



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:46 PM GMT

PDB ID : 4FXG
Title : Complement C4 in complex with MASP-2
Authors : Kidmose, R.T.; Laursen, N.S.; Andersen, G.R.
Deposited on : 2012-07-03
Resolution : 3.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

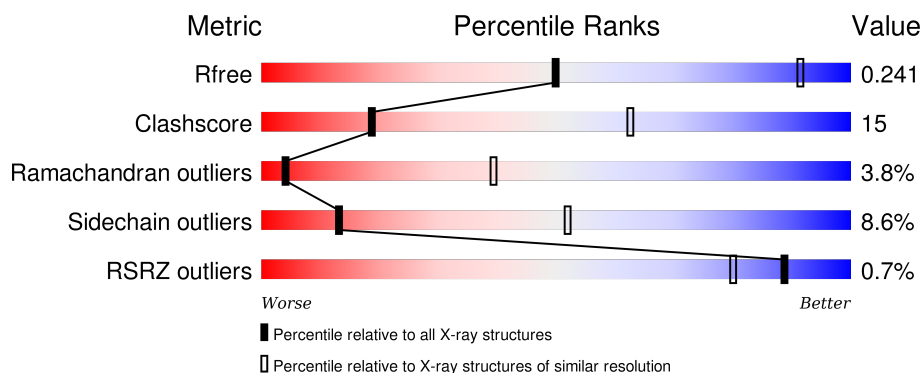
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.75 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}	91344	1268 (4.02-3.50)
Clashscore	102246	1407 (4.02-3.50)
Ramachandran outliers	100387	1346 (4.02-3.50)
Sidechain outliers	100360	1342 (4.02-3.50)
RSRZ outliers	91569	1276 (4.02-3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	656	 62% 33% . .
1	D	656	 63% 32% . .
2	B	767	 % 57% 35% . .
2	E	767	 2% 58% 35% . .
3	C	291	 55% 35% 8% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	F	291	<div><div></div><div>59%31%8%</div><div></div></div>
4	G	154	<div><div></div><div>70%21%6%</div><div></div></div>
4	I	154	<div><div>%</div><div></div><div>71%20%6%</div><div></div></div>
5	H	242	<div><div>%</div><div></div><div>64%31%5%</div><div></div></div>
5	J	242	<div><div>%</div><div></div><div>64%31%5%</div><div></div></div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 32218 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 Complement C4 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	651	Total	C	N	O	S	0	0	0
			5012	3185	872	939	16			
1	D	651	Total	C	N	O	S	0	0	0
			5012	3185	872	939	16			

- Molecule 2 is a protein called Complement C4-A alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	740	Total	C	N	O	S	0	0	0
			5718	3588	1002	1102	26			
2	E	740	Total	C	N	O	S	0	0	0
			5718	3588	1002	1102	26			

- Molecule 3 is a protein called Complement C4 gamma chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	287	Total	C	N	O	S	0	0	0
			2291	1437	407	430	17			
3	F	287	Total	C	N	O	S	0	0	0
			2291	1437	407	430	17			

- Molecule 4 is a protein called Mannan-binding lectin serine protease 2 A chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	145	Total	C	N	O	S	0	0	0
			1103	701	177	213	12			
4	I	145	Total	C	N	O	S	0	0	0
			1103	701	177	213	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	298	HIS	GLN	CONFLICT	UNP O00187
G	299	ALA	PRO	CONFLICT	UNP O00187
I	298	HIS	GLN	CONFLICT	UNP O00187
I	299	ALA	PRO	CONFLICT	UNP O00187

- Molecule 5 is a protein called Mannan-binding lectin serine protease 2 B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	H	242	Total	C	N	O	S	0	0	0
			1868	1190	317	351	10			
5	J	242	Total	C	N	O	S	0	0	0
			1868	1190	317	351	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	633	ALA	SER	ENGINEERED MUTATION	UNP O00187
J	633	ALA	SER	ENGINEERED MUTATION	UNP O00187

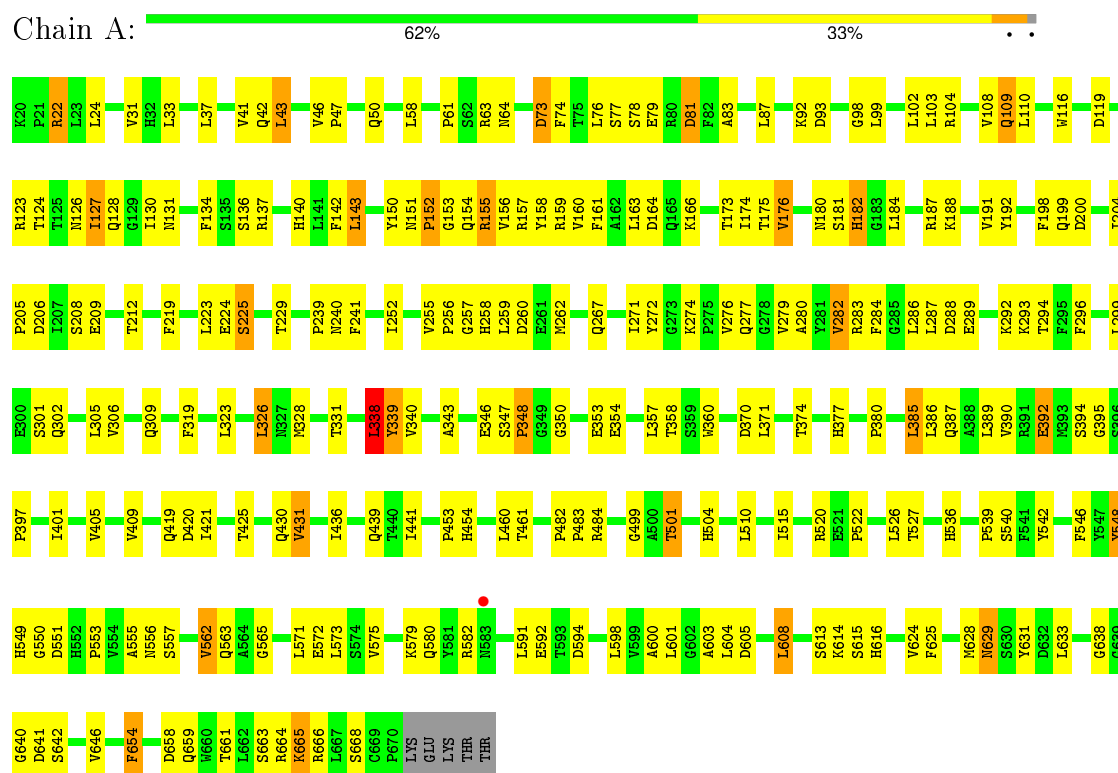
- Molecule 6 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	3	Total	C	N	O	0	0
			39	22	2	15		
6	B	3	Total	C	N	O	0	0
			39	22	2	15		
6	D	3	Total	C	N	O	0	0
			39	22	2	15		
6	B	3	Total	C	N	O	0	0
			39	22	2	15		
6	E	3	Total	C	N	O	0	0
			39	22	2	15		
6	E	3	Total	C	N	O	0	0
			39	22	2	15		

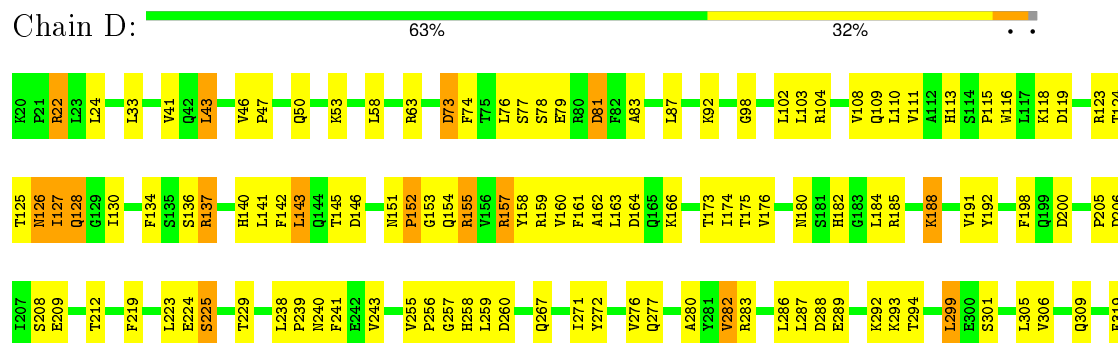
3 Residue-property plots

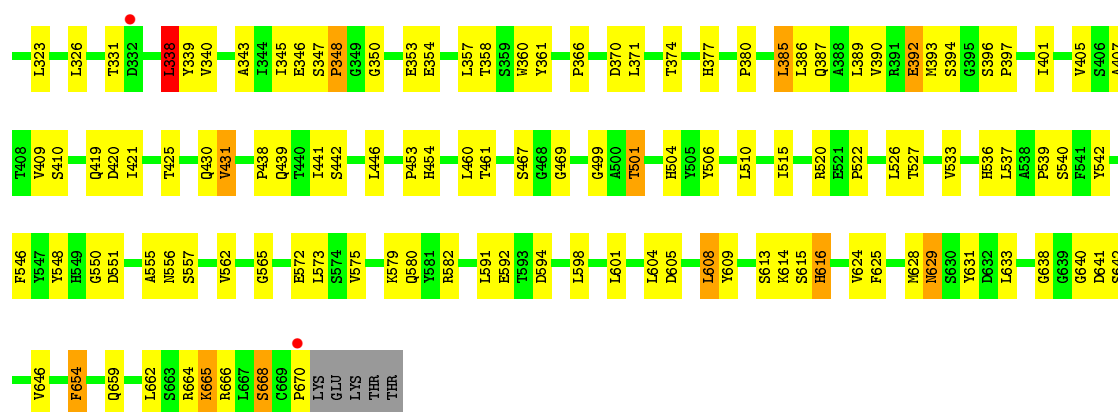
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Complement C4 beta chain

