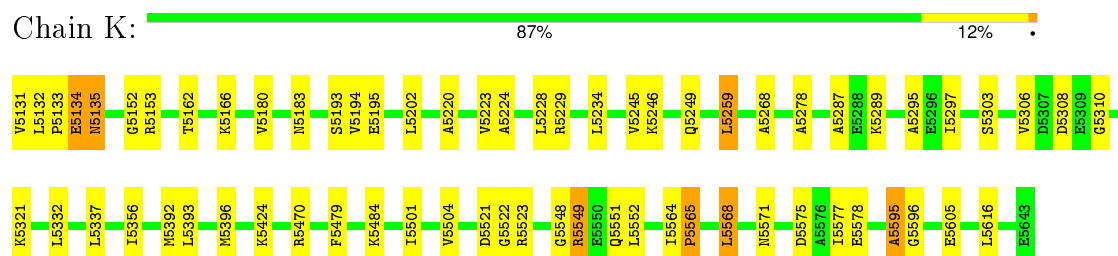
- Molecule 1: Chaperonin



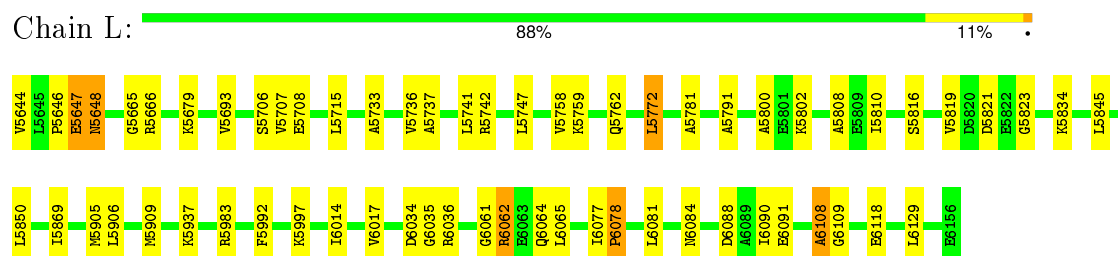
- Molecule 1: Chaperonin



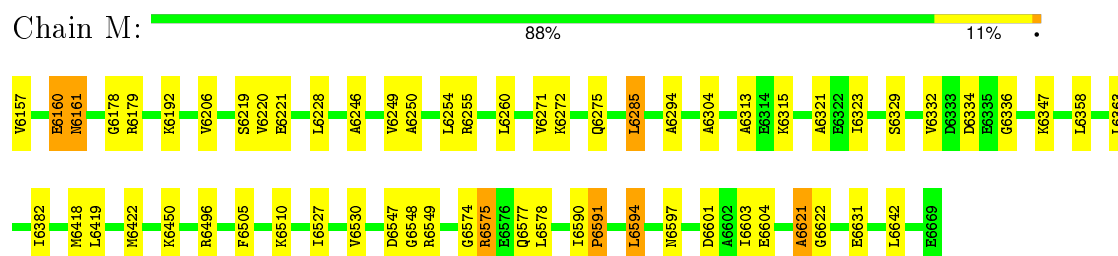
- Molecule 1: Chaperonin



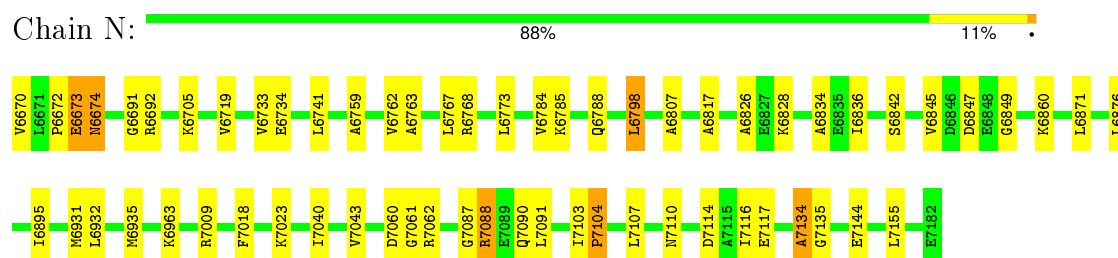
- Molecule 1: Chaperonin




- Molecule 1: Chaperonin

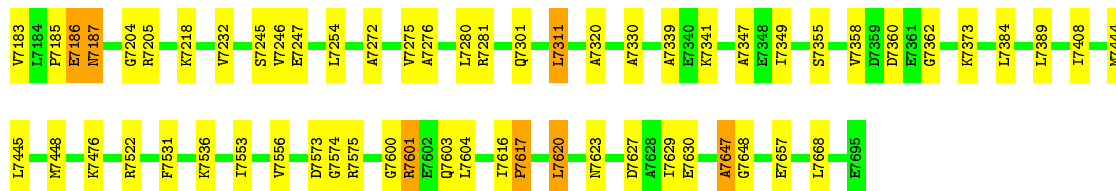


- Molecule 1: Chaperonin




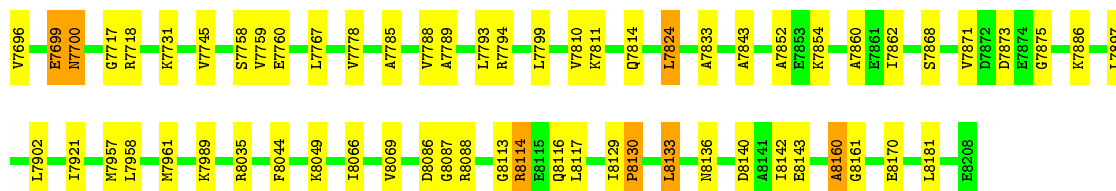
- Molecule 1: Chaperonin

Chain O:  88% 10% .



- Molecule 1: Chaperonin

Chain P:  88% 11% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D	Depositor
Number of images	Not provided	Depositor
Resolution determination method	FSC at 0.5 cut-off	Depositor
CTF correction method	Not provided	Depositor
Microscope	JEOL 2010F	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Gatan 4Kx4K CCD camera	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 2$	RMSZ	# $ Z > 2$
1	A	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	B	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	C	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	D	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	E	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	F	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	G	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	H	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	I	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	J	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	K	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	L	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	M	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	N	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	O	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
1	P	0.89	3/3875 (0.1%)	0.76	1/5214 (0.0%)
All	All	0.89	48/62000 (0.1%)	0.76	16/83424 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
1	C	0	3
1	D	0	3
1	E	0	3
1	F	0	3
1	G	0	3
1	H	0	3
1	I	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
1	J	0	3
1	K	0	3
1	L	0	3
1	M	0	3
1	N	0	3
1	O	0	3
1	P	0	3
All	All	0	48

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	4621	GLU	C-O	-5.72	1.12	1.23
1	L	5647	GLU	C-O	-5.72	1.12	1.23
1	N	6673	GLU	C-O	-5.72	1.12	1.23
1	P	7699	GLU	C-O	-5.72	1.12	1.23
1	K	5134	GLU	C-O	-5.71	1.12	1.23
1	M	6160	GLU	C-O	-5.71	1.12	1.23
1	I	4108	GLU	C-O	-5.69	1.12	1.23
1	O	7186	GLU	C-O	-5.69	1.12	1.23
1	A	4	GLU	C-O	-5.67	1.12	1.23
1	B	517	GLU	C-O	-5.67	1.12	1.23
1	C	1030	GLU	C-O	-5.67	1.12	1.23
1	D	1543	GLU	C-O	-5.67	1.12	1.23
1	E	2056	GLU	C-O	-5.67	1.12	1.23
1	F	2569	GLU	C-O	-5.67	1.12	1.23
1	G	3082	GLU	C-O	-5.67	1.12	1.23
1	H	3595	GLU	C-O	-5.67	1.12	1.23
1	M	6160	GLU	C-N	5.44	1.46	1.34
1	A	4	GLU	C-N	5.44	1.46	1.34
1	C	1030	GLU	C-N	5.44	1.46	1.34
1	E	2056	GLU	C-N	5.44	1.46	1.34
1	G	3082	GLU	C-N	5.44	1.46	1.34
1	K	5134	GLU	C-N	5.44	1.46	1.34
1	B	517	GLU	C-N	5.41	1.46	1.34
1	D	1543	GLU	C-N	5.41	1.46	1.34
1	F	2569	GLU	C-N	5.41	1.46	1.34
1	H	3595	GLU	C-N	5.41	1.46	1.34
1	J	4621	GLU	C-N	5.41	1.46	1.34
1	L	5647	GLU	C-N	5.41	1.46	1.34
1	O	7186	GLU	C-N	5.40	1.46	1.34
1	I	4108	GLU	C-N	5.40	1.46	1.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	6673	GLU	C-N	5.38	1.46	1.34
1	P	7699	GLU	C-N	5.38	1.46	1.34
1	B	948	PRO	N-CD	5.28	1.55	1.47
1	D	1974	PRO	N-CD	5.28	1.55	1.47
1	F	3000	PRO	N-CD	5.28	1.55	1.47
1	H	4026	PRO	N-CD	5.28	1.55	1.47
1	J	5052	PRO	N-CD	5.28	1.55	1.47
1	L	6078	PRO	N-CD	5.28	1.55	1.47
1	M	6591	PRO	N-CD	5.28	1.55	1.47
1	O	7617	PRO	N-CD	5.28	1.55	1.47
1	N	7104	PRO	N-CD	5.24	1.55	1.47
1	P	8130	PRO	N-CD	5.24	1.55	1.47
1	A	435	PRO	N-CD	5.21	1.55	1.47
1	C	1461	PRO	N-CD	5.21	1.55	1.47
1	E	2487	PRO	N-CD	5.21	1.55	1.47
1	G	3513	PRO	N-CD	5.21	1.55	1.47
1	I	4539	PRO	N-CD	5.21	1.55	1.47
1	K	5565	PRO	N-CD	5.21	1.55	1.47

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	7134	ALA	CB-CA-C	5.10	117.76	110.10
1	P	8160	ALA	CB-CA-C	5.10	117.76	110.10
1	I	4569	ALA	CB-CA-C	5.09	117.74	110.10
1	K	5595	ALA	CB-CA-C	5.09	117.74	110.10
1	M	6621	ALA	CB-CA-C	5.09	117.74	110.10
1	O	7647	ALA	CB-CA-C	5.09	117.74	110.10
1	B	978	ALA	CB-CA-C	5.09	117.73	110.10
1	D	2004	ALA	CB-CA-C	5.09	117.73	110.10
1	F	3030	ALA	CB-CA-C	5.09	117.73	110.10
1	H	4056	ALA	CB-CA-C	5.09	117.73	110.10
1	A	465	ALA	CB-CA-C	5.08	117.73	110.10
1	C	1491	ALA	CB-CA-C	5.08	117.73	110.10
1	E	2517	ALA	CB-CA-C	5.08	117.73	110.10
1	G	3543	ALA	CB-CA-C	5.08	117.73	110.10
1	J	5082	ALA	CB-CA-C	5.07	117.70	110.10
1	L	6108	ALA	CB-CA-C	5.07	117.70	110.10

There are no chirality outliers.

All (48) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119	GLN	Mainchain
1	A	138	ALA	Mainchain
1	A	475	GLU	Mainchain
1	B	632	GLN	Mainchain
1	B	651	ALA	Mainchain
1	B	988	GLU	Mainchain
1	C	1145	GLN	Mainchain
1	C	1164	ALA	Mainchain
1	C	1501	GLU	Mainchain
1	D	1658	GLN	Mainchain
1	D	1677	ALA	Mainchain
1	D	2014	GLU	Mainchain
1	E	2171	GLN	Mainchain
1	E	2190	ALA	Mainchain
1	E	2527	GLU	Mainchain
1	F	2684	GLN	Mainchain
1	F	2703	ALA	Mainchain
1	F	3040	GLU	Mainchain
1	G	3197	GLN	Mainchain
1	G	3216	ALA	Mainchain
1	G	3553	GLU	Mainchain
1	H	3710	GLN	Mainchain
1	H	3729	ALA	Mainchain
1	H	4066	GLU	Mainchain
1	I	4223	GLN	Mainchain
1	I	4242	ALA	Mainchain
1	I	4579	GLU	Mainchain
1	J	4736	GLN	Mainchain
1	J	4755	ALA	Mainchain
1	J	5092	GLU	Mainchain
1	K	5249	GLN	Mainchain
1	K	5268	ALA	Mainchain
1	K	5605	GLU	Mainchain
1	L	5762	GLN	Mainchain
1	L	5781	ALA	Mainchain
1	L	6118	GLU	Mainchain
1	M	6275	GLN	Mainchain
1	M	6294	ALA	Mainchain
1	M	6631	GLU	Mainchain
1	N	6788	GLN	Mainchain
1	N	6807	ALA	Mainchain
1	N	7144	GLU	Mainchain
1	O	7301	GLN	Mainchain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	O	7320	ALA	Mainchain
1	O	7657	GLU	Mainchain
1	P	7814	GLN	Mainchain
1	P	7833	ALA	Mainchain
1	P	8170	GLU	Mainchain

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	3852	0	3996	88	0
1	B	3852	0	3993	85	0
1	C	3852	0	3993	83	0
1	D	3852	0	3993	83	0
1	E	3852	0	3993	81	0
1	F	3852	0	3993	86	0
1	G	3852	0	3993	85	0
1	H	3852	0	3993	85	0
1	I	3852	0	3993	85	0
1	J	3852	0	3993	85	0
1	K	3852	0	3993	87	0
1	L	3852	0	3993	83	0
1	M	3852	0	3993	83	0
1	N	3852	0	3993	83	0
1	O	3852	0	3993	82	0
1	P	3852	0	3993	86	0
All	All	61632	0	63891	902	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 7.

All (902) 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:1984:ASP:OD1	1:N:7091:LEU:HD21	1.45	1.17
1:D:1961:LEU:HD21	1:N:7114:ASP:OD1	1.45	1.17

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3500:LEU:HD21	1:K:5575:ASP:OD1	1.44	1.16
1:A:422:LEU:HD21	1:I:4549:ASP:OD1	1.44	1.16
1:H:4013:LEU:HD21	1:J:5062:ASP:OD1	1.45	1.16
1:G:3523:ASP:OD1	1:K:5552:LEU:HD21	1.44	1.16
1:B:935:LEU:HD21	1:P:8140:ASP:OD1	1.45	1.16
1:A:445:ASP:OD1	1:I:4526:LEU:HD21	1.44	1.16
1:F:3010:ASP:OD1	1:L:6065:LEU:HD21	1.45	1.16
1:H:4036:ASP:OD1	1:J:5039:LEU:HD21	1.45	1.16
1:F:2987:LEU:HD21	1:L:6088:ASP:OD1	1.45	1.15
1:E:2497:ASP:OD1	1:M:6578:LEU:HD21	1.44	1.15
1:C:1448:LEU:HD21	1:O:7627:ASP:OD1	1.44	1.15
1:B:958:ASP:OD1	1:P:8117:LEU:HD21	1.45	1.15
1:A:421:GLN:NE2	1:I:4552:GLU:OE2	1.81	1.14
1:G:3526:GLU:OE2	1:K:5551:GLN:NE2	1.81	1.14
1:E:2474:LEU:HD21	1:M:6601:ASP:OD1	1.44	1.13
1:C:1471:ASP:OD1	1:O:7604:LEU:HD21	1.44	1.13
1:D:1987:GLU:OE2	1:N:7090:GLN:NE2	1.81	1.12
1:F:3013:GLU:OE2	1:L:6064:GLN:NE2	1.81	1.12
1:C:1447:GLN:NE2	1:O:7630:GLU:OE2	1.81	1.12
1:D:1960:GLN:NE2	1:N:7117:GLU:OE2	1.81	1.12
1:E:2500:GLU:OE2	1:M:6577:GLN:NE2	1.81	1.12
1:B:934:GLN:NE2	1:P:8143:GLU:OE2	1.81	1.12
1:H:4012:GLN:NE2	1:J:5065:GLU:OE2	1.81	1.12
1:A:448:GLU:OE2	1:I:4525:GLN:NE2	1.81	1.12
1:G:3499:GLN:NE2	1:K:5578:GLU:OE2	1.81	1.12
1:H:4039:GLU:OE2	1:J:5038:GLN:NE2	1.81	1.12
1:E:2473:GLN:NE2	1:M:6604:GLU:OE2	1.81	1.11
1:C:1474:GLU:OE2	1:O:7603:GLN:NE2	1.81	1.11
1:F:2986:GLN:NE2	1:L:6091:GLU:OE2	1.81	1.10
1:B:961:GLU:OE2	1:P:8116:GLN:NE2	1.81	1.10
1:F:2986:GLN:NE2	1:L:6091:GLU:CD	2.15	1.01
1:B:961:GLU:CD	1:P:8116:GLN:NE2	2.15	1.01
1:D:1987:GLU:CD	1:N:7090:GLN:NE2	2.15	1.00
1:D:1960:GLN:NE2	1:N:7117:GLU:CD	2.15	1.00
1:C:1447:GLN:NE2	1:O:7630:GLU:CD	2.15	1.00
1:A:448:GLU:CD	1:I:4525:GLN:NE2	2.15	1.00
1:E:2500:GLU:CD	1:M:6577:GLN:NE2	2.15	1.00
1:G:3499:GLN:NE2	1:K:5578:GLU:CD	2.15	1.00
1:E:2473:GLN:NE2	1:M:6604:GLU:CD	2.15	0.99
1:H:4012:GLN:NE2	1:J:5065:GLU:CD	2.15	0.99
1:H:4039:GLU:CD	1:J:5038:GLN:NE2	2.15	0.99

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1474:GLU:CD	1:O:7603:GLN:NE2	2.15	0.99
1:F:3013:GLU:CD	1:L:6064:GLN:NE2	2.15	0.99
1:B:934:GLN:NE2	1:P:8143:GLU:CD	2.15	0.99
1:G:3526:GLU:CD	1:K:5551:GLN:NE2	2.15	0.98
1:A:421:GLN:NE2	1:I:4552:GLU:CD	2.15	0.98
1:D:1987:GLU:OE1	1:N:7090:GLN:CD	2.10	0.90
1:D:1960:GLN:CD	1:N:7117:GLU:OE1	2.10	0.90
1:A:421:GLN:CD	1:I:4552:GLU:OE1	2.10	0.90
1:G:3526:GLU:OE1	1:K:5551:GLN:CD	2.10	0.90
1:C:1447:GLN:CD	1:O:7630:GLU:OE1	2.10	0.89
1:E:2500:GLU:OE1	1:M:6577:GLN:CD	2.10	0.89
1:F:3013:GLU:OE1	1:L:6064:GLN:CD	2.10	0.89
1:B:934:GLN:CD	1:P:8143:GLU:OE1	2.10	0.89
1:E:2473:GLN:CD	1:M:6604:GLU:OE1	2.10	0.89
1:C:1474:GLU:OE1	1:O:7603:GLN:CD	2.10	0.89
1:B:961:GLU:OE1	1:P:8116:GLN:CD	2.10	0.89
1:F:2986:GLN:CD	1:L:6091:GLU:OE1	2.10	0.89
1:H:4012:GLN:CD	1:J:5065:GLU:OE1	2.10	0.89
1:H:4039:GLU:OE1	1:J:5038:GLN:CD	2.10	0.89
1:A:448:GLU:OE1	1:I:4525:GLN:CD	2.10	0.88
1:G:3499:GLN:CD	1:K:5578:GLU:OE1	2.10	0.88
1:B:960:ILE:CB	1:P:8117:LEU:HG	2.05	0.87
1:C:1473:ILE:CB	1:O:7604:LEU:HG	2.05	0.87
1:A:422:LEU:HG	1:I:4551:ILE:CB	2.05	0.87
1:G:3525:ILE:CB	1:K:5552:LEU:HG	2.05	0.87
1:F:2987:LEU:HG	1:L:6090:ILE:CB	2.05	0.87
1:E:2474:LEU:HG	1:M:6603:ILE:CB	2.05	0.87
1:D:1986:ILE:CB	1:N:7091:LEU:HG	2.05	0.87
1:D:1961:LEU:HG	1:N:7116:ILE:CB	2.05	0.87
1:E:2474:LEU:HG	1:M:6603:ILE:HB	1.57	0.87
1:C:1473:ILE:HB	1:O:7604:LEU:HG	1.57	0.87
1:D:1961:LEU:HG	1:N:7116:ILE:HB	1.57	0.86
1:C:1448:LEU:HG	1:O:7629:ILE:CB	2.05	0.86
1:D:1986:ILE:HB	1:N:7091:LEU:HG	1.57	0.86
1:E:2499:ILE:CB	1:M:6578:LEU:HG	2.05	0.86
1:G:3500:LEU:HG	1:K:5577:ILE:CB	2.05	0.86
1:B:935:LEU:HG	1:P:8142:ILE:CB	2.05	0.86
1:F:2987:LEU:HG	1:L:6090:ILE:HB	1.57	0.86
1:A:447:ILE:CB	1:I:4526:LEU:HG	2.05	0.86
1:F:3012:ILE:CB	1:L:6065:LEU:HG	2.05	0.86
1:H:4038:ILE:CB	1:J:5039:LEU:HG	2.05	0.86