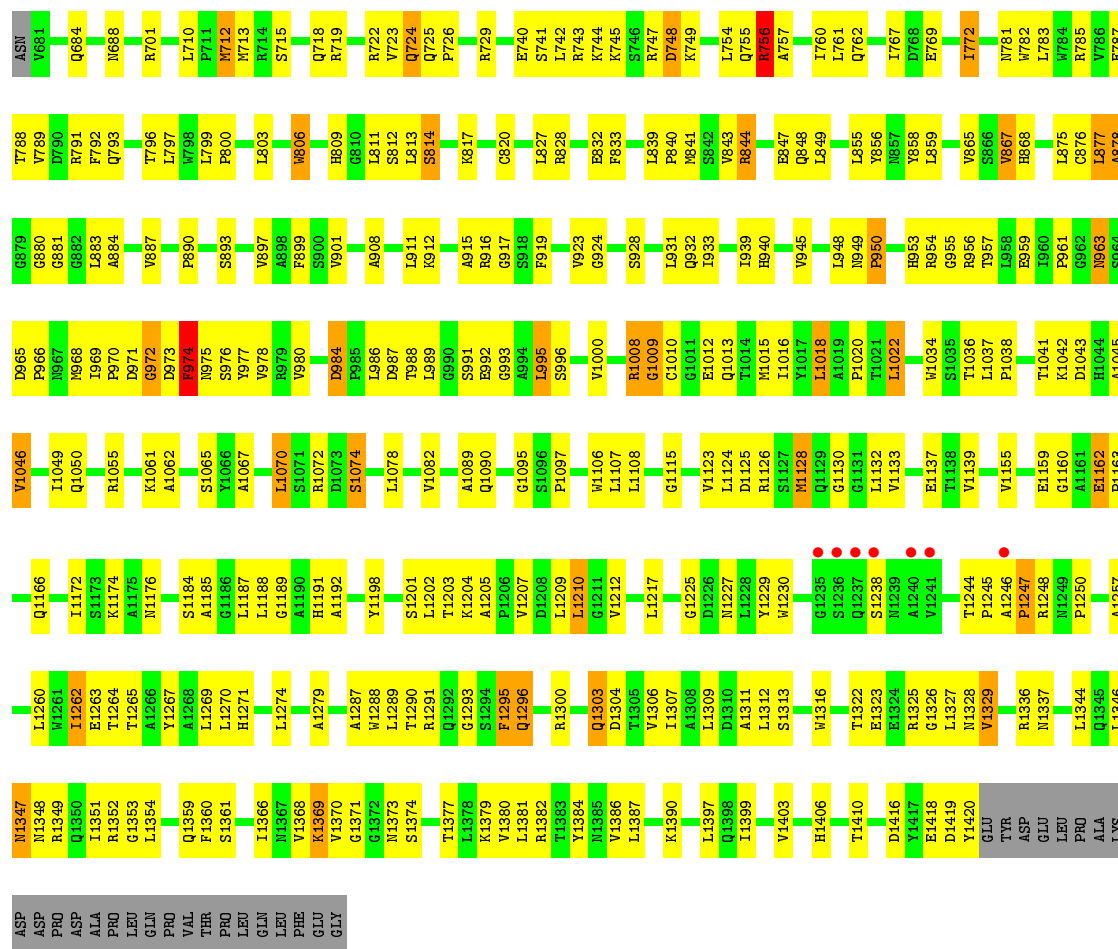


• Molecule 1: Complement C4 beta chain

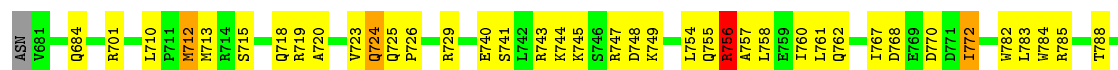


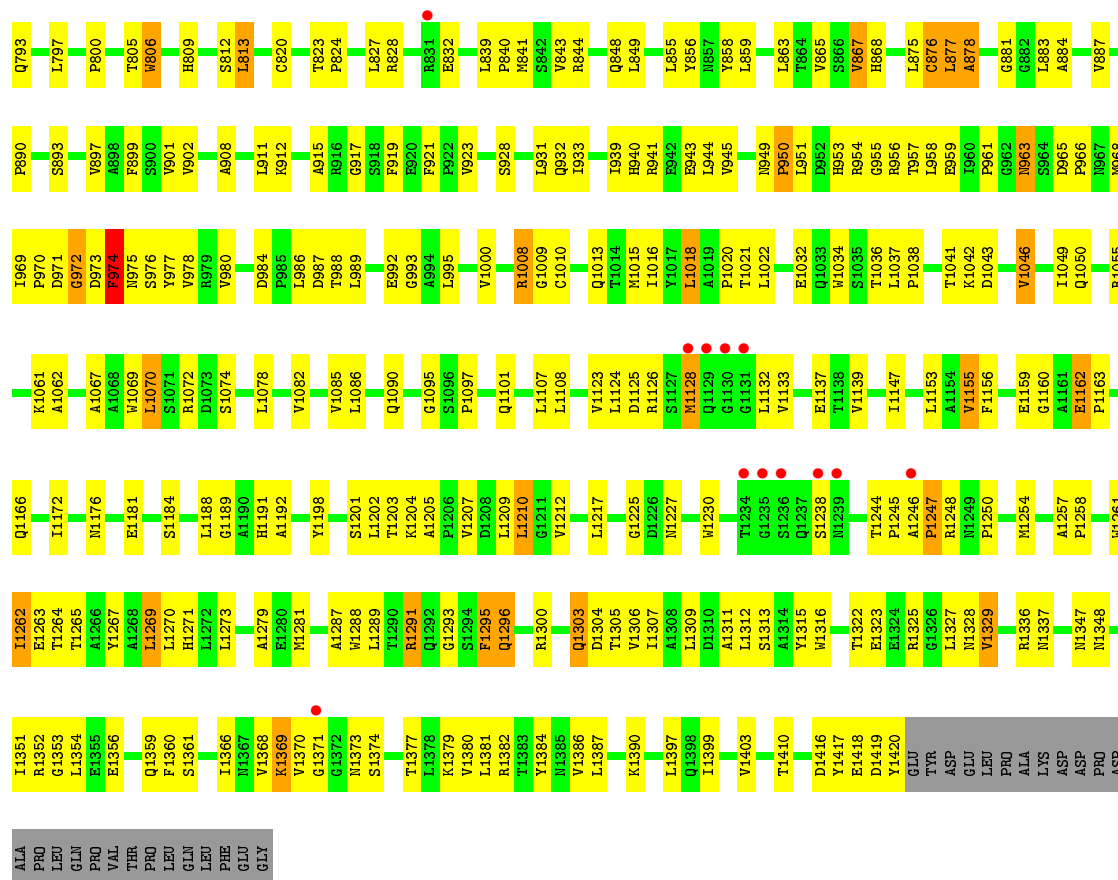


• Molecule 2: Complement C4-A alpha chain



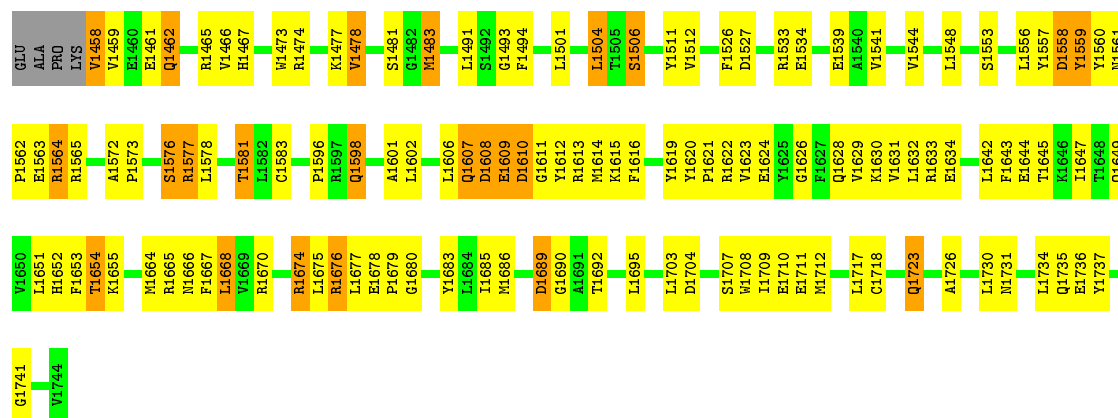
• Molecule 2: Complement C4-A alpha chain





• Molecule 3: Complement C4 gamma chain

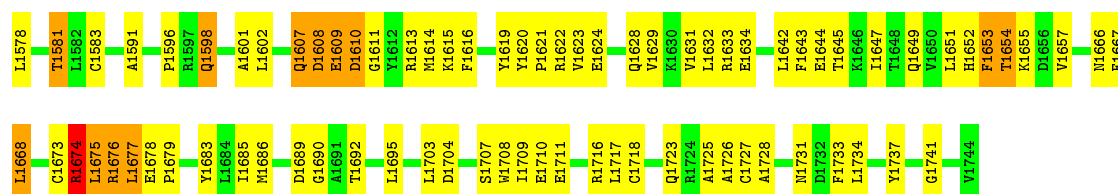
Chain C: 55% 35% 8%



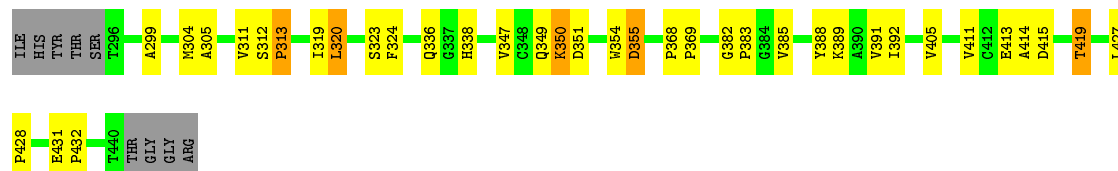
• Molecule 3: Complement C4 gamma chain

Chain F: 59% 31% 8%

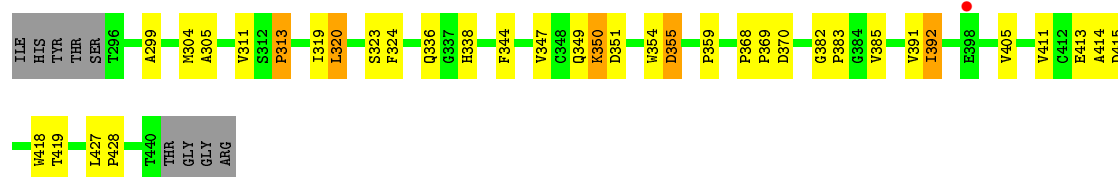




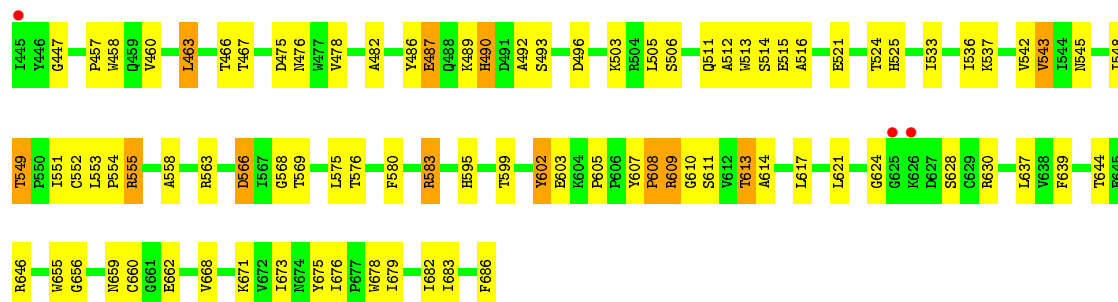
- Molecule 4: Mannan-binding lectin serine protease 2 A chain