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:960:ILE:HB	1:P:8117:LEU:HG	1.57	0.86
1:H:4013:LEU:HG	1:J:5064:ILE:CB	2.05	0.86
1:C:1448:LEU:HG	1:O:7629:ILE:HB	1.57	0.86
1:E:2499:ILE:HB	1:M:6578:LEU:HG	1.57	0.85
1:A:422:LEU:CD2	1:I:4549:ASP:OD1	2.25	0.85
1:G:3523:ASP:OD1	1:K:5552:LEU:CD2	2.25	0.85
1:G:3500:LEU:HG	1:K:5577:ILE:HB	1.57	0.85
1:A:447:ILE:HB	1:I:4526:LEU:HG	1.57	0.85
1:H:4013:LEU:CD2	1:J:5062:ASP:OD1	2.25	0.84
1:B:935:LEU:HG	1:P:8142:ILE:HB	1.57	0.84
1:A:445:ASP:OD1	1:I:4526:LEU:CD2	2.25	0.84
1:F:3012:ILE:HB	1:L:6065:LEU:HG	1.57	0.84
1:H:4036:ASP:OD1	1:J:5039:LEU:CD2	2.25	0.84
1:G:3500:LEU:CD2	1:K:5575:ASP:OD1	2.25	0.84
1:H:4013:LEU:HG	1:J:5064:ILE:HB	1.57	0.84
1:H:4038:ILE:HB	1:J:5039:LEU:HG	1.57	0.84
1:A:422:LEU:HG	1:I:4551:ILE:HB	1.57	0.84
1:G:3525:ILE:HB	1:K:5552:LEU:HG	1.57	0.84
1:F:3010:ASP:OD1	1:L:6065:LEU:CD2	2.25	0.84
1:B:935:LEU:CD2	1:P:8140:ASP:OD1	2.25	0.84
1:C:1471:ASP:OD1	1:O:7604:LEU:CD2	2.25	0.83
1:E:2474:LEU:CD2	1:M:6601:ASP:OD1	2.25	0.83
1:C:1448:LEU:CG	1:O:7629:ILE:HB	2.09	0.83
1:E:2499:ILE:HB	1:M:6578:LEU:CG	2.09	0.83
1:E:2474:LEU:CG	1:M:6603:ILE:HB	2.09	0.83
1:C:1473:ILE:HB	1:O:7604:LEU:CG	2.09	0.83
1:D:1961:LEU:CG	1:N:7116:ILE:HB	2.09	0.83
1:F:2987:LEU:CG	1:L:6090:ILE:HB	2.09	0.83
1:B:960:ILE:HB	1:P:8117:LEU:CG	2.09	0.83
1:G:3500:LEU:CG	1:K:5577:ILE:HB	2.09	0.83
1:D:1986:ILE:HB	1:N:7091:LEU:CG	2.09	0.83
1:A:422:LEU:CG	1:I:4551:ILE:HB	2.09	0.83
1:G:3525:ILE:HB	1:K:5552:LEU:CG	2.09	0.83
1:A:447:ILE:HB	1:I:4526:LEU:CG	2.09	0.83
1:D:1984:ASP:OD1	1:N:7091:LEU:CD2	2.25	0.82
1:B:935:LEU:CG	1:P:8142:ILE:HB	2.09	0.82
1:D:1961:LEU:CD2	1:N:7114:ASP:OD1	2.25	0.82
1:F:3012:ILE:HB	1:L:6065:LEU:CG	2.09	0.82
1:H:4038:ILE:HB	1:J:5039:LEU:CG	2.09	0.82
1:H:4013:LEU:CG	1:J:5064:ILE:HB	2.09	0.82
1:F:2987:LEU:CD2	1:L:6088:ASP:OD1	2.25	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:958:ASP:OD1	1:P:8117:LEU:CD2	2.25	0.81
1:E:2497:ASP:OD1	1:M:6578:LEU:CD2	2.25	0.81
1:C:1448:LEU:CD2	1:O:7627:ASP:OD1	2.25	0.80
1:F:3013:GLU:OE1	1:L:6064:GLN:NE2	2.17	0.78
1:B:934:GLN:NE2	1:P:8143:GLU:OE1	2.17	0.78
1:H:4012:GLN:NE2	1:J:5065:GLU:OE1	2.17	0.78
1:H:4039:GLU:OE1	1:J:5038:GLN:NE2	2.17	0.78
1:B:961:GLU:OE1	1:P:8116:GLN:NE2	2.17	0.77
1:A:421:GLN:NE2	1:I:4552:GLU:OE1	2.17	0.77
1:G:3526:GLU:OE1	1:K:5551:GLN:NE2	2.17	0.77
1:F:2986:GLN:NE2	1:L:6091:GLU:OE1	2.17	0.77
1:E:2473:GLN:NE2	1:M:6604:GLU:OE1	2.17	0.77
1:C:1474:GLU:OE1	1:O:7603:GLN:NE2	2.17	0.77
1:D:1960:GLN:NE2	1:N:7117:GLU:OE1	2.17	0.77
1:E:2500:GLU:OE1	1:M:6577:GLN:NE2	2.17	0.77
1:D:1987:GLU:OE1	1:N:7090:GLN:NE2	2.17	0.76
1:C:1447:GLN:NE2	1:O:7630:GLU:OE1	2.17	0.76
1:A:448:GLU:OE1	1:I:4525:GLN:NE2	2.17	0.76
1:G:3499:GLN:NE2	1:K:5578:GLU:OE1	2.17	0.76
1:H:4038:ILE:CG2	1:J:5039:LEU:HG	2.18	0.73
1:H:4013:LEU:HG	1:J:5064:ILE:CG2	2.19	0.73
1:B:960:ILE:CG2	1:P:8117:LEU:HG	2.19	0.73
1:F:2987:LEU:HG	1:L:6090:ILE:CG2	2.19	0.73
1:C:1473:ILE:CG2	1:O:7604:LEU:HG	2.19	0.73
1:E:2474:LEU:HG	1:M:6603:ILE:CG2	2.19	0.73
1:A:447:ILE:CG2	1:I:4526:LEU:HG	2.19	0.73
1:D:1986:ILE:CG2	1:N:7091:LEU:HG	2.19	0.73
1:D:1961:LEU:HG	1:N:7116:ILE:CG2	2.19	0.73
1:G:3500:LEU:HG	1:K:5577:ILE:CG2	2.19	0.73
1:M:6590:ILE:HB	1:M:6591:PRO:HD3	1.71	0.73
1:A:422:LEU:HG	1:I:4551:ILE:CG2	2.19	0.72
1:B:935:LEU:HG	1:P:8142:ILE:CG2	2.19	0.72
1:F:3012:ILE:CG2	1:L:6065:LEU:HG	2.18	0.72
1:C:1460:ILE:HB	1:C:1461:PRO:HD3	1.71	0.72
1:A:434:ILE:HB	1:A:435:PRO:HD3	1.71	0.72
1:K:5564:ILE:HB	1:K:5565:PRO:HD3	1.71	0.72
1:G:3525:ILE:CG2	1:K:5552:LEU:HG	2.19	0.72
1:C:1448:LEU:HG	1:O:7629:ILE:CG2	2.19	0.72
1:D:1973:ILE:HB	1:D:1974:PRO:HD3	1.71	0.72
1:N:7103:ILE:HB	1:N:7104:PRO:HD3	1.71	0.72
1:E:2499:ILE:CG2	1:M:6578:LEU:HG	2.19	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:8129:ILE:HB	1:P:8130:PRO:HD3	1.71	0.71
1:F:2999:ILE:HB	1:F:3000:PRO:HD3	1.71	0.71
1:B:947:ILE:HB	1:B:948:PRO:HD3	1.71	0.71
1:J:5051:ILE:HB	1:J:5052:PRO:HD3	1.71	0.71
1:L:6077:ILE:HB	1:L:6078:PRO:HD3	1.71	0.71
1:I:4538:ILE:HB	1:I:4539:PRO:HD3	1.71	0.71
1:G:3512:ILE:HB	1:G:3513:PRO:HD3	1.71	0.71
1:H:4025:ILE:HB	1:H:4026:PRO:HD3	1.71	0.71
1:E:2486:ILE:HB	1:E:2487:PRO:HD3	1.71	0.70
1:O:7616:ILE:HB	1:O:7617:PRO:HD3	1.71	0.70
1:F:2987:LEU:CD2	1:L:6090:ILE:HB	2.22	0.70
1:B:960:ILE:HB	1:P:8117:LEU:CD2	2.22	0.70
1:H:4013:LEU:CD2	1:J:5064:ILE:HB	2.22	0.70
1:H:4038:ILE:HB	1:J:5039:LEU:CD2	2.22	0.69
1:G:3500:LEU:CD2	1:K:5577:ILE:HB	2.22	0.69
1:A:447:ILE:HB	1:I:4526:LEU:CD2	2.22	0.69
1:G:3525:ILE:HB	1:K:5552:LEU:CD2	2.22	0.69
1:C:1448:LEU:CD2	1:O:7629:ILE:HB	2.22	0.69
1:D:1986:ILE:HB	1:N:7091:LEU:CD2	2.22	0.69
1:A:422:LEU:CD2	1:I:4551:ILE:HB	2.22	0.69
1:E:2499:ILE:HB	1:M:6578:LEU:CD2	2.22	0.69
1:E:2474:LEU:CD2	1:M:6603:ILE:HB	2.22	0.69
1:D:1961:LEU:CD2	1:N:7116:ILE:HB	2.22	0.69
1:F:3012:ILE:HB	1:L:6065:LEU:CD2	2.22	0.69
1:B:935:LEU:CD2	1:P:8142:ILE:HB	2.22	0.69
1:C:1473:ILE:HB	1:O:7604:LEU:CD2	2.22	0.69
1:B:960:ILE:HG21	1:P:8117:LEU:HG	1.77	0.66
1:F:2987:LEU:HG	1:L:6090:ILE:HG21	1.77	0.66
1:G:3500:LEU:HG	1:K:5577:ILE:HG21	1.78	0.66
1:H:4013:LEU:HG	1:J:5064:ILE:HG21	1.77	0.66
1:A:447:ILE:HG21	1:I:4526:LEU:HG	1.78	0.66
1:H:4038:ILE:HG21	1:J:5039:LEU:HG	1.77	0.66
1:A:422:LEU:HG	1:I:4551:ILE:HG21	1.77	0.66
1:G:3525:ILE:HG21	1:K:5552:LEU:HG	1.78	0.66
1:E:2474:LEU:HG	1:M:6603:ILE:HG21	1.78	0.66
1:C:1473:ILE:HG21	1:O:7604:LEU:HG	1.78	0.66
1:F:3012:ILE:HG21	1:L:6065:LEU:HG	1.77	0.65
1:B:935:LEU:HG	1:P:8142:ILE:HG21	1.77	0.65
1:D:1961:LEU:HG	1:N:7116:ILE:HG21	1.77	0.65
1:D:1986:ILE:HG21	1:N:7091:LEU:HG	1.77	0.65
1:E:2499:ILE:HG21	1:M:6578:LEU:HG	1.78	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1448:LEU:HG	1:O:7629:ILE:HG21	1.78	0.64
1:D:1698:LYS:HA	1:D:1698:LYS:HE2	1.81	0.63
1:N:6828:LYS:HE2	1:N:6828:LYS:HA	1.81	0.63
1:D:1986:ILE:CD1	1:N:7091:LEU:HG	2.29	0.63
1:D:1961:LEU:HG	1:N:7116:ILE:CD1	2.29	0.63
1:B:960:ILE:CD1	1:P:8117:LEU:HG	2.29	0.62
1:F:2724:LYS:HA	1:F:2724:LYS:HE2	1.81	0.62
1:F:2987:LEU:HG	1:L:6090:ILE:CD1	2.29	0.62
1:P:7854:LYS:HE2	1:P:7854:LYS:HA	1.81	0.62
1:G:3500:LEU:HG	1:K:5577:ILE:CD1	2.30	0.62
1:A:447:ILE:CD1	1:I:4526:LEU:HG	2.30	0.62
1:G:3525:ILE:CD1	1:K:5552:LEU:HG	2.30	0.62
1:E:2474:LEU:HG	1:M:6603:ILE:CD1	2.30	0.62
1:C:1473:ILE:CD1	1:O:7604:LEU:HG	2.30	0.62
1:C:1185:LYS:HA	1:C:1185:LYS:HE2	1.81	0.62
1:A:422:LEU:HG	1:I:4551:ILE:CD1	2.30	0.62
1:B:935:LEU:HD21	1:P:8142:ILE:HB	1.82	0.62
1:B:935:LEU:HG	1:P:8142:ILE:CD1	2.29	0.62
1:F:3012:ILE:HB	1:L:6065:LEU:HD21	1.82	0.62
1:F:3012:ILE:CD1	1:L:6065:LEU:HG	2.29	0.62
1:F:2987:LEU:HD21	1:L:6090:ILE:HB	1.82	0.62
1:B:960:ILE:HB	1:P:8117:LEU:HD21	1.82	0.62
1:M:6315:LYS:HE2	1:M:6315:LYS:HA	1.81	0.62
1:H:4013:LEU:HG	1:J:5064:ILE:CD1	2.29	0.62
1:D:1986:ILE:HB	1:N:7091:LEU:HD21	1.82	0.62
1:D:1961:LEU:HD21	1:N:7116:ILE:HB	1.82	0.62
1:G:3500:LEU:HD21	1:K:5577:ILE:HB	1.82	0.62
1:H:4038:ILE:CD1	1:J:5039:LEU:HG	2.29	0.62
1:O:7341:LYS:HE2	1:O:7341:LYS:HA	1.81	0.62
1:I:4263:LYS:HE2	1:I:4263:LYS:HA	1.81	0.62
1:A:447:ILE:HB	1:I:4526:LEU:HD21	1.82	0.61
1:E:2499:ILE:HB	1:M:6578:LEU:HD21	1.82	0.61
1:C:1448:LEU:HD21	1:O:7629:ILE:HB	1.82	0.61
1:G:3237:LYS:HA	1:G:3237:LYS:HE2	1.81	0.61
1:L:5802:LYS:HA	1:L:5802:LYS:HE2	1.81	0.61
1:E:2211:LYS:HE2	1:E:2211:LYS:HA	1.81	0.61
1:G:3525:ILE:HB	1:K:5552:LEU:HD21	1.82	0.61
1:E:2499:ILE:CD1	1:M:6578:LEU:HG	2.30	0.61
1:B:672:LYS:HA	1:B:672:LYS:HE2	1.81	0.61
1:A:422:LEU:HD21	1:I:4551:ILE:HB	1.82	0.61
1:C:1448:LEU:HG	1:O:7629:ILE:CD1	2.30	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:5850:LEU:C	1:L:5850:LEU:HD23	2.21	0.61
1:C:1473:ILE:HB	1:O:7604:LEU:HD21	1.82	0.61
1:M:6363:LEU:HD23	1:M:6363:LEU:C	2.21	0.61
1:O:7389:LEU:HD23	1:O:7389:LEU:C	2.21	0.61
1:C:1233:LEU:HD23	1:C:1233:LEU:C	2.21	0.61
1:B:720:LEU:C	1:B:720:LEU:HD23	2.21	0.61
1:E:2474:LEU:HD21	1:M:6603:ILE:HB	1.82	0.61
1:H:3750:LYS:HA	1:H:3750:LYS:HE2	1.81	0.61
1:J:4776:LYS:HA	1:J:4776:LYS:HE2	1.81	0.61
1:E:2259:LEU:HD23	1:E:2259:LEU:C	2.21	0.61
1:P:7902:LEU:HD23	1:P:7902:LEU:C	2.21	0.61
1:A:207:LEU:HD23	1:A:207:LEU:C	2.21	0.61
1:A:159:LYS:HA	1:A:159:LYS:HE2	1.81	0.61
1:F:2772:LEU:C	1:F:2772:LEU:HD23	2.21	0.61
1:K:5337:LEU:C	1:K:5337:LEU:HD23	2.21	0.61
1:N:6876:LEU:C	1:N:6876:LEU:HD23	2.21	0.61
1:H:4013:LEU:HD21	1:J:5064:ILE:HB	1.82	0.60
1:K:5289:LYS:HE2	1:K:5289:LYS:HA	1.81	0.60
1:D:1746:LEU:C	1:D:1746:LEU:HD23	2.21	0.60
1:H:4038:ILE:HB	1:J:5039:LEU:HD21	1.82	0.60
1:I:4311:LEU:HD23	1:I:4311:LEU:C	2.21	0.60
1:G:3285:LEU:C	1:G:3285:LEU:HD23	2.21	0.60
1:J:4824:LEU:HD23	1:J:4824:LEU:C	2.21	0.60
1:H:3798:LEU:HD23	1:H:3798:LEU:C	2.21	0.60
1:G:3500:LEU:CD1	1:K:5577:ILE:CG2	2.82	0.58
1:A:422:LEU:CD1	1:I:4551:ILE:CG2	2.82	0.58
1:A:447:ILE:CG2	1:I:4526:LEU:CD1	2.82	0.58
1:D:1961:LEU:CD1	1:N:7116:ILE:CG2	2.81	0.58
1:H:4013:LEU:CD1	1:J:5064:ILE:CG2	2.81	0.58
1:G:3525:ILE:CG2	1:K:5552:LEU:CD1	2.82	0.58
1:B:935:LEU:CD1	1:P:8142:ILE:CG2	2.81	0.58
1:D:1986:ILE:CG2	1:N:7091:LEU:CD1	2.81	0.58
1:F:3012:ILE:CG2	1:L:6065:LEU:CD1	2.81	0.58
1:H:4038:ILE:CG2	1:J:5039:LEU:CD1	2.81	0.58
1:E:2474:LEU:CD1	1:M:6603:ILE:CG2	2.82	0.58
1:C:1473:ILE:CG2	1:O:7604:LEU:CD1	2.82	0.58
1:C:1448:LEU:CD1	1:O:7629:ILE:CG2	2.82	0.57
1:E:2499:ILE:CG2	1:M:6578:LEU:CD1	2.82	0.57
1:F:2987:LEU:CD1	1:L:6090:ILE:CG2	2.81	0.57
1:B:960:ILE:CG2	1:P:8117:LEU:CD1	2.81	0.57
1:G:3500:LEU:HD22	1:K:5575:ASP:OD2	2.05	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:445:ASP:OD2	1:I:4526:LEU:HD22	2.05	0.57
1:F:3010:ASP:OD2	1:L:6065:LEU:HD22	2.05	0.56
1:B:935:LEU:HD22	1:P:8140:ASP:OD2	2.05	0.56
1:F:2987:LEU:HD22	1:L:6088:ASP:OD2	2.05	0.56
1:A:422:LEU:HD22	1:I:4549:ASP:OD2	2.05	0.56
1:B:958:ASP:OD2	1:P:8117:LEU:HD22	2.05	0.56
1:G:3523:ASP:OD2	1:K:5552:LEU:HD22	2.05	0.56
1:J:4639:GLY:HA2	1:J:4689:LEU:HD22	1.87	0.56
1:D:1984:ASP:OD2	1:N:7091:LEU:HD22	2.05	0.56
1:D:1961:LEU:HD22	1:N:7114:ASP:OD2	2.05	0.56
1:C:1448:LEU:HD22	1:O:7627:ASP:OD2	2.05	0.56
1:C:1471:ASP:OD2	1:O:7604:LEU:HD22	2.05	0.56
1:H:3613:GLY:HA2	1:H:3663:LEU:HD22	1.87	0.56
1:E:2497:ASP:OD2	1:M:6578:LEU:HD22	2.05	0.56
1:E:2474:LEU:HD22	1:M:6601:ASP:OD2	2.05	0.56
1:N:6691:GLY:HA2	1:N:6741:LEU:HD22	1.87	0.56
1:D:1561:GLY:HA2	1:D:1611:LEU:HD22	1.87	0.56
1:I:4126:GLY:HA2	1:I:4176:LEU:HD22	1.87	0.56
1:G:3100:GLY:HA2	1:G:3150:LEU:HD22	1.87	0.56
1:H:4036:ASP:OD2	1:J:5039:LEU:HD22	2.05	0.56
1:E:2497:ASP:CG	1:M:6578:LEU:CD2	2.75	0.55
1:C:1448:LEU:CD2	1:O:7627:ASP:CG	2.75	0.55
1:L:5665:GLY:HA2	1:L:5715:LEU:HD22	1.87	0.55
1:H:4013:LEU:HD22	1:J:5062:ASP:OD2	2.05	0.55
1:B:958:ASP:CG	1:P:8117:LEU:CD2	2.75	0.55
1:A:22:GLY:HA2	1:A:72:LEU:HD22	1.87	0.55
1:B:535:GLY:HA2	1:B:585:LEU:HD22	1.87	0.55
1:F:2987:LEU:CD2	1:L:6088:ASP:CG	2.75	0.55
1:K:5152:GLY:HA2	1:K:5202:LEU:HD22	1.87	0.55
1:D:1984:ASP:CG	1:N:7091:LEU:CD2	2.75	0.55
1:D:1961:LEU:CD2	1:N:7114:ASP:CG	2.75	0.55
1:O:7204:GLY:HA2	1:O:7254:LEU:HD22	1.87	0.55
1:E:2074:GLY:HA2	1:E:2124:LEU:HD22	1.87	0.55
1:C:1048:GLY:HA2	1:C:1098:LEU:HD22	1.87	0.55
1:G:3523:ASP:CG	1:K:5552:LEU:CD2	2.75	0.55
1:A:422:LEU:CD2	1:I:4549:ASP:CG	2.75	0.55
1:M:6178:GLY:HA2	1:M:6228:LEU:HD22	1.87	0.55
1:G:3500:LEU:HD21	1:K:5575:ASP:CG	2.25	0.55
1:A:445:ASP:CG	1:I:4526:LEU:HD21	2.25	0.55
1:B:935:LEU:CD2	1:P:8140:ASP:CG	2.75	0.54
1:C:1471:ASP:CG	1:O:7604:LEU:CD2	2.75	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:7717:GLY:HA2	1:P:7767:LEU:HD22	1.87	0.54
1:F:3010:ASP:CG	1:L:6065:LEU:CD2	2.75	0.54
1:E:2474:LEU:CD2	1:M:6601:ASP:CG	2.75	0.54
1:A:422:LEU:HD21	1:I:4549:ASP:CG	2.25	0.54
1:H:4013:LEU:CD2	1:J:5062:ASP:CG	2.75	0.54
1:H:4036:ASP:CG	1:J:5039:LEU:CD2	2.75	0.54
1:G:3523:ASP:CG	1:K:5552:LEU:HD21	2.25	0.54
1:A:167:ILE:HB	1:A:202:LEU:HB2	1.89	0.54
1:K:5297:ILE:HB	1:K:5332:LEU:HB2	1.89	0.54
1:F:2587:GLY:HA2	1:F:2637:LEU:HD22	1.87	0.54
1:B:680:ILE:HB	1:B:715:LEU:HB2	1.89	0.54
1:A:445:ASP:CG	1:I:4526:LEU:CD2	2.75	0.54
1:L:5810:ILE:HB	1:L:5845:LEU:HB2	1.89	0.54
1:F:2732:ILE:HB	1:F:2767:LEU:HB2	1.89	0.54
1:H:4036:ASP:CG	1:J:5039:LEU:HD21	2.26	0.54
1:P:7862:ILE:HB	1:P:7897:LEU:HB2	1.89	0.54
1:G:3500:LEU:CD2	1:K:5575:ASP:CG	2.75	0.54
1:O:7349:ILE:HB	1:O:7384:LEU:HB2	1.89	0.54
1:C:1193:ILE:HB	1:C:1228:LEU:HB2	1.89	0.54
1:M:6323:ILE:HB	1:M:6358:LEU:HB2	1.89	0.54
1:E:2219:ILE:HB	1:E:2254:LEU:HB2	1.89	0.54
1:H:3758:ILE:HB	1:H:3793:LEU:HB2	1.89	0.54
1:J:4784:ILE:HB	1:J:4819:LEU:HB2	1.89	0.53
1:N:6932:LEU:C	1:N:6932:LEU:HD23	2.29	0.53
1:D:1802:LEU:HD23	1:D:1802:LEU:C	2.29	0.53
1:N:6836:ILE:HB	1:N:6871:LEU:HB2	1.89	0.53
1:E:2315:LEU:C	1:E:2315:LEU:HD23	2.29	0.53
1:D:1706:ILE:HB	1:D:1741:LEU:HB2	1.89	0.53
1:I:4271:ILE:HB	1:I:4306:LEU:HB2	1.89	0.53
1:O:7445:LEU:HD23	1:O:7445:LEU:C	2.29	0.53
1:G:3245:ILE:HB	1:G:3280:LEU:HB2	1.89	0.53
1:E:2230:ASP:O	1:E:2232:GLY:HA2	2.09	0.52
1:O:7360:ASP:O	1:O:7362:GLY:HA2	2.10	0.52
1:F:3010:ASP:CG	1:L:6065:LEU:HD21	2.26	0.52
1:F:2743:ASP:O	1:F:2745:GLY:HA2	2.10	0.52
1:D:1986:ILE:HG22	1:N:7091:LEU:CD1	2.39	0.52
1:N:6847:ASP:O	1:N:6849:GLY:HA2	2.10	0.52
1:P:7873:ASP:O	1:P:7875:GLY:HA2	2.10	0.52
1:D:1717:ASP:O	1:D:1719:GLY:HA2	2.10	0.52
1:M:6419:LEU:HD23	1:M:6419:LEU:C	2.29	0.52
1:J:4880:LEU:C	1:J:4880:LEU:HD23	2.29	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1961:LEU:CD1	1:N:7116:ILE:HG22	2.40	0.52
1:B:935:LEU:HD21	1:P:8140:ASP:CG	2.26	0.52
1:H:3854:LEU:C	1:H:3854:LEU:HD23	2.29	0.52
1:M:6334:ASP:O	1:M:6336:GLY:HA2	2.10	0.52
1:C:1204:ASP:O	1:C:1206:GLY:HA2	2.09	0.52
1:B:935:LEU:CD1	1:P:8142:ILE:HG22	2.39	0.52
1:F:3012:ILE:HG22	1:L:6065:LEU:CD1	2.39	0.52
1:G:3256:ASP:O	1:G:3258:GLY:HA2	2.09	0.52
1:L:5906:LEU:HD23	1:L:5906:LEU:C	2.29	0.52
1:K:5393:LEU:C	1:K:5393:LEU:HD23	2.29	0.52
1:H:4013:LEU:CD1	1:J:5064:ILE:HG22	2.39	0.52
1:C:1448:LEU:CD1	1:O:7629:ILE:HG22	2.40	0.52
1:B:958:ASP:CG	1:P:8117:LEU:HD21	2.26	0.52
1:C:1289:LEU:C	1:C:1289:LEU:HD23	2.29	0.52
1:A:263:LEU:C	1:A:263:LEU:HD23	2.29	0.52
1:L:5821:ASP:O	1:L:5823:GLY:HA2	2.10	0.52
1:H:4038:ILE:HG22	1:J:5039:LEU:CD1	2.39	0.52
1:E:2499:ILE:HG22	1:M:6578:LEU:CD1	2.40	0.52
1:B:691:ASP:O	1:B:693:GLY:HA2	2.10	0.52
1:B:776:LEU:HD23	1:B:776:LEU:C	2.29	0.52
1:P:7958:LEU:C	1:P:7958:LEU:HD23	2.29	0.52
1:G:3341:LEU:C	1:G:3341:LEU:HD23	2.29	0.52
1:I:4282:ASP:O	1:I:4284:GLY:HA2	2.10	0.52
1:I:4367:LEU:C	1:I:4367:LEU:HD23	2.29	0.52
1:F:2828:LEU:HD23	1:F:2828:LEU:C	2.29	0.52
1:F:2987:LEU:HD21	1:L:6088:ASP:CG	2.26	0.51
1:C:1473:ILE:HG22	1:O:7604:LEU:CD1	2.40	0.51
1:H:4038:ILE:CG2	1:J:5039:LEU:CG	2.89	0.51
1:F:2987:LEU:CG	1:L:6090:ILE:CG2	2.89	0.51
1:A:422:LEU:CD1	1:I:4551:ILE:HG22	2.40	0.51
1:H:4013:LEU:CG	1:J:5064:ILE:CG2	2.89	0.51
1:E:2474:LEU:CD1	1:M:6603:ILE:HG22	2.40	0.51
1:B:960:ILE:HG22	1:P:8117:LEU:CD1	2.39	0.51
1:H:3769:ASP:O	1:H:3771:GLY:HA2	2.10	0.51
1:H:4013:LEU:HD11	1:J:5064:ILE:HG22	1.93	0.51
1:G:3525:ILE:HG22	1:K:5552:LEU:CD1	2.40	0.51
1:K:5308:ASP:O	1:K:5310:GLY:HA2	2.10	0.51
1:G:3500:LEU:CD1	1:K:5577:ILE:HG22	2.40	0.51
1:A:447:ILE:HG22	1:I:4526:LEU:CD1	2.40	0.51
1:H:4038:ILE:HG22	1:J:5039:LEU:HD11	1.93	0.51
1:F:2987:LEU:CD1	1:L:6090:ILE:HG22	2.40	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3012:ILE:CG2	1:L:6065:LEU:CG	2.89	0.51
1:A:178:ASP:O	1:A:180:GLY:HA2	2.09	0.51
1:J:4795:ASP:O	1:J:4797:GLY:HA2	2.10	0.51
1:G:3500:LEU:CD2	1:K:5575:ASP:OD2	2.59	0.51
1:B:935:LEU:CG	1:P:8142:ILE:CG2	2.89	0.51
1:A:445:ASP:OD2	1:I:4526:LEU:CD2	2.59	0.51
1:K:5356:ILE:N	1:K:5356:ILE:HD12	2.26	0.51
1:A:422:LEU:CD2	1:I:4549:ASP:OD2	2.59	0.51
1:G:3523:ASP:OD2	1:K:5552:LEU:CD2	2.59	0.51
1:B:935:LEU:CD2	1:P:8140:ASP:OD2	2.59	0.51
1:C:1448:LEU:CD2	1:O:7627:ASP:OD2	2.59	0.51
1:M:6382:ILE:HD12	1:M:6382:ILE:N	2.26	0.51
1:L:5869:ILE:N	1:L:5869:ILE:HD12	2.26	0.51
1:N:6895:ILE:N	1:N:6895:ILE:HD12	2.26	0.51
1:D:1986:ILE:CG2	1:N:7091:LEU:CG	2.89	0.50
1:F:3010:ASP:OD2	1:L:6065:LEU:CD2	2.59	0.50
1:H:4036:ASP:OD2	1:J:5039:LEU:CD2	2.59	0.50
1:E:2497:ASP:OD2	1:M:6578:LEU:CD2	2.59	0.50
1:A:226:ILE:N	1:A:226:ILE:HD12	2.27	0.50
1:D:1765:ILE:N	1:D:1765:ILE:HD12	2.27	0.50
1:C:1252:ILE:HD12	1:C:1252:ILE:N	2.27	0.50
1:B:739:ILE:HD12	1:B:739:ILE:N	2.27	0.50
1:D:1961:LEU:CG	1:N:7116:ILE:CG2	2.89	0.50
1:H:4013:LEU:CD2	1:J:5062:ASP:OD2	2.59	0.50
1:D:1540:VAL:O	1:E:2116:VAL:HA	2.12	0.50
1:B:514:VAL:O	1:C:1090:VAL:HA	2.12	0.50
1:O:7408:ILE:N	1:O:7408:ILE:HD12	2.26	0.50
1:E:2474:LEU:CD2	1:M:6601:ASP:OD2	2.59	0.50
1:C:1471:ASP:OD2	1:O:7604:LEU:CD2	2.59	0.50
1:L:5644:VAL:O	1:M:6220:VAL:HA	2.12	0.50
1:N:6670:VAL:O	1:O:7246:VAL:HA	2.12	0.50
1:I:4105:VAL:O	1:J:4681:VAL:HA	2.12	0.50
1:E:2278:ILE:N	1:E:2278:ILE:HD12	2.27	0.50
1:D:1984:ASP:OD2	1:N:7091:LEU:CD2	2.59	0.50
1:A:64:VAL:HA	1:H:3592:VAL:O	2.12	0.50
1:D:1961:LEU:CD2	1:N:7114:ASP:OD2	2.59	0.50
1:G:3079:VAL:O	1:H:3655:VAL:HA	2.12	0.50
1:G:3114:LYS:HB2	1:G:3519:ASN:HB3	1.94	0.50
1:H:3817:ILE:HD12	1:H:3817:ILE:N	2.27	0.50
1:J:4843:ILE:N	1:J:4843:ILE:HD12	2.26	0.50
1:I:4140:LYS:HB2	1:I:4545:ASN:HB3	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1986:ILE:HG22	1:N:7091:LEU:HD11	1.93	0.50
1:B:935:LEU:HD11	1:P:8142:ILE:HG22	1.93	0.50
1:F:2566:VAL:O	1:G:3142:VAL:HA	2.12	0.50
1:J:4618:VAL:O	1:K:5194:VAL:HA	2.12	0.50
1:D:1961:LEU:HD11	1:N:7116:ILE:HG22	1.93	0.50
1:F:3012:ILE:HG22	1:L:6065:LEU:HD11	1.93	0.50
1:F:2987:LEU:HD11	1:L:6090:ILE:HG22	1.93	0.50
1:A:447:ILE:CG2	1:I:4526:LEU:CG	2.89	0.50
1:F:2987:LEU:CD2	1:L:6088:ASP:OD2	2.59	0.50
1:B:960:ILE:HG22	1:P:8117:LEU:HD11	1.93	0.50
1:B:958:ASP:OD2	1:P:8117:LEU:CD2	2.59	0.50
1:L:5647:GLU:O	1:L:5648:ASN:CB	2.60	0.50
1:I:4168:VAL:HA	1:P:7696:VAL:O	2.12	0.50
1:B:517:GLU:O	1:B:518:ASN:CB	2.60	0.50
1:G:3500:LEU:CG	1:K:5577:ILE:CG2	2.89	0.49
1:C:1473:ILE:CG2	1:O:7604:LEU:CG	2.89	0.49
1:E:2056:GLU:O	1:E:2057:ASN:CB	2.60	0.49
1:M:6160:GLU:O	1:M:6161:ASN:CB	2.60	0.49
1:G:3304:ILE:N	1:G:3304:ILE:HD12	2.27	0.49
1:P:7921:ILE:N	1:P:7921:ILE:HD12	2.26	0.49
1:I:4330:ILE:N	1:I:4330:ILE:HD12	2.26	0.49
1:O:7183:VAL:O	1:P:7759:VAL:HA	2.12	0.49
1:C:1448:LEU:HD11	1:O:7629:ILE:HG22	1.93	0.49
1:C:1030:GLU:O	1:C:1031:ASN:CB	2.60	0.49
1:O:7186:GLU:O	1:O:7187:ASN:CB	2.60	0.49
1:E:2499:ILE:HG22	1:M:6578:LEU:HD11	1.93	0.49
1:E:2053:VAL:O	1:F:2629:VAL:HA	2.12	0.49
1:F:2791:ILE:N	1:F:2791:ILE:HD12	2.27	0.49
1:E:2474:LEU:CG	1:M:6603:ILE:CG2	2.89	0.49
1:P:7731:LYS:HB2	1:P:8136:ASN:HB3	1.94	0.49
1:C:1027:VAL:O	1:D:1603:VAL:HA	2.12	0.49
1:F:2601:LYS:HB2	1:F:3006:ASN:HB3	1.94	0.49
1:E:2474:LEU:HD11	1:M:6603:ILE:HG22	1.93	0.49
1:C:1473:ILE:HG22	1:O:7604:LEU:HD11	1.93	0.49
1:H:3627:LYS:HB2	1:H:4032:ASN:HB3	1.94	0.49
1:P:7699:GLU:O	1:P:7700:ASN:CB	2.60	0.49
1:A:447:ILE:HG22	1:I:4526:LEU:HD11	1.93	0.49
1:F:2569:GLU:O	1:F:2570:ASN:CB	2.60	0.49
1:D:1575:LYS:HB2	1:D:1980:ASN:HB3	1.94	0.49
1:K:5131:VAL:O	1:L:5707:VAL:HA	2.12	0.49
1:E:2088:LYS:HB2	1:E:2493:ASN:HB3	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:6157:VAL:O	1:N:6733:VAL:HA	2.12	0.49
1:D:1543:GLU:O	1:D:1544:ASN:CB	2.60	0.49
1:G:3500:LEU:HD11	1:K:5577:ILE:HG22	1.93	0.49
1:J:4653:LYS:HB2	1:J:5058:ASN:HB3	1.94	0.49
1:N:6673:GLU:O	1:N:6674:ASN:CB	2.60	0.49
1:O:7218:LYS:HB2	1:O:7623:ASN:HB3	1.94	0.49