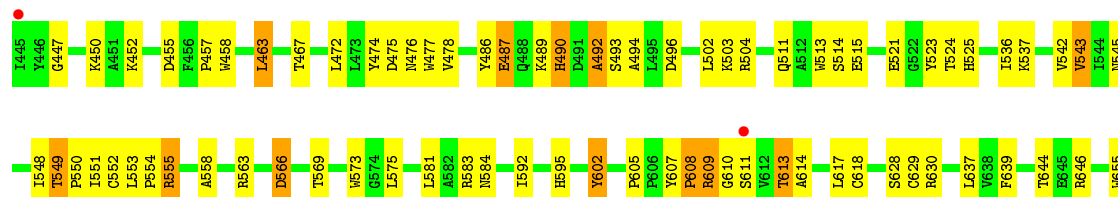
- Molecule 4: Mannan-binding lectin serine protease 2 A chain



- Molecule 5: Mannan-binding lectin serine protease 2 B chain



- Molecule 5: Mannan-binding lectin serine protease 2 B chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	99.01Å 215.01Å 142.86Å 90.00° 110.11° 90.00°	Depositor
Resolution (Å)	48.97 – 3.75 48.97 – 3.75	Depositor EDS
% Data completeness (in resolution range)	98.6 (48.97-3.75) 98.6 (48.97-3.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 3.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.174 , 0.241 0.174 , 0.241	Depositor DCC
R_{free} test set	1726 reflections (3.05%)	DCC
Wilson B-factor (Å ²)	118.2	Xtriage
Anisotropy	0.553	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 66.6	EDS
Estimated twinning fraction	0.083 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 56608 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	32218	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: BMA, NAG, TYS

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	0.31	0/5128	0.58	1/6961 (0.0%)
1	D	0.33	0/5128	0.58	1/6961 (0.0%)
2	B	0.32	0/5799	0.63	3/7875 (0.0%)
2	E	0.32	0/5799	0.61	2/7875 (0.0%)
3	C	0.35	0/2338	0.64	0/3158
3	F	0.35	0/2338	0.64	1/3158 (0.0%)
4	G	0.33	0/1136	0.60	0/1549
4	I	0.34	0/1136	0.60	0/1549
5	H	0.28	0/1916	0.50	0/2604
5	J	0.32	0/1916	0.53	0/2604
All	All	0.32	0/32634	0.60	8/44294 (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	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	756	ARG	NE-CZ-NH2	19.88	130.24	120.30
2	E	756	ARG	NE-CZ-NH2	16.11	128.36	120.30
2	B	756	ARG	NE-CZ-NH1	-9.44	115.58	120.30
2	E	756	ARG	NE-CZ-NH1	-6.74	116.93	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	338	LEU	CA-CB-CG	6.03	129.17	115.30
1	D	338	LEU	CA-CB-CG	5.50	127.94	115.30
3	F	1675	LEU	CA-CB-CG	-5.27	103.18	115.30
2	B	756	ARG	CD-NE-CZ	-5.15	116.39	123.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	225	SER	Peptide
1	D	225	SER	Peptide

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	5012	0	5025	140	0
1	D	5012	0	5025	140	0
2	B	5718	0	5645	220	0
2	E	5718	0	5645	217	0
3	C	2291	0	2228	90	0
3	F	2291	0	2228	81	0
4	G	1103	0	1051	20	0
4	I	1103	0	1051	18	0
5	H	1868	0	1803	62	0
5	J	1868	0	1803	61	0
6	A	39	0	34	0	0
6	B	78	0	68	2	0
6	D	39	0	34	0	0
6	E	78	0	68	2	0
All	All	32218	0	31708	984	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 15.

All (984) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:756:ARG:HG2	5:J:655:TRP:HA	1.40	1.01
2:E:756:ARG:HG2	5:H:655:TRP:HA	1.56	0.87
3:C:1631:VAL:HA	3:C:1645:THR:HG22	1.54	0.86
1:D:143:LEU:HB3	1:D:160:VAL:HG23	1.56	0.86
2:E:848:GLN:HE21	3:F:1548:LEU:HD22	1.43	0.83
2:B:978:VAL:HG13	2:B:1360:PHE:HA	1.61	0.82
1:A:143:LEU:HB3	1:A:160:VAL:HG23	1.60	0.82
2:E:978:VAL:HG13	2:E:1360:PHE:HA	1.61	0.80
1:A:205:PRO:HG2	1:A:208:SER:HB2	1.63	0.79
2:E:710:LEU:HD22	2:E:719:ARG:HE	1.47	0.79
3:C:1598:GLN:HG3	3:C:1676:ARG:HD2	1.65	0.78
2:E:715:SER:HB2	2:E:718:GLN:HB3	1.65	0.77
1:A:370:ASP:HB3	1:A:389:LEU:HB3	1.66	0.76
2:B:848:GLN:HE21	3:C:1548:LEU:HD22	1.52	0.75
2:B:715:SER:HB2	2:B:718:GLN:HB3	1.68	0.75
3:F:1629:VAL:HG12	3:F:1647:ILE:HA	1.67	0.75
3:F:1598:GLN:HG3	3:F:1676:ARG:HD2	1.70	0.74
1:D:573:LEU:HD22	1:D:591:LEU:HD22	1.69	0.74
2:B:945:VAL:HG12	2:B:1379:LYS:HG2	1.70	0.73
2:E:1325:ARG:HG2	2:E:1374:SER:HB3	1.69	0.73
5:H:457:PRO:HB2	5:H:549:THR:H	1.54	0.73
2:B:1325:ARG:HG2	2:B:1374:SER:HB3	1.70	0.72
2:B:1416:ASP:O	2:B:1418:GLU:N	2.23	0.72
2:E:726:PRO:HA	2:E:729:ARG:HB3	1.72	0.72
2:B:710:LEU:HD21	3:C:1511:TYR:HE2	1.55	0.72
1:D:572:GLU:HB3	1:D:592:GLU:HB2	1.72	0.71
3:F:1461:GLU:HG2	3:F:1462:GLN:HG3	1.72	0.71
3:C:1629:VAL:HG12	3:C:1647:ILE:HA	1.72	0.71
2:E:1295:PHE:HD2	2:E:1381:LEU:HB3	1.54	0.71
2:B:949:ASN:HD22	2:B:955:GLY:HA3	1.55	0.71
2:E:887:VAL:HG21	2:E:897:VAL:HG22	1.72	0.71
1:D:605:ASP:HA	2:E:806:TRP:HB3	1.73	0.71
2:E:1416:ASP:O	2:E:1418:GLU:N	2.24	0.71
5:J:457:PRO:HB2	5:J:549:THR:H	1.55	0.71
3:C:1642:LEU:HD13	3:C:1668:LEU:HD23	1.72	0.71
3:F:1631:VAL:HA	3:F:1645:THR:HG22	1.72	0.71
1:D:357:LEU:HG	2:E:772:ILE:HG12	1.74	0.70
3:F:1642:LEU:HD11	3:F:1666:ASN:HB3	1.72	0.70
3:C:1634:GLU:HB2	3:C:1643:PHE:HD1	1.57	0.70
1:A:572:GLU:HB3	1:A:592:GLU:HB2	1.73	0.69
5:J:602:TYR:HE1	5:J:668:VAL:HG22	1.58	0.69
2:B:989:LEU:HD11	2:B:1351:ILE:H	1.58	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:LEU:HD23	1:A:130:ILE:HD11	1.75	0.69
1:A:136:SER:HB2	1:A:224:GLU:HG2	1.75	0.69
2:B:1008:ARG:HD3	2:B:1016:ILE:HG21	1.75	0.69
1:A:58:LEU:HG	1:A:87:LEU:HD21	1.74	0.69
1:D:58:LEU:HG	1:D:87:LEU:HD21	1.75	0.68
4:I:305:ALA:HB2	4:I:311:VAL:HG23	1.75	0.68
1:A:357:LEU:HG	2:B:772:ILE:HG12	1.75	0.68
2:E:840:PRO:HB3	3:F:1493:GLY:HA2	1.73	0.68
2:E:976:SER:H	2:E:1336:ARG:HH22	1.41	0.68
1:A:573:LEU:HD22	1:A:591:LEU:HD22	1.73	0.68
2:B:1128:MET:HE1	2:B:1192:ALA:H	1.59	0.68
3:F:1642:LEU:HD13	3:F:1668:LEU:HD23	1.76	0.68
2:B:1126:ARG:NH1	2:B:1263:GLU:OE1	2.27	0.68
2:B:710:LEU:HD22	2:B:719:ARG:HE	1.58	0.67
2:B:1295:PHE:HD2	2:B:1381:LEU:HB3	1.59	0.67
1:A:293:LYS:HZ3	1:A:340:VAL:HG21	1.59	0.67
3:F:1609:GLU:O	3:F:1611:GLY:N	2.27	0.67
1:D:205:PRO:HG2	1:D:208:SER:HB3	1.76	0.67
2:B:1174:LYS:HA	1:D:123:ARG:HH12	1.58	0.67
5:H:671:LYS:HE2	5:H:673:ILE:HD11	1.77	0.67
3:C:1609:GLU:O	3:C:1611:GLY:N	2.28	0.67
1:D:136:SER:HB2	1:D:224:GLU:HG2	1.76	0.67
2:B:755:GLN:C	2:B:756:ARG:HD3	2.14	0.67
1:D:409:VAL:HG12	1:D:441:ILE:HD13	1.77	0.66
5:J:671:LYS:HE2	5:J:673:ILE:HD11	1.78	0.66
1:D:370:ASP:HB3	1:D:389:LEU:HB3	1.76	0.66
2:E:832:GLU:HB3	2:E:859:LEU:HD13	1.75	0.66
2:B:783:LEU:HD12	2:B:797:LEU:HD12	1.78	0.66
3:C:1461:GLU:HG2	3:C:1462:GLN:HG3	1.76	0.66
2:B:726:PRO:HA	2:B:729:ARG:HB3	1.75	0.66
2:B:684:GLN:HE22	2:B:767:ILE:H	1.43	0.66
1:A:605:ASP:HA	2:B:806:TRP:HB3	1.76	0.66
2:B:976:SER:H	2:B:1336:ARG:HH22	1.44	0.66
4:I:313:PRO:HG2	4:I:324:PHE:HA	1.78	0.65
1:A:47:PRO:HG2	1:A:50:GLN:HB2	1.77	0.65
3:C:1642:LEU:HD11	3:C:1666:ASN:HB3	1.78	0.65
2:B:887:VAL:HG21	2:B:897:VAL:HG22	1.76	0.65
2:E:945:VAL:HG12	2:E:1379:LYS:HG2	1.77	0.65
2:E:710:LEU:HD13	2:E:719:ARG:HH21	1.62	0.65
2:E:1124:LEU:HD21	2:E:1303:GLN:HG3	1.78	0.65
3:C:1620:TYR:HB3	3:C:1621:PRO:HD3	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:992:GLU:HG3	2:B:1037:LEU:HD13	1.79	0.65
2:E:710:LEU:HD21	3:F:1511:TYR:HE2	1.61	0.64
3:C:1651:LEU:H	3:C:1651:LEU:HD12	1.62	0.64
2:B:950:PRO:HG3	2:B:1370:VAL:HG11	1.79	0.64
2:E:950:PRO:HG3	2:E:1370:VAL:HG11	1.79	0.64
3:C:1596:PRO:HD3	3:C:1704:ASP:HA	1.79	0.64
2:B:908:ALA:HB1	2:B:932:GLN:HA	1.80	0.64
5:J:554:PRO:HD2	5:J:676:ILE:HD11	1.78	0.64
2:E:961:PRO:HG2	2:E:1366:ILE:HD12	1.79	0.64
1:D:81:ASP:HB2	1:D:520:ARG:HE	1.62	0.64
4:G:305:ALA:HB2	4:G:311:VAL:HG23	1.79	0.64
3:F:1616:PHE:HA	3:F:1621:PRO:HD2	1.79	0.63
1:D:604:LEU:HD22	1:D:608:LEU:HD11	1.78	0.63
3:F:1704:ASP:N	3:F:1704:ASP:OD1	2.31	0.63
2:E:1328:ASN:H	2:E:1371:GLY:H	1.46	0.63
2:B:832:GLU:HB3	2:B:859:LEU:HD13	1.79	0.63
1:D:110:LEU:HD23	1:D:130:ILE:HD11	1.81	0.63
1:A:604:LEU:HD22	1:A:608:LEU:HD11	1.80	0.62
2:E:1207:VAL:HA	2:E:1210:LEU:HB2	1.81	0.62
2:E:684:GLN:HE22	2:E:767:ILE:H	1.46	0.62
2:B:840:PRO:HB3	3:C:1493:GLY:HA2	1.80	0.62
1:A:425:THR:HA	1:A:431:VAL:HG23	1.80	0.62
1:D:504:HIS:ND1	1:D:522:PRO:HA	2.14	0.62
2:B:1187:LEU:N	1:D:662:LEU:HD21	2.13	0.62
3:C:1601:ALA:HB2	3:C:1711:GLU:HG3	1.82	0.62
3:C:1613:ARG:NH1	3:C:1710:GLU:OE1	2.28	0.62
1:D:419:GLN:HE21	1:D:421:ILE:HD11	1.65	0.62
2:B:1328:ASN:H	2:B:1371:GLY:H	1.47	0.62
5:J:463:LEU:HD12	5:J:467:THR:HG22	1.82	0.62
5:J:602:TYR:HE1	5:J:668:VAL:CG2	2.13	0.62
2:B:912:LYS:HD2	2:B:928:SER:HB2	1.82	0.62
2:B:1203:THR:O	2:B:1205:ALA:N	2.33	0.62
2:E:949:ASN:HD22	2:E:955:GLY:HA3	1.64	0.61
1:A:504:HIS:CD2	1:A:520:ARG:HD2	2.35	0.61
1:A:173:THR:HG22	1:A:192:TYR:HA	1.81	0.61
2:B:812:SER:HB3	2:B:820:CYS:HB3	1.82	0.61
2:E:839:LEU:HA	3:F:1544:VAL:HG21	1.82	0.61
2:E:1203:THR:O	2:E:1205:ALA:N	2.33	0.61
5:H:463:LEU:HD12	5:H:467:THR:HG22	1.81	0.61
2:E:1295:PHE:CD2	2:E:1381:LEU:HB3	2.35	0.61
3:C:1616:PHE:HA	3:C:1621:PRO:HD2	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:425:THR:HA	1:D:431:VAL:HG23	1.83	0.61
1:D:47:PRO:HG2	1:D:50:GLN:HB2	1.82	0.61
2:E:1090:GLN:NE2	2:E:1095:GLY:O	2.32	0.61
1:A:640:GLY:HA3	1:A:646:VAL:HG23	1.82	0.61
1:A:575:VAL:HB	1:A:579:LYS:HG2	1.83	0.61
4:G:313:PRO:HG2	4:G:324:PHE:HA	1.82	0.61
3:F:1651:LEU:H	3:F:1651:LEU:HD12	1.65	0.61
2:B:992:GLU:OE1	2:B:1352:ARG:NH2	2.33	0.61
2:E:972:GLY:HA2	2:E:1387:LEU:HD23	1.82	0.60
3:F:1634:GLU:HB2	3:F:1643:PHE:HD1	1.66	0.60
2:B:972:GLY:HA2	2:B:1387:LEU:HD23	1.82	0.60
1:A:116:TRP:HA	1:A:119:ASP:HB3	1.83	0.60
2:E:992:GLU:OE1	2:E:1352:ARG:NH2	2.33	0.60
2:E:1265:THR:HG21	2:E:1288:TRP:CZ3	2.36	0.60
1:A:155:ARG:NE	1:A:157:ARG:HD2	2.16	0.60
2:B:1139:VAL:HG11	2:B:1188:LEU:HD21	1.83	0.60
2:B:1191:HIS:HA	2:B:1264:THR:HG23	1.84	0.60