1:N:6705:LYS:HB2	1:N:7110:ASN:HB3	1.94	0.49
1:A:1:VAL:O	1:B:577:VAL:HA	2.12	0.49
1:A:4:GLU:O	1:A:5:ASN:CB	2.60	0.49
1:K:5166:LYS:HB2	1:K:5571:ASN:HB3	1.94	0.49
1:K:5134:GLU:O	1:K:5135:ASN:CB	2.60	0.49
1:A:36:LYS:HB2	1:A:441:ASN:HB3	1.94	0.49
1:L:5679:LYS:HB2	1:L:6084:ASN:HB3	1.94	0.49
1:B:549:LYS:HB2	1:B:954:ASN:HB3	1.94	0.49
1:I:4108:GLU:O	1:I:4109:ASN:CB	2.60	0.49
1:A:422:LEU:HD11	1:I:4551:ILE:HG22	1.93	0.48
1:G:3525:ILE:HG22	1:K:5552:LEU:HD11	1.93	0.48
1:C:1062:LYS:HB2	1:C:1467:ASN:HB3	1.94	0.48
1:M:6192:LYS:HB2	1:M:6597:ASN:HB3	1.94	0.48
1:G:3082:GLU:O	1:G:3083:ASN:CB	2.60	0.48
1:G:3525:ILE:CG2	1:K:5552:LEU:CG	2.89	0.48
1:A:422:LEU:CG	1:I:4551:ILE:CG2	2.89	0.48
1:E:2499:ILE:CG2	1:M:6578:LEU:CG	2.89	0.48
1:E:2497:ASP:CG	1:M:6578:LEU:HD21	2.25	0.48
1:D:1987:GLU:HG2	1:N:7088:ARG:NH2	2.29	0.48
1:H:4039:GLU:HG2	1:J:5036:ARG:NH2	2.29	0.48
1:H:3595:GLU:O	1:H:3596:ASN:CB	2.60	0.48
1:C:1448:LEU:HD21	1:O:7627:ASP:CG	2.25	0.48
1:C:1448:LEU:CG	1:O:7629:ILE:CG2	2.89	0.48
1:C:1445:ARG:NH2	1:O:7630:GLU:HG2	2.29	0.48
1:E:2500:GLU:HG2	1:M:6575:ARG:NH2	2.29	0.48
1:B:932:ARG:NH2	1:P:8143:GLU:HG2	2.29	0.48
1:H:4010:ARG:NH2	1:J:5065:GLU:HG2	2.29	0.48
1:F:2984:ARG:NH2	1:L:6091:GLU:HG2	2.29	0.48
1:J:4621:GLU:O	1:J:4622:ASN:CB	2.60	0.48
1:B:960:ILE:CG2	1:P:8117:LEU:CG	2.89	0.48
1:F:3013:GLU:HG2	1:L:6062:ARG:NH2	2.29	0.48
1:D:1958:ARG:NH2	1:N:7117:GLU:HG2	2.29	0.48
1:B:961:GLU:HG2	1:P:8114:ARG:NH2	2.29	0.48
1:G:3526:GLU:HG2	1:K:5549:ARG:NH2	2.29	0.47
1:A:419:ARG:NH2	1:I:4552:GLU:HG2	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3497:ARG:NH2	1:K:5578:GLU:HG2	2.29	0.47
1:E:2471:ARG:NH2	1:M:6604:GLU:HG2	2.29	0.47
1:C:1474:GLU:HG2	1:O:7601:ARG:NH2	2.29	0.47
1:A:448:GLU:HG2	1:I:4523:ARG:NH2	2.29	0.47
1:C:1471:ASP:CG	1:O:7604:LEU:HD21	2.25	0.47
1:E:2474:LEU:HD21	1:M:6601:ASP:CG	2.25	0.47
1:E:2243:LYS:HB2	1:E:2423:ILE:HD12	1.97	0.46
1:O:7373:LYS:HB2	1:O:7553:ILE:HD12	1.97	0.46
1:F:2756:LYS:HB2	1:F:2936:ILE:HD12	1.97	0.46
1:H:3782:LYS:HB2	1:H:3962:ILE:HD12	1.97	0.46
1:J:4880:LEU:O	1:J:4880:LEU:HD23	2.16	0.46
1:H:3854:LEU:HD23	1:H:3854:LEU:O	2.16	0.46
1:P:7886:LYS:HB2	1:P:8066:ILE:HD12	1.98	0.46
1:J:4808:LYS:HB2	1:J:4988:ILE:HD12	1.98	0.46
1:D:1730:LYS:HB2	1:D:1910:ILE:HD12	1.97	0.46
1:M:6419:LEU:HD23	1:M:6419:LEU:O	2.16	0.46
1:K:5393:LEU:O	1:K:5393:LEU:HD23	2.16	0.46
1:D:1801:MET:O	1:D:1805:MET:HG2	2.16	0.46
1:N:6932:LEU:O	1:N:6932:LEU:HD23	2.16	0.45
1:D:1802:LEU:HD23	1:D:1802:LEU:O	2.16	0.45
1:A:263:LEU:O	1:A:263:LEU:HD23	2.16	0.45
1:B:704:LYS:HB2	1:B:884:ILE:HD12	1.97	0.45
1:N:6860:LYS:HB2	1:N:7040:ILE:HD12	1.98	0.45
1:N:6931:MET:O	1:N:6935:MET:HG2	2.17	0.45
1:P:7852:ALA:HB2	1:P:8069:VAL:HG22	1.99	0.45
1:C:1289:LEU:O	1:C:1289:LEU:HD23	2.16	0.45
1:K:5392:MET:O	1:K:5396:MET:HG2	2.16	0.45
1:A:262:MET:O	1:A:266:MET:HG2	2.16	0.45
1:F:2722:ALA:HB2	1:F:2939:VAL:HG22	1.99	0.45
1:L:5834:LYS:HB2	1:L:6014:ILE:HD12	1.98	0.45
1:G:3341:LEU:O	1:G:3341:LEU:HD23	2.16	0.45
1:I:4367:LEU:O	1:I:4367:LEU:HD23	2.16	0.45
1:E:2209:ALA:HB2	1:E:2426:VAL:HG22	1.99	0.45
1:C:1288:MET:O	1:C:1292:MET:HG2	2.16	0.45
1:O:7339:ALA:HB2	1:O:7556:VAL:HG22	1.99	0.45
1:O:7444:MET:O	1:O:7448:MET:HG2	2.16	0.45
1:H:3748:ALA:HB2	1:H:3965:VAL:HG22	1.99	0.45
1:L:6034:ASP:C	1:L:6036:ARG:H	2.20	0.45
1:J:4774:ALA:HB2	1:J:4991:VAL:HG22	1.99	0.45
1:A:191:LYS:HB2	1:A:371:ILE:HD12	1.97	0.45
1:M:6418:MET:O	1:M:6422:MET:HG2	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:5906:LEU:O	1:L:5906:LEU:HD23	2.16	0.45
1:E:2314:MET:O	1:E:2318:MET:HG2	2.16	0.45
1:K:5321:LYS:HB2	1:K:5501:ILE:HD12	1.97	0.45
1:J:4879:MET:O	1:J:4883:MET:HG2	2.16	0.45
1:M:6347:LYS:HB2	1:M:6527:ILE:HD12	1.97	0.45
1:C:1217:LYS:HB2	1:C:1397:ILE:HD12	1.97	0.45
1:H:3853:MET:O	1:H:3857:MET:HG2	2.16	0.45
1:B:904:ASP:C	1:B:906:ARG:H	2.20	0.45
1:I:4261:ALA:HB2	1:I:4478:VAL:HG22	1.99	0.45
1:G:3235:ALA:HB2	1:G:3452:VAL:HG22	1.99	0.45
1:B:776:LEU:O	1:B:776:LEU:HD23	2.16	0.45
1:E:2315:LEU:HD23	1:E:2315:LEU:O	2.16	0.45
1:K:5521:ASP:C	1:K:5523:ARG:H	2.20	0.45
1:A:391:ASP:C	1:A:393:ARG:H	2.20	0.45
1:G:3269:LYS:HB2	1:G:3449:ILE:HD12	1.97	0.45
1:I:4295:LYS:HB2	1:I:4475:ILE:HD12	1.97	0.45
1:O:7445:LEU:O	1:O:7445:LEU:HD23	2.16	0.45
1:P:7958:LEU:O	1:P:7958:LEU:HD23	2.16	0.45
1:F:2828:LEU:HD23	1:F:2828:LEU:O	2.16	0.45
1:N:6826:ALA:HB2	1:N:7043:VAL:HG22	1.99	0.45
1:K:5287:ALA:HB2	1:K:5504:VAL:HG22	1.99	0.45
1:N:7060:ASP:C	1:N:7062:ARG:H	2.20	0.45
1:P:8086:ASP:C	1:P:8088:ARG:H	2.20	0.45
1:D:1696:ALA:HB2	1:D:1913:VAL:HG22	1.99	0.45
1:D:1930:ASP:C	1:D:1932:ARG:H	2.20	0.45
1:A:157:ALA:HB2	1:A:374:VAL:HG22	1.99	0.45
1:D:1629:ALA:O	1:D:1633:ALA:CB	2.66	0.45
1:B:775:MET:O	1:B:779:MET:HG2	2.16	0.45
1:N:6759:ALA:O	1:N:6763:ALA:CB	2.66	0.44
1:M:6547:ASP:C	1:M:6549:ARG:H	2.20	0.44
1:C:1417:ASP:C	1:C:1419:ARG:H	2.20	0.44
1:F:2956:ASP:C	1:F:2958:ARG:H	2.20	0.44
1:L:5905:MET:O	1:L:5909:MET:HG2	2.17	0.44
1:B:603:ALA:O	1:B:607:ALA:CB	2.66	0.44
1:M:6313:ALA:HB2	1:M:6530:VAL:HG22	1.99	0.44
1:H:3681:ALA:O	1:H:3685:ALA:CB	2.66	0.44
1:P:7957:MET:O	1:P:7961:MET:HG2	2.16	0.44
1:J:5008:ASP:C	1:J:5010:ARG:H	2.20	0.44
1:L:5800:ALA:HB2	1:L:6017:VAL:HG22	1.99	0.44
1:L:5733:ALA:O	1:L:5737:ALA:CB	2.66	0.44
1:J:4707:ALA:O	1:J:4711:ALA:CB	2.66	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:670:ALA:HB2	1:B:887:VAL:HG22	1.99	0.44
1:G:3340:MET:O	1:G:3344:MET:HG2	2.16	0.44
1:H:3982:ASP:C	1:H:3984:ARG:H	2.20	0.44
1:C:1183:ALA:HB2	1:C:1400:VAL:HG22	1.99	0.44
1:F:2827:MET:O	1:F:2831:MET:HG2	2.16	0.44
1:F:2655:ALA:O	1:F:2659:ALA:CB	2.66	0.44
1:I:4495:ASP:C	1:I:4497:ARG:H	2.20	0.44
1:E:2142:ALA:O	1:E:2146:ALA:CB	2.65	0.44
1:G:3469:ASP:C	1:G:3471:ARG:H	2.20	0.44
1:C:1116:ALA:O	1:C:1120:ALA:CB	2.65	0.44
1:I:4366:MET:O	1:I:4370:MET:HG2	2.16	0.44
1:P:7785:ALA:O	1:P:7789:ALA:CB	2.66	0.44
1:O:7272:ALA:O	1:O:7276:ALA:CB	2.66	0.44
1:K:5131:VAL:O	1:L:5708:GLU:N	2.51	0.44
1:M:6246:ALA:O	1:M:6250:ALA:CB	2.66	0.44
1:B:514:VAL:O	1:C:1091:GLU:N	2.51	0.43
1:K:5220:ALA:O	1:K:5224:ALA:CB	2.66	0.43
1:A:90:ALA:O	1:A:94:ALA:CB	2.65	0.43
1:A:1:VAL:O	1:B:578:GLU:N	2.51	0.43
1:C:1199:SER:O	1:C:1202:VAL:HG12	2.19	0.43
1:L:5816:SER:O	1:L:5819:VAL:HG12	2.19	0.43
1:B:686:SER:O	1:B:689:VAL:HG12	2.19	0.43
1:M:6157:VAL:O	1:N:6734:GLU:N	2.51	0.43
1:E:2225:SER:O	1:E:2228:VAL:HG12	2.19	0.43
1:O:7355:SER:O	1:O:7358:VAL:HG12	2.18	0.43
1:G:3168:ALA:O	1:G:3172:ALA:CB	2.65	0.43
1:G:3372:LYS:NZ	1:G:3372:LYS:HB3	2.34	0.43
1:I:4194:ALA:O	1:I:4198:ALA:CB	2.66	0.43
1:O:7183:VAL:O	1:P:7760:GLU:N	2.51	0.43
1:A:173:SER:O	1:A:176:VAL:HG12	2.19	0.43
1:M:6329:SER:O	1:M:6332:VAL:HG12	2.19	0.43
1:I:4398:LYS:NZ	1:I:4398:LYS:HB3	2.34	0.43
1:E:2346:LYS:NZ	1:E:2346:LYS:HB3	2.34	0.43
1:K:5303:SER:O	1:K:5306:VAL:HG12	2.19	0.43
1:C:1320:LYS:HB3	1:C:1320:LYS:NZ	2.34	0.43
1:A:294:LYS:HB3	1:A:294:LYS:NZ	2.34	0.43
1:D:1540:VAL:O	1:E:2117:GLU:N	2.51	0.43
1:L:5644:VAL:O	1:M:6221:GLU:N	2.52	0.43
1:A:65:GLU:N	1:H:3592:VAL:O	2.51	0.43
1:C:1027:VAL:O	1:D:1604:GLU:N	2.51	0.43
1:E:2443:ASP:C	1:E:2445:ARG:H	2.20	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:7476:LYS:HB3	1:O:7476:LYS:NZ	2.34	0.43
1:K:5424:LYS:NZ	1:K:5424:LYS:HB3	2.34	0.43
1:K:5564:ILE:HB	1:K:5565:PRO:CD	2.46	0.43
1:O:7573:ASP:C	1:O:7575:ARG:H	2.20	0.43
1:M:6450:LYS:NZ	1:M:6450:LYS:HB3	2.34	0.43
1:N:6670:VAL:O	1:O:7247:GLU:N	2.52	0.43
1:E:2053:VAL:O	1:F:2630:GLU:N	2.51	0.43
1:D:1833:LYS:NZ	1:D:1833:LYS:HB3	2.34	0.43
1:N:6963:LYS:HB3	1:N:6963:LYS:NZ	2.34	0.43
1:A:434:ILE:HB	1:A:435:PRO:CD	2.46	0.43
1:J:4618:VAL:O	1:K:5195:GLU:N	2.52	0.43
1:H:3764:SER:O	1:H:3767:VAL:HG12	2.19	0.43
1:I:4154:VAL:O	1:I:4154:VAL:HG13	2.19	0.43
1:F:2738:SER:O	1:F:2741:VAL:HG12	2.19	0.43
1:H:4009:GLY:O	1:H:4012:GLN:HG2	2.19	0.43
1:M:6590:ILE:HB	1:M:6591:PRO:CD	2.46	0.43
1:I:4105:VAL:O	1:J:4682:GLU:N	2.51	0.43
1:P:7868:SER:O	1:P:7871:VAL:HG12	2.19	0.43
1:G:3251:SER:O	1:G:3254:VAL:HG12	2.19	0.43
1:J:4790:SER:O	1:J:4793:VAL:HG12	2.19	0.43
1:I:4277:SER:O	1:I:4280:VAL:HG12	2.18	0.43
1:D:1986:ILE:HD12	1:N:7091:LEU:HG	2.01	0.42
1:G:3525:ILE:HD12	1:K:5552:LEU:HG	2.01	0.42
1:N:7087:GLY:O	1:N:7090:GLN:HG2	2.19	0.42
1:D:1957:GLY:O	1:D:1960:GLN:HG2	2.19	0.42
1:J:5035:GLY:O	1:J:5038:GLN:HG2	2.19	0.42
1:C:1460:ILE:HB	1:C:1461:PRO:CD	2.46	0.42
1:F:2566:VAL:O	1:G:3143:GLU:N	2.51	0.42
1:D:1632:VAL:CG1	1:D:1633:ALA:N	2.82	0.42
1:N:6762:VAL:CG1	1:N:6763:ALA:N	2.82	0.42
1:H:3684:VAL:CG1	1:H:3685:ALA:N	2.82	0.42
1:J:4710:VAL:CG1	1:J:4711:ALA:N	2.82	0.42
1:P:7745:VAL:HG13	1:P:7745:VAL:O	2.19	0.42
1:L:5937:LYS:NZ	1:L:5937:LYS:HB3	2.34	0.42
1:F:2859:LYS:HB3	1:F:2859:LYS:NZ	2.34	0.42
1:B:807:LYS:NZ	1:B:807:LYS:HB3	2.34	0.42
1:D:1961:LEU:HG	1:N:7116:ILE:HD12	2.01	0.42
1:F:2655:ALA:O	1:F:2659:ALA:HB2	2.20	0.42
1:E:2145:VAL:CG1	1:E:2146:ALA:N	2.82	0.42
1:O:7275:VAL:CG1	1:O:7276:ALA:N	2.82	0.42
1:N:6842:SER:O	1:N:6845:VAL:HG12	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3128:VAL:HG13	1:G:3128:VAL:O	2.19	0.42
1:F:2615:VAL:HG13	1:F:2615:VAL:O	2.19	0.42
1:A:422:LEU:HG	1:I:4551:ILE:HD12	2.02	0.42
1:C:1444:GLY:O	1:C:1447:GLN:HG2	2.19	0.42
1:M:6574:GLY:O	1:M:6577:GLN:HG2	2.19	0.42
1:D:1629:ALA:O	1:D:1633:ALA:HB2	2.20	0.42
1:B:606:VAL:CG1	1:B:607:ALA:N	2.82	0.42
1:L:5736:VAL:CG1	1:L:5737:ALA:N	2.82	0.42
1:H:3641:VAL:HG13	1:H:3641:VAL:O	2.19	0.42
1:J:4911:LYS:HB3	1:J:4911:LYS:NZ	2.34	0.42
1:J:4667:VAL:O	1:J:4667:VAL:HG13	2.19	0.42
1:H:3885:LYS:HB3	1:H:3885:LYS:NZ	2.34	0.42
1:G:3079:VAL:O	1:H:3656:GLU:N	2.51	0.42
1:I:4169:GLU:N	1:P:7696:VAL:O	2.52	0.42