4:I:413:GLU:HG3	4:I:414:ALA:H	1.67	0.60
3:F:1613:ARG:NH1	3:F:1710:GLU:OE1	2.28	0.60
3:C:1624:GLU:HB3	3:C:1654:THR:HG21	1.83	0.60
2:E:989:LEU:HD11	2:E:1351:ILE:H	1.65	0.60
3:F:1596:PRO:HD3	3:F:1704:ASP:HA	1.84	0.60
1:D:640:GLY:HA3	1:D:646:VAL:HG23	1.84	0.60
2:E:980:VAL:HG22	2:E:1380:VAL:HG12	1.84	0.60
1:D:116:TRP:HA	1:D:119:ASP:HB3	1.84	0.60
5:J:537:LYS:NZ	5:J:686:PHE:OXT	2.33	0.60
2:B:755:GLN:O	2:B:756:ARG:HD3	2.02	0.59
2:B:1128:MET:HG2	2:B:1189:GLY:HA3	1.84	0.59
2:B:992:GLU:O	2:B:1352:ARG:NH2	2.36	0.59
2:B:961:PRO:HG2	2:B:1366:ILE:HD12	1.85	0.59
5:H:602:TYR:CE2	5:H:655:TRP:CZ3	2.91	0.59
2:B:993:GLY:HA2	2:B:1352:ARG:NH1	2.18	0.59
2:E:992:GLU:O	2:E:1352:ARG:NH2	2.36	0.59
2:E:1419:ASP:O	2:E:1420:TYS:HB3	2.01	0.59
4:G:391:VAL:HG22	4:G:411:VAL:HG23	1.83	0.59
2:B:1209:LEU:HA	2:B:1212:VAL:HG12	1.85	0.59
3:C:1704:ASP:N	3:C:1704:ASP:OD1	2.34	0.58
1:D:556:ASN:HA	1:D:646:VAL:HG21	1.84	0.58
1:A:661:THR:O	1:A:661:THR:OG1	2.21	0.58
1:D:143:LEU:HD11	1:D:229:THR:H	1.68	0.58
2:E:908:ALA:HB1	2:E:932:GLN:HA	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1008:ARG:HD3	2:E:1016:ILE:HG21	1.83	0.58
2:B:1265:THR:HG21	2:B:1288:TRP:CZ3	2.39	0.58
2:E:986:LEU:HD21	2:E:1377:THR:HB	1.85	0.58
2:B:865:VAL:HG11	2:B:915:ALA:HB1	1.86	0.58
2:E:1097:PRO:HB3	2:E:1155:VAL:HG22	1.86	0.58
2:E:993:GLY:HA2	2:E:1352:ARG:NH1	2.17	0.58
1:D:151:ASN:O	1:D:153:GLY:N	2.37	0.58
2:E:755:GLN:C	2:E:756:ARG:HD3	2.23	0.58
2:B:1329:VAL:HG23	2:B:1368:VAL:HA	1.85	0.58
2:B:1009:GLY:O	2:B:1055:ARG:NH2	2.37	0.58
2:E:1128:MET:HG2	2:E:1189:GLY:HA3	1.86	0.58
2:E:963:ASN:N	2:E:963:ASN:OD1	2.36	0.58
1:A:504:HIS:ND1	1:A:522:PRO:HA	2.18	0.58
2:E:1009:GLY:O	2:E:1055:ARG:NH2	2.37	0.57
3:F:1628:GLN:HB3	3:F:1649:GLN:HB2	1.85	0.57
2:B:1097:PRO:HB3	2:B:1155:VAL:HG22	1.86	0.57
2:B:980:VAL:HG22	2:B:1380:VAL:HG12	1.86	0.57
2:E:754:LEU:HD22	5:H:607:TYR:HD1	1.69	0.57
2:B:1090:GLN:NE2	2:B:1095:GLY:O	2.33	0.57
2:B:1419:ASP:O	2:B:1420:TYR:HB3	2.03	0.57
1:A:664:ARG:HG3	1:A:665:LYS:H	1.69	0.57
4:G:299:ALA:HA	4:G:319:ILE:HG12	1.85	0.57
2:B:1130:GLY:HA3	1:D:104:ARG:CZ	2.34	0.57
5:H:555:ARG:HG2	5:H:558:ALA:HB2	1.86	0.57
5:H:496:ASP:OD1	5:H:511:GLN:NE2	2.37	0.57
2:B:710:LEU:HD21	3:C:1511:TYR:CE2	2.38	0.57
1:A:633:LEU:HB3	1:A:664:ARG:NH2	2.19	0.57
2:B:1207:VAL:HA	2:B:1210:LEU:HB2	1.85	0.57
3:C:1474:ARG:NH1	3:C:1481:SER:HB3	2.20	0.57
3:C:1628:GLN:HB3	3:C:1649:GLN:HB2	1.86	0.57
1:A:409:VAL:HG12	1:A:441:ILE:HD13	1.86	0.57
1:D:255:VAL:O	1:D:257:GLY:N	2.36	0.57
5:H:595:HIS:NE2	5:H:613:THR:O	2.37	0.57
1:D:280:ALA:HB2	1:D:305:LEU:HD21	1.87	0.57
3:F:1655:LYS:NZ	3:F:1690:GLY:O	2.37	0.57
2:B:1227:ASN:OD1	2:B:1291:ARG:NH1	2.37	0.57
1:A:142:PHE:HB2	1:A:161:PHE:HB2	1.87	0.57
2:E:1078:LEU:O	2:E:1082:VAL:HG23	2.04	0.57
2:E:1128:MET:HE1	2:E:1192:ALA:H	1.69	0.57
2:E:745:LYS:O	2:E:748:ASP:HB2	2.05	0.57
3:C:1667:PHE:HD2	3:C:1703:LEU:HD21	1.69	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1620:TYR:HB3	3:F:1621:PRO:HD3	1.86	0.56
2:E:1352:ARG:O	2:E:1354:LEU:N	2.34	0.56
2:E:1139:VAL:HG11	2:E:1188:LEU:HD21	1.87	0.56
1:D:575:VAL:HB	1:D:579:LYS:HG2	1.87	0.56
1:D:24:LEU:HD22	1:D:654:PHE:HE2	1.69	0.56
1:A:43:LEU:HD22	1:A:76:LEU:HG	1.88	0.56
1:D:664:ARG:HG3	1:D:665:LYS:H	1.69	0.56
2:B:1172:ILE:O	2:B:1176:ASN:ND2	2.31	0.56
5:H:543:VAL:O	5:H:545:ASN:ND2	2.39	0.56
4:I:313:PRO:HD2	4:I:324:PHE:HB2	1.87	0.56
1:A:539:PRO:HD2	1:A:629:ASN:ND2	2.20	0.56
2:B:782:TRP:CG	2:B:800:PRO:HG2	2.41	0.56
5:J:608:PRO:O	5:J:610:GLY:N	2.37	0.56
1:A:389:LEU:HD13	1:A:430:GLN:HG2	1.87	0.56
1:A:241:PHE:CD2	1:A:276:VAL:HG21	2.41	0.56
2:E:969:ILE:H	2:E:969:ILE:HD12	1.71	0.56
3:C:1655:LYS:NZ	3:C:1690:GLY:O	2.38	0.56
2:E:754:LEU:HB2	5:H:656:GLY:O	2.06	0.56
3:F:1596:PRO:HG2	3:F:1675:LEU:HD13	1.86	0.56
3:F:1474:ARG:NH1	3:F:1481:SER:HB3	2.21	0.56
2:B:969:ILE:HB	2:B:970:PRO:HD3	1.87	0.56
3:C:1624:GLU:O	3:C:1654:THR:HB	2.06	0.55
2:B:917:GLY:HA3	2:B:923:VAL:H	1.69	0.55
1:A:181:SER:O	1:A:182:HIS:ND1	2.38	0.55
1:A:63:ARG:HD2	1:A:98:GLY:HA3	1.89	0.55
2:B:1371:GLY:HA2	6:B:1504:NAG:C7	2.37	0.55
2:E:993:GLY:HA2	2:E:1352:ARG:HH12	1.72	0.55
1:A:271:ILE:HD12	1:A:271:ILE:H	1.72	0.55
2:E:867:VAL:HG21	2:E:897:VAL:HG11	1.88	0.55
1:D:286:LEU:HA	1:D:339:TYR:HB2	1.89	0.55
3:F:1601:ALA:HB2	3:F:1711:GLU:HG3	1.87	0.55
2:B:1352:ARG:O	2:B:1354:LEU:N	2.31	0.55
2:B:1416:ASP:N	2:B:1416:ASP:OD1	2.39	0.55
3:F:1573:PRO:O	3:F:1576:SER:HB3	2.07	0.55
5:H:608:PRO:O	5:H:610:GLY:N	2.36	0.55
3:F:1473:TRP:HB3	3:F:1533:ARG:HA	1.88	0.55
1:A:22:ARG:NH2	1:A:658:ASP:OD2	2.40	0.55
2:E:1191:HIS:HA	2:E:1264:THR:HG23	1.87	0.55
1:A:277:GLN:O	1:A:348:PRO:HD3	2.07	0.55
1:A:255:VAL:O	1:A:257:GLY:N	2.40	0.55
2:B:1078:LEU:O	2:B:1082:VAL:HG23	2.07	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1623:VAL:HG11	3:F:1686:MET:HB2	1.87	0.55
1:A:81:ASP:HB2	1:A:520:ARG:HE	1.72	0.54
4:G:413:GLU:HG3	4:G:414:ALA:H	1.72	0.54
5:J:477:TRP:NE1	5:J:683:ILE:HG23	2.22	0.54
2:B:1202:LEU:HD13	2:B:1274:LEU:HD21	1.89	0.54
2:B:963:ASN:N	2:B:963:ASN:OD1	2.39	0.54
1:D:92:LYS:HD3	1:D:92:LYS:H	1.72	0.54
2:B:1185:ALA:O	1:D:662:LEU:HD22	2.07	0.54
2:B:1034:TRP:CE3	2:B:1042:LYS:HG2	2.43	0.54
5:H:576:THR:HG21	5:H:583:ARG:NH2	2.22	0.54
3:C:1473:TRP:HB3	3:C:1533:ARG:HA	1.89	0.54
2:E:1371:GLY:HA2	6:E:1504:NAG:C7	2.37	0.54
3:C:1686:MET:HG3	3:C:1708:TRP:HB3	1.88	0.54
2:E:760:ILE:HG23	2:E:1410:THR:HG21	1.89	0.54
3:C:1573:PRO:O	3:C:1576:SER:HB3	2.07	0.54
1:A:374:THR:OG1	1:A:387:GLN:O	2.25	0.54
1:D:277:GLN:O	1:D:348:PRO:HD3	2.06	0.54
1:D:271:ILE:HD12	1:D:271:ILE:H	1.72	0.54
5:H:602:TYR:HE2	5:H:655:TRP:CZ3	2.26	0.54
2:B:966:PRO:HD3	2:B:1382:ARG:CZ	2.38	0.54
2:E:710:LEU:HD21	3:F:1511:TYR:CE2	2.40	0.54
3:C:1615:LYS:HA	3:C:1619:TYR:HB2	1.90	0.54
5:H:659:ASN:HB3	5:H:662:GLU:HB2	1.90	0.54
1:A:267:GLN:HG3	1:A:309:GLN:HG3	1.89	0.54
5:J:673:ILE:HA	5:J:676:ILE:HG12	1.88	0.54
2:B:875:LEU:HD23	2:B:901:VAL:HG21	1.89	0.54
1:D:267:GLN:HG3	1:D:309:GLN:HG3	1.90	0.54
2:E:856:TYR:OH	3:F:1458:VAL:O	2.26	0.54
3:C:1614:MET:C	3:C:1616:PHE:H	2.10	0.54
2:B:1265:THR:HG21	2:B:1288:TRP:HZ3	1.73	0.54
2:B:1406:HIS:ND1	3:C:1465:ARG:O	2.32	0.54
2:E:1020:PRO:HD3	2:E:1306:VAL:HG12	1.90	0.54
1:A:109:GLN:NE2	1:A:131:ASN:OD1	2.41	0.54
1:A:151:ASN:O	1:A:153:GLY:N	2.41	0.54
1:A:143:LEU:HD11	1:A:229:THR:H	1.72	0.53
2:E:1416:ASP:OD1	2:E:1416:ASP:N	2.41	0.53
2:B:969:ILE:H	2:B:969:ILE:HD12	1.72	0.53