1:N:6759:ALA:O	1:N:6763:ALA:HB2	2.20	0.42
1:P:7785:ALA:O	1:P:7789:ALA:HB2	2.20	0.42
1:I:4194:ALA:O	1:I:4198:ALA:HB2	2.20	0.42
1:H:3931:ARG:HB2	1:H:3940:PHE:CE1	2.55	0.42
1:M:6496:ARG:HB2	1:M:6505:PHE:CE1	2.55	0.42
1:C:1366:ARG:HB2	1:C:1375:PHE:CE1	2.55	0.42
1:O:7522:ARG:HB2	1:O:7531:PHE:CE1	2.55	0.42
1:D:1712:SER:O	1:D:1715:VAL:HG12	2.19	0.42
1:D:1589:VAL:O	1:D:1589:VAL:HG13	2.19	0.42
1:M:6594:LEU:HD12	1:M:6594:LEU:HA	1.86	0.42
1:E:2392:ARG:HB2	1:E:2401:PHE:CE1	2.55	0.42
1:B:603:ALA:O	1:B:607:ALA:HB2	2.20	0.42
1:L:5733:ALA:O	1:L:5737:ALA:HB2	2.20	0.42
1:K:5223:VAL:CG1	1:K:5224:ALA:N	2.82	0.42
1:G:3168:ALA:O	1:G:3172:ALA:HB2	2.20	0.42
1:D:1879:ARG:HB2	1:D:1888:PHE:CE1	2.55	0.42
1:J:4957:ARG:HB2	1:J:4966:PHE:CE1	2.55	0.42
1:P:7989:LYS:HB3	1:P:7989:LYS:NZ	2.34	0.42
1:N:6719:VAL:HG13	1:N:6719:VAL:O	2.19	0.42
1:F:2905:ARG:HB2	1:F:2914:PHE:CE1	2.55	0.42
1:N:7009:ARG:HB2	1:N:7018:PHE:CE1	2.55	0.42
1:B:853:ARG:HB2	1:B:862:PHE:CE1	2.55	0.42
1:P:8129:ILE:HB	1:P:8130:PRO:CD	2.46	0.42
1:G:3171:VAL:CG1	1:G:3172:ALA:N	2.82	0.42
1:P:8035:ARG:HB2	1:P:8044:PHE:CE1	2.55	0.42
1:L:5983:ARG:HB2	1:L:5992:PHE:CE1	2.55	0.42
1:H:3681:ALA:O	1:H:3685:ALA:HB2	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:4707:ALA:O	1:J:4711:ALA:HB2	2.20	0.42
1:E:2142:ALA:O	1:E:2146:ALA:HB2	2.20	0.42
1:M:6249:VAL:CG1	1:M:6250:ALA:N	2.82	0.42
1:K:5220:ALA:O	1:K:5224:ALA:HB2	2.20	0.42
1:A:93:VAL:CG1	1:A:94:ALA:N	2.82	0.42
1:C:1464:LEU:HA	1:C:1464:LEU:HD12	1.86	0.42
1:E:2102:VAL:HG13	1:E:2102:VAL:O	2.19	0.42
1:O:7232:VAL:HG13	1:O:7232:VAL:O	2.19	0.42
1:H:4038:ILE:HG21	1:J:5039:LEU:CG	2.49	0.42
1:F:2983:GLY:O	1:F:2986:GLN:HG2	2.19	0.42
1:C:1119:VAL:CG1	1:C:1120:ALA:N	2.82	0.42
1:O:7272:ALA:O	1:O:7276:ALA:HB2	2.20	0.42
1:A:90:ALA:O	1:A:94:ALA:HB2	2.20	0.42
1:I:4197:VAL:CG1	1:I:4198:ALA:N	2.82	0.42
1:A:23:ARG:NH1	1:A:99:ARG:HD3	2.35	0.42
1:M:6206:VAL:O	1:M:6206:VAL:HG13	2.19	0.42
1:C:1076:VAL:HG13	1:C:1076:VAL:O	2.19	0.42
1:N:6817:ALA:HB1	1:N:6834:ALA:HA	2.02	0.42
1:H:4013:LEU:CG	1:J:5064:ILE:HG21	2.49	0.42
1:E:2499:ILE:HD12	1:M:6578:LEU:HG	2.01	0.42
1:B:960:ILE:HD12	1:P:8117:LEU:HG	2.01	0.42
1:E:2474:LEU:CG	1:M:6603:ILE:CB	2.80	0.42
1:I:4522:GLY:O	1:I:4525:GLN:HG2	2.19	0.42
1:O:7600:GLY:O	1:O:7603:GLN:HG2	2.19	0.42
1:P:8113:GLY:O	1:P:8116:GLN:HG2	2.19	0.42
1:D:1687:ALA:HB1	1:D:1704:ALA:HA	2.02	0.42
1:B:931:GLY:O	1:B:934:GLN:HG2	2.19	0.42
1:G:3496:GLY:O	1:G:3499:GLN:HG2	2.19	0.42
1:E:2470:GLY:O	1:E:2473:GLN:HG2	2.19	0.42
1:F:2999:ILE:HB	1:F:3000:PRO:CD	2.46	0.42
1:K:5153:ARG:NH1	1:K:5229:ARG:HD3	2.35	0.42
1:F:2987:LEU:HG	1:L:6090:ILE:HD12	2.01	0.41
1:M:6246:ALA:O	1:M:6250:ALA:HB2	2.20	0.41
1:G:3101:ARG:NH1	1:G:3177:ARG:HD3	2.35	0.41
1:K:5568:LEU:HD12	1:K:5568:LEU:HA	1.86	0.41
1:L:5693:VAL:O	1:L:5693:VAL:HG13	2.19	0.41
1:P:7718:ARG:NH1	1:P:7794:ARG:HD3	2.35	0.41
1:A:418:GLY:O	1:A:421:GLN:HG2	2.19	0.41
1:L:6061:GLY:O	1:L:6064:GLN:HG2	2.19	0.41
1:C:1116:ALA:O	1:C:1120:ALA:HB2	2.20	0.41
1:E:2200:ALA:HB1	1:E:2217:ALA:HA	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:4127:ARG:NH1	1:I:4203:ARG:HD3	2.35	0.41
1:F:2588:ARG:NH1	1:F:2664:ARG:HD3	2.35	0.41
1:O:7330:ALA:HB1	1:O:7347:ALA:HA	2.02	0.41
1:B:563:VAL:HG13	1:B:563:VAL:O	2.19	0.41
1:K:5548:GLY:O	1:K:5551:GLN:HG2	2.19	0.41
1:C:1448:LEU:HG	1:O:7629:ILE:HD12	2.02	0.41
1:I:4444:ARG:HB2	1:I:4453:PHE:CE1	2.55	0.41
1:A:340:ARG:HB2	1:A:349:PHE:CE1	2.55	0.41
1:M:6304:ALA:HB1	1:M:6321:ALA:HA	2.02	0.41
1:G:3418:ARG:HB2	1:G:3427:PHE:CE1	2.55	0.41
1:P:8133:LEU:HA	1:P:8133:LEU:HD12	1.86	0.41
1:A:50:VAL:HG13	1:A:50:VAL:O	2.19	0.41
1:K:5470:ARG:HB2	1:K:5479:PHE:CE1	2.55	0.41
1:C:1473:ILE:CB	1:O:7604:LEU:CG	2.80	0.41
1:P:7788:VAL:CG1	1:P:7789:ALA:N	2.82	0.41
1:C:1049:ARG:NH1	1:C:1125:ARG:HD3	2.35	0.41
1:C:1174:ALA:HB1	1:C:1191:ALA:HA	2.02	0.41
1:M:6179:ARG:NH1	1:M:6255:ARG:HD3	2.35	0.41
1:K:5180:VAL:O	1:K:5180:VAL:HG13	2.19	0.41
1:A:438:LEU:HD12	1:A:438:LEU:HA	1.86	0.41
1:H:4038:ILE:HD12	1:J:5039:LEU:HG	2.01	0.41
1:B:960:ILE:HG21	1:P:8117:LEU:CG	2.49	0.41
1:E:2181:LEU:HB3	1:E:2538:LEU:HD11	2.03	0.41
1:F:3003:LEU:HD12	1:F:3003:LEU:HA	1.86	0.41
1:F:2987:LEU:CG	1:L:6090:ILE:HG21	2.49	0.41
1:F:2658:VAL:CG1	1:F:2659:ALA:N	2.82	0.41
1:O:7311:LEU:HB3	1:O:7668:LEU:HD11	2.03	0.41
1:B:628:VAL:HG13	1:B:629:LYS:N	2.36	0.41
1:B:536:ARG:NH1	1:B:612:ARG:HD3	2.35	0.41
1:B:661:ALA:HB1	1:B:678:ALA:HA	2.02	0.41
1:L:5791:ALA:HB1	1:L:5808:ALA:HA	2.02	0.41
1:A:63:SER:O	1:H:3594:PRO:HD3	2.21	0.41
1:J:4640:ARG:NH1	1:J:4716:ARG:HD3	2.35	0.41
1:D:1542:PRO:HD3	1:E:2115:SER:O	2.21	0.41
1:D:1562:ARG:NH1	1:D:1638:ARG:HD3	2.35	0.41
1:O:7185:PRO:HD3	1:P:7758:SER:O	2.21	0.41
1:H:4013:LEU:HG	1:J:5064:ILE:HD12	2.01	0.41
1:E:2055:PRO:HD3	1:F:2628:SER:O	2.21	0.41
1:L:5666:ARG:NH1	1:L:5742:ARG:HD3	2.35	0.41
1:L:5758:VAL:HG13	1:L:5759:LYS:N	2.36	0.41
1:N:6692:ARG:NH1	1:N:6768:ARG:HD3	2.35	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1155:LEU:HB3	1:C:1512:LEU:HD11	2.03	0.41
1:N:6784:VAL:HG13	1:N:6785:LYS:N	2.36	0.41
1:B:516:PRO:HD3	1:C:1089:SER:O	2.21	0.41
1:H:3706:VAL:HG13	1:H:3707:LYS:N	2.36	0.41
1:H:3614:ARG:NH1	1:H:3690:ARG:HD3	2.35	0.41
1:D:1654:VAL:HG13	1:D:1655:LYS:N	2.36	0.41
1:D:1984:ASP:CG	1:N:7091:LEU:HD21	2.26	0.41
1:G:3081:PRO:HD3	1:H:3654:SER:O	2.21	0.41
1:L:5646:PRO:HD3	1:M:6219:SER:O	2.21	0.41
1:L:5772:LEU:HB3	1:L:6129:LEU:HD11	2.03	0.41
1:K:5132:LEU:HA	1:K:5133:PRO:HD3	1.95	0.41
1:M:6285:LEU:HB3	1:M:6642:LEU:HD11	2.03	0.41
1:J:4732:VAL:HG13	1:J:4733:LYS:N	2.36	0.41
1:I:4107:PRO:HD3	1:J:4680:SER:O	2.21	0.41
1:A:422:LEU:CG	1:I:4551:ILE:CB	2.80	0.41
1:N:6672:PRO:HD3	1:O:7245:SER:O	2.21	0.41
1:F:2680:VAL:HG13	1:F:2681:LYS:N	2.36	0.41
1:A:2:LEU:HA	1:A:3:PRO:HD3	1.95	0.41
1:B:642:LEU:HB3	1:B:999:LEU:HD11	2.03	0.41
1:N:6798:LEU:HB3	1:N:7155:LEU:HD11	2.03	0.41
1:F:2713:ALA:HB1	1:F:2730:ALA:HA	2.02	0.41
1:J:4620:PRO:HD3	1:K:5193:SER:O	2.21	0.41
1:H:4013:LEU:CG	1:J:5064:ILE:CB	2.80	0.41
1:H:4038:ILE:HD11	1:J:4721:LEU:CD2	2.51	0.41
1:A:3:PRO:HD3	1:B:576:SER:O	2.21	0.41
1:D:1668:LEU:HB3	1:D:2025:LEU:HD11	2.03	0.41
1:P:7843:ALA:HB1	1:P:7860:ALA:HA	2.02	0.41
1:C:1141:VAL:HG13	1:C:1142:LYS:N	2.36	0.41
1:G:3207:LEU:HB3	1:G:3564:LEU:HD11	2.03	0.41
1:P:7810:VAL:HG13	1:P:7811:LYS:N	2.36	0.41
1:H:3695:LEU:CD2	1:J:5064:ILE:HD11	2.52	0.40
1:F:3012:ILE:HD11	1:L:5747:LEU:CD2	2.51	0.40
1:N:7103:ILE:HB	1:N:7104:PRO:CD	2.46	0.40
1:G:3082:GLU:O	1:G:3083:ASN:HB3	2.21	0.40
1:K:5133:PRO:HD3	1:L:5706:SER:O	2.21	0.40
1:I:4233:LEU:HB3	1:I:4590:LEU:HD11	2.03	0.40
1:J:4765:ALA:HB1	1:J:4782:ALA:HA	2.02	0.40
1:A:129:LEU:HB3	1:A:486:LEU:HD11	2.03	0.40
1:I:4542:LEU:HD12	1:I:4542:LEU:HA	1.86	0.40
1:M:6271:VAL:HG13	1:M:6272:LYS:N	2.36	0.40
1:D:1961:LEU:HD21	1:N:7114:ASP:CG	2.26	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:617:LEU:CD2	1:P:8142:ILE:HD11	2.52	0.40
1:H:3739:ALA:HB1	1:H:3756:ALA:HA	2.02	0.40
1:I:4219:VAL:HG13	1:I:4220:LYS:N	2.36	0.40
1:K:5259:LEU:HB3	1:K:5616:LEU:HD11	2.03	0.40
1:K:5278:ALA:HB1	1:K:5295:ALA:HA	2.02	0.40
1:F:2648:VAL:HG12	1:F:2648:VAL:O	2.21	0.40
1:G:3193:VAL:HG13	1:G:3194:LYS:N	2.36	0.40
1:F:3012:ILE:HG21	1:L:6065:LEU:CG	2.49	0.40
1:I:4108:GLU:O	1:I:4109:ASN:HB3	2.21	0.40
1:P:7824:LEU:HB3	1:P:8181:LEU:HD11	2.03	0.40
1:E:2075:ARG:NH1	1:E:2151:ARG:HD3	2.35	0.40
1:A:148:ALA:HB1	1:A:165:ALA:HA	2.02	0.40
1:D:1986:ILE:HD11	1:N:6773:LEU:CD2	2.51	0.40
1:D:1643:LEU:CD2	1:N:7116:ILE:HD11	2.52	0.40
1:A:419:ARG:NE	1:I:4549:ASP:OD2	2.54	0.40
1:B:935:LEU:CG	1:P:8142:ILE:HG21	2.49	0.40
1:A:447:ILE:HD11	1:I:4208:LEU:CD2	2.52	0.40
1:E:2499:ILE:HD11	1:M:6260:LEU:CD2	2.52	0.40
1:C:1130:LEU:CD2	1:O:7629:ILE:HD11	2.52	0.40
1:B:606:VAL:HG13	1:B:607:ALA:N	2.37	0.40
1:O:7205:ARG:NH1	1:O:7281:ARG:HD3	2.35	0.40
1:F:2694:LEU:HB3	1:F:3051:LEU:HD11	2.03	0.40
1:F:2568:PRO:HD3	1:G:3141:SER:O	2.21	0.40
1:A:32:THR:CG2	1:A:53:ASN:HB2	2.52	0.40
1:K:5162:THR:CG2	1:K:5183:ASN:HB2	2.52	0.40
1:O:7620:LEU:HA	1:O:7620:LEU:HD12	1.86	0.40
1:G:3516:LEU:HD12	1:G:3516:LEU:HA	1.86	0.40
1:P:7778:VAL:HG12	1:P:7778:VAL:O	2.22	0.40
1:A:104:LEU:CD2	1:I:4551:ILE:HD11	2.52	0.40
1:G:3523:ASP:OD2	1:K:5549:ARG:NE	2.54	0.40
1:G:3525:ILE:HD11	1:K:5234:LEU:CD2	2.52	0.40
1:G:3525:ILE:CB	1:K:5552:LEU:CG	2.80	0.40
1:H:4038:ILE:CB	1:J:5039:LEU:CG	2.80	0.40
1:B:960:ILE:HD11	1:P:7799:LEU:CD2	2.51	0.40
1:D:1973:ILE:HB	1:D:1974:PRO:CD	2.46	0.40
1:G:3226:ALA:HB1	1:G:3243:ALA:HA	2.02	0.40
1:K:5245:VAL:HG13	1:K:5246:LYS:N	2.36	0.40
1:I:4252:ALA:HB1	1:I:4269:ALA:HA	2.02	0.40
1:A:115:VAL:HG13	1:A:116:LYS:N	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	B	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	C	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	D	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	E	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	F	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	G	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	H	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	I	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	J	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	K	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	L	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	M	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	N	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	O	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
1	P	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	19	65
All	All	8176/8208 (100%)	7776 (95%)	320 (4%)	80 (1%)	24	65

All (80) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	B	518	ASN
1	C	1031	ASN
1	D	1544	ASN
1	E	2057	ASN
1	F	2570	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	3083	ASN
1	H	3596	ASN
1	I	4109	ASN
1	J	4622	ASN
1	K	5135	ASN
1	L	5648	ASN
1	M	6161	ASN
1	N	6674	ASN
1	O	7187	ASN
1	P	7700	ASN
1	A	354	LYS
1	A	465	ALA
1	A	466	GLY
1	B	867	LYS
1	B	978	ALA
1	B	979	GLY
1	C	1380	LYS
1	C	1491	ALA
1	C	1492	GLY
1	D	1893	LYS
1	D	2004	ALA
1	D	2005	GLY
1	E	2406	LYS
1	E	2517	ALA
1	E	2518	GLY
1	F	2919	LYS
1	F	3030	ALA
1	F	3031	GLY
1	G	3432	LYS
1	G	3543	ALA
1	G	3544	GLY
1	H	3945	LYS
1	H	4056	ALA
1	H	4057	GLY
1	I	4458	LYS
1	I	4569	ALA
1	I	4570	GLY
1	J	4971	LYS
1	J	5082	ALA
1	J	5083	GLY
1	K	5484	LYS
1	K	5595	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	K	5596	GLY
1	L	5997	LYS
1	L	6108	ALA
1	L	6109	GLY
1	M	6510	LYS
1	M	6621	ALA
1	M	6622	GLY
1	N	7023	LYS
1	N	7134	ALA
1	N	7135	GLY
1	O	7536	LYS
1	O	7647	ALA
1	O	7648	GLY
1	P	8049	LYS
1	P	8160	ALA
1	P	8161	GLY
1	A	392	GLY
1	B	905	GLY
1	C	1418	GLY
1	D	1931	GLY
1	E	2444	GLY
1	F	2957	GLY
1	G	3470	GLY
1	H	3983	GLY
1	I	4496	GLY
1	J	5009	GLY
1	K	5522	GLY
1	L	6035	GLY
1	M	6548	GLY
1	N	7061	GLY
1	O	7574	GLY
1	P	8087	GLY