2:E:812:SER:HB3	2:E:820:CYS:HB3	1.89	0.53
1:D:557:SER:OG	1:D:638:GLY:O	2.26	0.53
1:A:92:LYS:H	1:A:92:LYS:HD3	1.73	0.53
2:B:743:ARG:HG2	2:B:747:ARG:HH12	1.73	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:976:SER:O	2:E:1336:ARG:NH2	2.41	0.53
2:E:1209:LEU:HA	2:E:1212:VAL:HG12	1.89	0.53
2:E:1327:LEU:HB2	2:E:1370:VAL:HG13	1.91	0.53
3:F:1624:GLU:HB3	3:F:1654:THR:HG21	1.90	0.53
1:D:22:ARG:NH1	1:D:551:ASP:HA	2.24	0.53
3:C:1467:HIS:HB2	3:C:1539:GLU:OE1	2.08	0.53
1:D:338:LEU:H	1:D:338:LEU:HD23	1.74	0.53
2:B:976:SER:H	2:B:1336:ARG:NH2	2.06	0.53
3:F:1607:GLN:O	3:F:1609:GLU:N	2.42	0.53
1:A:191:VAL:HG22	1:A:192:TYR:O	2.08	0.53
3:F:1686:MET:HG3	3:F:1708:TRP:HB3	1.89	0.53
5:J:595:HIS:NE2	5:J:613:THR:O	2.40	0.53
2:E:755:GLN:O	2:E:756:ARG:HD3	2.09	0.53
5:H:458:TRP:CG	5:H:551:ILE:HB	2.44	0.53
2:E:1034:TRP:CE3	2:E:1042:LYS:HG2	2.44	0.53
2:B:1327:LEU:HB2	2:B:1370:VAL:HG13	1.91	0.52
2:E:1265:THR:HG21	2:E:1288:TRP:HZ3	1.74	0.52
2:B:971:ASP:O	2:B:973:ASP:N	2.38	0.52
1:A:557:SER:OG	1:A:638:GLY:O	2.26	0.52
2:B:1015:MET:HA	2:B:1018:LEU:HD12	1.92	0.52
5:J:452:LYS:N	5:J:455:ASP:OD2	2.42	0.52
2:E:745:LYS:C	2:E:748:ASP:HB2	2.29	0.52
1:A:603:ALA:O	2:B:781:ASN:ND2	2.41	0.52
2:B:1123:VAL:HG12	2:B:1124:LEU:HD12	1.90	0.52
2:E:1312:LEU:HD22	2:E:1316:TRP:CZ2	2.45	0.52
2:B:968:MET:HE1	2:B:1386:VAL:HG22	1.91	0.52
1:A:33:LEU:HD21	1:A:134:PHE:HB2	1.91	0.52
2:E:782:TRP:CG	2:E:800:PRO:HG2	2.45	0.52
3:F:1615:LYS:HA	3:F:1619:TYR:HB2	1.91	0.52
5:H:486:TYR:CE2	5:H:525:HIS:HB2	2.44	0.52
4:G:382:GLY:O	4:G:385:VAL:HG12	2.09	0.52
2:E:783:LEU:HD12	2:E:797:LEU:HD12	1.89	0.52
2:E:890:PRO:HB2	2:E:893:SER:HB2	1.91	0.52
3:C:1458:VAL:HG12	3:C:1459:VAL:HG23	1.91	0.52
3:C:1623:VAL:HG11	3:C:1686:MET:HB2	1.91	0.52
4:I:391:VAL:HG22	4:I:411:VAL:HG23	1.92	0.52
1:A:187:ARG:NH2	1:A:200:ASP:OD2	2.43	0.52
2:B:1038:PRO:HG2	2:B:1041:THR:HG23	1.92	0.52
2:B:1133:VAL:O	2:B:1137:GLU:HG2	2.10	0.52
5:J:542:VAL:HG11	5:J:548:ILE:HG21	1.92	0.52
2:B:715:SER:CB	2:B:718:GLN:HB3	2.39	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:908:ALA:HA	2:E:933:ILE:HG12	1.92	0.52
1:A:74:PHE:HD2	1:A:76:LEU:HD13	1.75	0.52
2:E:1015:MET:HA	2:E:1018:LEU:HD12	1.90	0.52
2:B:756:ARG:HG2	5:J:655:TRP:CA	2.28	0.51
2:E:965:ASP:HB3	2:E:1360:PHE:O	2.10	0.51
2:B:688:ASN:ND2	2:B:769:GLU:OE2	2.43	0.51
2:E:743:ARG:HG2	2:E:747:ARG:HH12	1.75	0.51
4:I:299:ALA:HA	4:I:319:ILE:HG12	1.92	0.51
2:B:986:LEU:HD21	2:B:1377:THR:HB	1.92	0.51
1:D:123:ARG:HG3	1:D:124:THR:H	1.75	0.51
5:J:611:SER:OG	5:J:611:SER:O	2.29	0.51
2:E:1172:ILE:O	2:E:1176:ASN:ND2	2.38	0.51
4:G:313:PRO:HD2	4:G:324:PHE:HB2	1.92	0.51
1:D:241:PHE:CD2	1:D:276:VAL:HG21	2.46	0.51
3:F:1478:VAL:HG11	3:F:1564:ARG:HH12	1.76	0.51
2:B:722:ARG:NH1	3:C:1534:GLU:OE1	2.44	0.51
2:E:875:LEU:HD23	2:E:901:VAL:HG21	1.93	0.51
2:B:1187:LEU:H	1:D:662:LEU:HD21	1.75	0.51
2:E:969:ILE:HB	2:E:970:PRO:HD3	1.92	0.51
5:J:659:ASN:HB3	5:J:662:GLU:HB2	1.92	0.51
1:D:293:LYS:HZ3	1:D:340:VAL:HG21	1.74	0.51
3:C:1667:PHE:CD2	3:C:1703:LEU:HD21	2.45	0.51
2:B:1399:ILE:HB	3:C:1556:LEU:HB2	1.92	0.51
1:D:289:GLU:N	1:D:289:GLU:OE2	2.43	0.51
3:C:1652:HIS:HB2	3:C:1737:TYR:CE2	2.46	0.51
5:J:555:ARG:HG2	5:J:558:ALA:HB2	1.92	0.51
3:C:1611:GLY:O	3:C:1615:LYS:HG3	2.10	0.51
3:C:1596:PRO:HG2	3:C:1675:LEU:HD13	1.92	0.51
5:H:503:LYS:HB2	5:H:506:SER:HB2	1.92	0.51
1:D:374:THR:OG1	1:D:387:GLN:O	2.27	0.51
1:A:174:ILE:HG22	1:A:219:PHE:HA	1.92	0.51
1:A:592:GLU:OE1	2:B:792:PHE:HB3	2.11	0.51
2:B:855:LEU:HD11	2:B:867:VAL:HG11	1.93	0.51
3:C:1704:ASP:O	3:C:1707:SER:HB2	2.11	0.51
2:B:839:LEU:HA	3:C:1544:VAL:HG21	1.93	0.51
2:E:843:VAL:O	2:E:933:ILE:HA	2.11	0.51
4:G:320:LEU:HD22	4:G:350:LYS:HA	1.92	0.51
2:B:710:LEU:HD13	2:B:719:ARG:HH21	1.76	0.51
5:J:458:TRP:CG	5:J:551:ILE:HB	2.46	0.51
2:B:961:PRO:HG2	2:B:1366:ILE:HB	1.93	0.51
1:D:241:PHE:CE1	1:D:354:GLU:HB2	2.45	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:953:HIS:HA	2:B:956:ARG:HB2	1.93	0.51
1:D:63:ARG:HD2	1:D:98:GLY:HA3	1.92	0.50
2:E:710:LEU:HD22	2:E:719:ARG:NE	2.23	0.50
2:E:1329:VAL:HG23	2:E:1368:VAL:HA	1.93	0.50
2:E:966:PRO:HD3	2:E:1382:ARG:CZ	2.41	0.50
2:E:976:SER:H	2:E:1336:ARG:NH2	2.08	0.50
1:A:159:ARG:NH2	1:A:601:LEU:O	2.33	0.50
5:H:673:ILE:HA	5:H:676:ILE:HG12	1.93	0.50
2:E:1371:GLY:HA2	6:E:1504:NAG:N2	2.25	0.50
5:J:496:ASP:OD1	5:J:511:GLN:NE2	2.44	0.50
2:E:1067:ALA:HB1	2:E:1072:ARG:HB3	1.93	0.50
1:D:389:LEU:HD13	1:D:430:GLN:HG2	1.93	0.50
4:G:323:SER:HB3	4:G:347:VAL:HG23	1.94	0.50
1:D:539:PRO:HD2	1:D:629:ASN:ND2	2.27	0.50
1:A:31:VAL:HB	1:A:37:LEU:HD22	1.92	0.50
1:D:79:GLU:O	1:D:520:ARG:NH2	2.45	0.50
2:E:1198:TYR:CE1	2:E:1270:LEU:HB3	2.47	0.50
1:A:280:ALA:HB2	1:A:305:LEU:HD21	1.94	0.50
2:E:1160:GLY:C	2:E:1163:PRO:HD2	2.32	0.50
5:H:569:THR:O	5:H:637:LEU:HD12	2.12	0.50
2:B:1174:LYS:O	1:D:123:ARG:NH2	2.43	0.50
2:B:1257:ALA:O	2:B:1300:ARG:HD2	2.12	0.50
3:C:1633:ARG:NH1	3:C:1644:GLU:OE2	2.45	0.50
2:E:1227:ASN:OD1	2:E:1291:ARG:NH1	2.45	0.50
2:B:1067:ALA:HB1	2:B:1072:ARG:HB3	1.94	0.50
2:E:917:GLY:HA3	2:E:923:VAL:H	1.75	0.50
2:B:1198:TYR:CE1	2:B:1270:LEU:HB3	2.46	0.50
3:C:1533:ARG:HH21	2:E:1166:GLN:HG3	1.77	0.50
2:B:987:ASP:N	2:B:987:ASP:OD1	2.44	0.50
2:E:1267:TYR:CZ	2:E:1307:ILE:HD13	2.47	0.50
3:C:1559:TYR:HD1	3:C:1560:TYR:H	1.58	0.49
2:B:843:VAL:O	2:B:933:ILE:HA	2.11	0.49
2:E:1269:LEU:HD12	2:E:1311:ALA:HB1	1.93	0.49
2:E:971:ASP:O	2:E:973:ASP:N	2.38	0.49
2:E:1265:THR:HG23	2:E:1289:LEU:HD21	1.93	0.49
3:F:1559:TYR:HD1	3:F:1560:TYR:H	1.58	0.49
5:H:457:PRO:HB2	5:H:549:THR:N	2.26	0.49
3:F:1678:GLU:HG2	3:F:1683:TYR:OH	2.12	0.49
2:E:1133:VAL:O	2:E:1137:GLU:HG2	2.12	0.49
5:J:489:LYS:HG3	5:J:490:HIS:H	1.77	0.49
2:B:1115:GLY:HA3	1:D:123:ARG:NH2	2.26	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1128:MET:SD	2:E:1191:HIS:HB3	2.52	0.49
1:D:118:LYS:HD2	1:D:125:THR:OG1	2.12	0.49
1:D:155:ARG:NE	1:D:157:ARG:HD2	2.26	0.49
1:D:380:PRO:HB3	1:D:439:GLN:HA	1.95	0.49
1:A:319:PHE:CZ	1:A:323:LEU:HD11	2.48	0.49
1:A:140:HIS:HB2	1:A:163:LEU:HB2	1.94	0.49
3:F:1737:TYR:HA	3:F:1741:GLY:HA2	1.94	0.49
1:A:289:GLU:OE2	1:A:289:GLU:N	2.45	0.49
2:B:986:LEU:HD13	2:B:1290:THR:HG21	1.95	0.49
2:B:1217:LEU:O	2:B:1230:TRP:HZ3	1.96	0.49
5:H:602:TYR:CE2	5:H:655:TRP:HZ3	2.30	0.49
2:B:966:PRO:HG2	2:B:1360:PHE:CZ	2.48	0.49
2:B:867:VAL:HG21	2:B:897:VAL:HG11	1.94	0.49
3:F:1602:LEU:HD22	3:F:1726:ALA:HB1	1.93	0.49
1:D:53:LYS:HE3	1:D:115:PRO:HG2	1.95	0.49
5:H:617:LEU:HD22	5:H:671:LYS:HA	1.95	0.49