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	B	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	C	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	D	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	E	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	F	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	G	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	H	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	I	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	J	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	K	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	L	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	M	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	N	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	O	414/414 (100%)	410 (99%)	4 (1%)	82	92
1	P	414/414 (100%)	410 (99%)	4 (1%)	82	92
All	All	6624/6624 (100%)	6560 (99%)	64 (1%)	83	92

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	98	LEU
1	A	129	LEU
1	A	419	ARG
1	A	438	LEU
1	B	611	LEU
1	B	642	LEU
1	B	932	ARG
1	B	951	LEU
1	C	1124	LEU
1	C	1155	LEU
1	C	1445	ARG
1	C	1464	LEU
1	D	1637	LEU
1	D	1668	LEU
1	D	1958	ARG
1	D	1977	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	2150	LEU
1	E	2181	LEU
1	E	2471	ARG
1	E	2490	LEU
1	F	2663	LEU
1	F	2694	LEU
1	F	2984	ARG
1	F	3003	LEU
1	G	3176	LEU
1	G	3207	LEU
1	G	3497	ARG
1	G	3516	LEU
1	H	3689	LEU
1	H	3720	LEU
1	H	4010	ARG
1	H	4029	LEU
1	I	4202	LEU
1	I	4233	LEU
1	I	4523	ARG
1	I	4542	LEU
1	J	4715	LEU
1	J	4746	LEU
1	J	5036	ARG
1	J	5055	LEU
1	K	5228	LEU
1	K	5259	LEU
1	K	5549	ARG
1	K	5568	LEU
1	L	5741	LEU
1	L	5772	LEU
1	L	6062	ARG
1	L	6081	LEU
1	M	6254	LEU
1	M	6285	LEU
1	M	6575	ARG
1	M	6594	LEU
1	N	6767	LEU
1	N	6798	LEU
1	N	7088	ARG
1	N	7107	LEU
1	O	7280	LEU
1	O	7311	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	O	7601	ARG
1	O	7620	LEU
1	P	7793	LEU
1	P	7824	LEU
1	P	8114	ARG
1	P	8133	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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.