2:E:1181:GLU:O	2:E:1184:SER:OG	2.26	0.49
3:F:1703:LEU:HD22	3:F:1709:ILE:HD11	1.95	0.49
3:C:1717:LEU:HD11	3:C:1723:GLN:HG2	1.95	0.49
1:A:137:ARG:HG2	1:A:631:TYR:HE1	1.78	0.48
3:C:1608:ASP:O	3:C:1610:ASP:N	2.45	0.48
2:E:1225:GLY:N	2:E:1247:PRO:HB3	2.28	0.48
5:J:617:LEU:HD22	5:J:671:LYS:HA	1.95	0.48
3:F:1704:ASP:O	3:F:1707:SER:HB2	2.13	0.48
3:F:1576:SER:O	3:F:1578:LEU:N	2.46	0.48
3:F:1608:ASP:O	3:F:1610:ASP:N	2.46	0.48
2:E:1123:VAL:HG12	2:E:1124:LEU:HD12	1.96	0.48
3:F:1652:HIS:HB2	3:F:1737:TYR:CE2	2.48	0.48
5:H:553:LEU:HD11	5:H:679:ILE:HG21	1.96	0.48
1:D:126:ASN:O	1:D:128:GLN:N	2.46	0.48
1:A:286:LEU:HA	1:A:339:TYR:HB2	1.96	0.48
5:J:644:THR:O	5:J:646:ARG:HG2	2.13	0.48
2:E:741:SER:HB3	2:E:745:LYS:NZ	2.29	0.48
2:E:745:LYS:HA	2:E:748:ASP:HB2	1.95	0.48
3:F:1458:VAL:HG12	3:F:1459:VAL:HG23	1.96	0.48
3:C:1602:LEU:HD22	3:C:1726:ALA:HB1	1.96	0.48
5:H:489:LYS:HG3	5:H:490:HIS:H	1.78	0.48
5:J:553:LEU:HD11	5:J:679:ILE:HG21	1.95	0.48
1:D:338:LEU:HD22	1:D:361:TYR:CE2	2.48	0.48
5:J:475:ASP:O	5:J:542:VAL:HG23	2.13	0.48
3:C:1466:VAL:HG13	3:C:1494:PHE:HE2	1.78	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:855:LEU:HD11	2:E:867:VAL:HG11	1.95	0.48
1:A:123:ARG:HG3	1:A:124:THR:H	1.78	0.48
1:A:370:ASP:O	1:A:371:LEU:HD23	2.13	0.48
1:A:151:ASN:O	1:A:154:GLN:HG3	2.14	0.48
5:J:521:GLU:H	5:J:521:GLU:CD	2.16	0.48
3:F:1624:GLU:O	3:F:1654:THR:HB	2.13	0.48
2:B:1225:GLY:N	2:B:1247:PRO:HB3	2.29	0.48
1:D:613:SER:C	1:D:615:SER:H	2.17	0.48
1:D:565:GLY:HA3	1:D:625:PHE:HE2	1.78	0.48
5:J:457:PRO:HB2	5:J:549:THR:N	2.26	0.48
2:E:1368:VAL:HG12	2:E:1370:VAL:HG22	1.95	0.48
2:B:908:ALA:CB	2:B:932:GLN:HA	2.44	0.48
1:D:140:HIS:HB2	1:D:163:LEU:HB2	1.96	0.48
3:C:1678:GLU:HG2	3:C:1683:TYR:OH	2.14	0.48
2:B:968:MET:HE2	2:B:1384:TYR:CE1	2.49	0.47
2:B:1128:MET:SD	2:B:1191:HIS:HB3	2.54	0.47
2:B:1371:GLY:HA2	6:B:1504:NAG:N2	2.29	0.47
1:A:255:VAL:HG21	1:A:454:HIS:ND1	2.29	0.47
1:D:410:SER:O	1:D:442:SER:N	2.44	0.47
5:H:644:THR:O	5:H:646:ARG:HG2	2.13	0.47
2:B:741:SER:HB3	2:B:745:LYS:HE3	1.97	0.47
2:B:1354:LEU:HA	2:B:1354:LEU:HD13	1.68	0.47
2:E:941:ARG:NH2	2:E:943:GLU:OE1	2.47	0.47
1:D:510:LEU:HB2	1:D:542:TYR:HB2	1.96	0.47
1:A:293:LYS:HZ1	1:A:340:VAL:HG11	1.79	0.47
5:J:595:HIS:HE2	5:J:614:ALA:HA	1.79	0.47
2:E:1399:ILE:HB	3:F:1556:LEU:HB2	1.95	0.47
1:A:580:GLN:HG3	2:B:828:ARG:HB3	1.96	0.47
2:B:974:PHE:HB3	2:B:975:ASN:H	1.57	0.47
2:E:953:HIS:HA	2:E:956:ARG:HB2	1.97	0.47
5:H:475:ASP:O	5:H:542:VAL:HG23	2.15	0.47
5:J:655:TRP:CE3	5:J:668:VAL:HG21	2.49	0.47
2:B:965:ASP:HB3	2:B:1360:PHE:O	2.14	0.47
5:H:458:TRP:CE3	5:H:551:ILE:HD13	2.49	0.47
1:D:293:LYS:HZ1	1:D:340:VAL:HG11	1.80	0.47
5:J:563:ARG:O	5:J:566:ASP:HB2	2.14	0.47
1:A:613:SER:C	1:A:615:SER:H	2.18	0.47
1:A:565:GLY:HA3	1:A:625:PHE:HE2	1.79	0.47
1:A:24:LEU:HD22	1:A:654:PHE:HE2	1.79	0.47
2:B:939:ILE:HG22	2:B:940:HIS:H	1.79	0.47
1:A:390:VAL:HG11	1:A:401:ILE:HG21	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:33:LEU:HD21	1:D:134:PHE:HB2	1.97	0.47
2:B:741:SER:HB3	2:B:745:LYS:NZ	2.30	0.47
1:D:390:VAL:HG11	1:D:401:ILE:HG21	1.96	0.47
1:D:74:PHE:HD2	1:D:76:LEU:HD13	1.80	0.47
1:D:272:TYR:HA	2:E:858:TYR:CE2	2.50	0.47
2:B:1022:LEU:HD21	2:B:1089:ALA:HB2	1.96	0.47
2:E:848:GLN:HG2	3:F:1548:LEU:HD22	1.97	0.47
2:E:1090:GLN:HE22	2:E:1095:GLY:C	2.18	0.47
2:B:1265:THR:HG23	2:B:1289:LEU:HD21	1.97	0.47
2:B:974:PHE:HE2	3:C:1670:ARG:HH22	1.61	0.47
1:D:206:ASP:OD1	1:D:206:ASP:N	2.46	0.47
2:B:811:LEU:HA	2:B:811:LEU:HD23	1.72	0.47
2:B:916:ARG:HA	2:B:924:GLY:HA2	1.97	0.47
2:E:992:GLU:HG3	2:E:1037:LEU:HD13	1.97	0.47
1:A:198:PHE:CZ	1:A:200:ASP:HB2	2.50	0.47
4:I:320:LEU:HD22	4:I:350:LYS:HA	1.97	0.47
1:A:206:ASP:N	1:A:206:ASP:OD1	2.45	0.47
1:A:546:PHE:HB3	1:A:555:ALA:HB2	1.96	0.47
3:F:1614:MET:C	3:F:1616:PHE:H	2.16	0.46
2:E:1207:VAL:HG22	5:J:503:LYS:HE2	1.96	0.46
1:A:79:GLU:O	1:A:520:ARG:NH2	2.48	0.46
1:A:556:ASN:HA	1:A:646:VAL:HG21	1.97	0.46
4:I:413:GLU:HG3	4:I:414:ALA:N	2.27	0.46
1:A:633:LEU:HB3	1:A:664:ARG:HH21	1.80	0.46
5:J:592:ILE:HD11	5:J:639:PHE:CZ	2.51	0.46
3:C:1616:PHE:CD2	3:C:1621:PRO:HG2	2.50	0.46
1:D:104:ARG:HA	1:D:104:ARG:HD2	1.62	0.46
2:B:856:TYR:OH	3:C:1458:VAL:O	2.33	0.46
1:D:504:HIS:CD2	1:D:520:ARG:HD2	2.50	0.46
1:D:102:LEU:C	1:D:104:ARG:H	2.17	0.46
1:A:239:PRO:HB3	1:A:354:GLU:CD	2.36	0.46
1:D:613:SER:OG	1:D:615:SER:O	2.34	0.46
5:H:537:LYS:NZ	5:H:686:PHE:OXT	2.41	0.46
1:D:633:LEU:HB3	1:D:664:ARG:NH2	2.31	0.46
1:D:460:LEU:HD12	1:D:461:THR:H	1.80	0.46
1:D:546:PHE:HB3	1:D:555:ALA:HB2	1.96	0.46
1:D:255:VAL:HG21	1:D:454:HIS:ND1	2.30	0.46
1:A:377:HIS:CE1	1:A:641:ASP:HA	2.50	0.46
1:A:392:GLU:OE1	1:A:397:PRO:HD3	2.16	0.46
2:B:993:GLY:HA2	2:B:1352:ARG:HH12	1.78	0.46
2:B:1287:ALA:O	2:B:1291:ARG:HD3	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:743:ARG:HG2	2:B:747:ARG:NH1	2.31	0.46
2:E:1270:LEU:HD21	2:E:1311:ALA:HA	1.98	0.46
5:H:542:VAL:HG11	5:H:548:ILE:HG21	1.98	0.46
1:D:173:THR:HG22	1:D:192:TYR:HA	1.97	0.46
3:C:1483:MET:HA	3:C:1526:PHE:O	2.16	0.46
1:D:108:VAL:HG22	1:D:109:GLN:H	1.80	0.46
1:D:499:GLY:O	1:D:501:THR:HG22	2.16	0.46
1:D:41:VAL:HG23	1:D:83:ALA:HB3	1.98	0.46
2:E:1038:PRO:HG2	2:E:1041:THR:HG23	1.97	0.46
1:A:594:ASP:N	1:A:594:ASP:OD1	2.48	0.46
1:A:338:LEU:H	1:A:338:LEU:HD23	1.81	0.46
3:C:1558:ASP:HB3	3:C:1561:ASN:HB2	1.98	0.46
2:B:1295:PHE:CD2	2:B:1381:LEU:HB3	2.44	0.46
2:E:944:LEU:HB2	2:E:1380:VAL:HG23	1.98	0.46
1:D:385:LEU:HD12	1:D:387:GLN:HG3	1.98	0.46
4:I:323:SER:HB3	4:I:347:VAL:HG23	1.98	0.46
5:J:607:TYR:O	5:J:609:ARG:N	2.48	0.46
4:I:427:LEU:HD23	4:I:428:PRO:HD2	1.98	0.46
3:F:1651:LEU:HD21	3:F:1734:LEU:HD22	1.98	0.46
3:F:1717:LEU:HD11	3:F:1723:GLN:HG2	1.98	0.46
1:D:624:VAL:O	1:D:628:MET:HG3	2.16	0.46
2:E:1262:ILE:H	2:E:1262:ILE:HG12	1.58	0.46
5:H:458:TRP:CD2	5:H:551:ILE:HD13	2.50	0.46
5:J:595:HIS:NE2	5:J:614:ALA:HA	2.30	0.46
2:B:1217:LEU:HG	2:B:1230:TRP:CZ3	2.50	0.46
5:J:478:VAL:HB	5:J:536:ILE:HB	1.98	0.46
3:F:1653:PHE:CD2	3:F:1657:VAL:HA	2.51	0.46
5:J:504:ARG:HB2	5:J:573:TRP:CD1	2.51	0.46
1:D:22:ARG:HH12	1:D:551:ASP:HA	1.81	0.46
2:E:768:ASP:OD2	2:E:770:ASP:HB2	2.16	0.46
2:E:968:MET:HE1	2:E:1386:VAL:HG22	1.98	0.46
2:E:1337:ASN:OD1	2:E:1359:GLN:NE2	2.49	0.46
2:B:908:ALA:HA	2:B:933:ILE:HG12	1.98	0.45
1:D:287:LEU:HB3	1:D:288:ASP:H	1.46	0.45
1:A:510:LEU:HB2	1:A:542:TYR:HB2	1.98	0.45
2:E:878:ALA:HB1	2:E:883:LEU:HD23	1.98	0.45
2:B:848:GLN:HG2	3:C:1548:LEU:HD22	1.96	0.45
1:D:123:ARG:HB3	1:D:127:ILE:HD13	1.98	0.45
2:B:968:MET:SD	2:B:970:PRO:HD2	2.56	0.45
1:A:108:VAL:HG22	1:A:109:GLN:H	1.81	0.45
3:F:1667:PHE:CE2	3:F:1685:ILE:HG21	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:712:MET:SD	2:E:712:MET:N	2.89	0.45
2:B:1095:GLY:O	2:B:1097:PRO:HD3	2.16	0.45
5:H:478:VAL:HB	5:H:536:ILE:HB	1.98	0.45
1:D:609:TYR:OH	1:D:616:HIS:O	2.28	0.45
1:D:533:VAL:HA	1:D:537:LEU:HD22	1.98	0.45
5:J:502:LEU:HD23	5:J:502:LEU:HA	1.77	0.45
2:B:1225:GLY:H	2:B:1247:PRO:HB3	1.81	0.45
1:A:600:ALA:HB3	2:B:811:LEU:HB2	1.98	0.45
1:D:73:ASP:OD1	1:D:73:ASP:N	2.49	0.45
5:J:602:TYR:CE1	5:J:668:VAL:HG22	2.45	0.45
5:J:553:LEU:HA	5:J:553:LEU:HD23	1.83	0.45
1:A:624:VAL:O	1:A:628:MET:HG3	2.16	0.45
1:A:272:TYR:HA	2:B:858:TYR:CE2	2.52	0.45
5:H:602:TYR:HE2	5:H:655:TRP:HZ3	1.64	0.45
3:C:1651:LEU:HD21	3:C:1734:LEU:HD22	1.99	0.45
2:E:968:MET:HE2	2:E:1384:TYR:CE1	2.52	0.45
2:B:954:ARG:O	2:B:957:THR:OG1	2.28	0.45
1:A:419:GLN:HE21	1:A:421:ILE:HD11	1.82	0.45
5:H:599:THR:O	5:H:603:GLU:HG2	2.16	0.45
2:B:1295:PHE:HD1	2:B:1296:GLN:N	2.15	0.45
3:C:1616:PHE:O	3:C:1621:PRO:HD2	2.16	0.45
2:E:961:PRO:HG2	2:E:1366:ILE:HB	1.98	0.45
2:E:1162:GLU:O	2:E:1166:GLN:HB2	2.16	0.45
2:E:797:LEU:HD23	2:E:797:LEU:HA	1.85	0.45
2:E:1070:LEU:C	2:E:1072:ARG:H	2.19	0.45
2:B:1020:PRO:HD3	2:B:1306:VAL:HG12	1.99	0.45
1:A:346:GLU:HG2	1:A:353:GLU:HG2	1.98	0.45
5:J:450:LYS:HD3	5:J:584:ASN:HB2	1.98	0.45
1:A:460:LEU:HD12	1:A:461:THR:H	1.81	0.45
3:C:1712:MET:HE2	3:C:1730:LEU:HD21	1.99	0.45
3:F:1631:VAL:HG12	3:F:1679:PRO:HA	1.99	0.45
3:C:1652:HIS:HB2	3:C:1737:TYR:HE2	1.81	0.45
2:B:1046:VAL:HA	2:B:1049:ILE:HD12	1.98	0.45
1:A:271:ILE:HG22	2:B:803:LEU:HD23	1.99	0.45
1:A:22:ARG:NH1	1:A:551:ASP:HA	2.31	0.45
1:A:150:TYR:CD2	1:A:156:VAL:HG12	2.51	0.45
3:F:1727:CYS:O	3:F:1731:ASN:HB2	2.16	0.45
2:E:1069:TRP:CD1	3:F:1513:SER:HB3	2.52	0.45
1:D:238:LEU:HA	1:D:239:PRO:HD3	1.76	0.45
5:J:543:VAL:O	5:J:545:ASN:ND2	2.47	0.45
5:H:476:ASN:N	5:H:476:ASN:OD1	2.50	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:715:SER:CB	2:E:718:GLN:HB3	2.42	0.45
2:B:1229:TYR:HB3	2:B:1288:TRP:CD2	2.52	0.45
1:A:385:LEU:HD12	1:A:387:GLN:HG3	1.99	0.45
3:F:1725:ALA:O	3:F:1728:ALA:HB3	2.17	0.45
2:B:740:GLU:O	2:B:744:LYS:HG2	2.17	0.45
2:B:1184:SER:OG	2:B:1185:ALA:N	2.50	0.44
2:B:987:ASP:O	2:B:991:SER:HB2	2.17	0.44
5:J:486:TYR:O	5:J:489:LYS:HG2	2.18	0.44
1:A:152:PRO:O	1:A:206:ASP:HA	2.18	0.44
2:B:868:HIS:HB3	2:B:884:ALA:HA	2.00	0.44
1:A:102:LEU:C	1:A:104:ARG:H	2.21	0.44
2:B:1191:HIS:HB2	2:B:1264:THR:OG1	2.17	0.44
1:A:604:LEU:HB3	1:A:605:ASP:H	1.45	0.44
2:E:1289:LEU:HA	2:E:1289:LEU:HD13	1.74	0.44
3:F:1563:GLU:HG2	3:F:1564:ARG:H	1.82	0.44
2:B:1201:SER:HG	2:B:1271:HIS:CE1	2.36	0.44
5:H:553:LEU:HA	5:H:553:LEU:HD23	1.84	0.44
1:D:319:PHE:CZ	1:D:323:LEU:HD11	2.52	0.44
5:J:472:LEU:HB3	5:J:550:PRO:HA	1.99	0.44
2:B:965:ASP:OD1	2:B:1382:ARG:HD3	2.17	0.44
1:D:409:VAL:HG11	1:D:438:PRO:HD2	2.00	0.44
2:B:684:GLN:HE22	2:B:767:ILE:N	2.11	0.44
2:E:684:GLN:HE22	2:E:767:ILE:N	2.11	0.44
4:G:312:SER:HB3	4:G:313:PRO:HD3	1.99	0.44
2:E:783:LEU:O	2:E:785:ARG:HG2	2.18	0.44
2:B:956:ARG:O	2:B:959:GLU:HG2	2.18	0.44
2:E:1244:THR:C	2:E:1246:ALA:H	2.21	0.44
1:A:123:ARG:HA	1:A:123:ARG:HD2	1.79	0.44
2:E:865:VAL:HG11	2:E:915:ALA:HB1	2.00	0.44
1:D:282:VAL:HG13	1:D:301:SER:HB3	2.00	0.44
2:E:945:VAL:HG23	2:E:1254:MET:HB3	2.00	0.44
1:D:163:LEU:HD21	2:E:813:LEU:HD11	2.00	0.44
2:E:912:LYS:HD2	2:E:928:SER:HB2	1.99	0.44
2:E:1000:VAL:HG11	2:E:1020:PRO:HG2	1.99	0.44
2:B:1124:LEU:HD21	2:B:1303:GLN:HG3	2.00	0.44
2:E:1198:TYR:CZ	2:E:1202:LEU:HD22	2.52	0.44
2:E:724:GLN:NE2	2:E:725:GLN:OE1	2.49	0.44
2:B:890:PRO:HB2	2:B:893:SER:HB2	1.99	0.44
1:D:598:LEU:HD23	2:E:788:THR:HG22	1.99	0.44
2:B:712:MET:SD	2:B:712:MET:N	2.90	0.44
2:E:757:ALA:O	5:H:630:ARG:HB3	2.16	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1581:THR:OG1	3:F:1583:CYS:SG	2.76	0.44
5:J:553:LEU:HD22	5:J:554:PRO:HD3	1.99	0.44
1:D:504:HIS:CE1	1:D:522:PRO:HA	2.52	0.44
1:D:152:PRO:O	1:D:206:ASP:HA	2.17	0.44
1:D:185:ARG:HH11	1:D:188:LYS:HB2	1.82	0.44
2:B:989:LEU:HD11	2:B:1351:ILE:N	2.28	0.44
1:D:43:LEU:HD22	1:D:76:LEU:HG	1.98	0.44
5:J:492:ALA:C	5:J:494:ALA:H	2.21	0.44
1:D:299:LEU:HA	1:D:299:LEU:HD13	1.84	0.44
2:B:1370:VAL:HG12	2:B:1373:ASN:H	1.83	0.44
1:A:571:LEU:HA	1:A:592:GLU:O	2.18	0.44
2:B:791:ARG:HB3	2:B:792:PHE:H	1.60	0.44
2:B:976:SER:O	2:B:1336:ARG:NH2	2.51	0.44
3:F:1614:MET:O	3:F:1616:PHE:N	2.40	0.44
5:H:595:HIS:NE2	5:H:614:ALA:HA	2.33	0.44
3:C:1626:GLY:HA2	3:C:1686:MET:HB3	2.00	0.44
2:B:1012:GLU:OE2	2:B:1303:GLN:HG2	2.18	0.44
2:E:747:ARG:C	2:E:749:LYS:H	2.19	0.44
1:A:380:PRO:HB3	1:A:439:GLN:HA	2.00	0.44
2:B:1262:ILE:H	2:B:1262:ILE:HG12	1.62	0.44
1:A:604:LEU:HA	1:A:604:LEU:HD23	1.79	0.44
2:B:1187:LEU:HD23	1:D:662:LEU:HD23	2.00	0.44
3:C:1664:MET:O	3:C:1665:ARG:NH1	2.49	0.44
1:D:174:ILE:HG22	1:D:219:PHE:HA	1.99	0.44
2:B:1397:LEU:HA	2:B:1397:LEU:HD23	1.78	0.44
5:H:655:TRP:CZ2	5:H:668:VAL:HG11	2.53	0.43
2:B:950:PRO:HB3	2:B:1370:VAL:CB	2.48	0.43
2:E:974:PHE:HB3	2:E:975:ASN:H	1.57	0.43
3:C:1607:GLN:O	3:C:1609:GLU:N	2.51	0.43
4:G:413:GLU:HG3	4:G:414:ALA:N	2.32	0.43
2:E:1018:LEU:O	2:E:1021:THR:N	2.51	0.43
2:B:1160:GLY:C	2:B:1163:PRO:HD2	2.38	0.43
1:D:142:PHE:HB2	1:D:161:PHE:HB2	2.00	0.43
1:A:73:ASP:OD1	1:A:73:ASP:N	2.51	0.43
3:C:1562:PRO:O	3:C:1565:ARG:NH1	2.51	0.43
2:B:992:GLU:HA	2:B:995:LEU:HB2	2.00	0.43
4:G:319:ILE:HG22	4:G:320:LEU:HG	2.00	0.43
5:H:595:HIS:HE2	5:H:614:ALA:HA	1.83	0.43
5:J:486:TYR:CE2	5:J:525:HIS:HB2	2.53	0.43
2:E:902:VAL:HG11	3:F:1591:ALA:HB2	1.99	0.43
2:B:844:ARG:N	2:B:847:GLU:OE1	2.51	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1281:MET:HE2	2:E:1281:MET:HB3	1.75	0.43
5:H:611:SER:O	5:H:611:SER:OG	2.31	0.43
1:D:594:ASP:OD1	1:D:594:ASP:N	2.49	0.43
5:H:607:TYR:O	5:H:609:ARG:N	2.50	0.43
2:B:950:PRO:HB3	2:B:1370:VAL:HB	2.00	0.43
2:B:1368:VAL:O	2:B:1370:VAL:HG23	2.18	0.43
2:B:877:LEU:HB3	2:B:881:GLY:N	2.33	0.43
2:E:939:ILE:HG22	2:E:940:HIS:H	1.83	0.43
4:I:355:ASP:N	4:I:355:ASP:OD1	2.51	0.43
5:H:655:TRP:CE2	5:H:668:VAL:HG11	2.54	0.43
2:E:966:PRO:HG2	2:E:1360:PHE:CZ	2.53	0.43
3:C:1616:PHE:CA	3:C:1621:PRO:HD2	2.48	0.43
2:B:1270:LEU:HD21	2:B:1311:ALA:HA	2.00	0.43
5:H:516:ALA:HB3	5:H:537:LYS:HB3	2.00	0.43
1:D:287:LEU:HA	1:D:287:LEU:HD23	1.88	0.43
2:E:823:THR:HA	2:E:824:PRO:HD3	1.84	0.43
2:B:878:ALA:HB1	2:B:883:LEU:HD23	2.00	0.43
1:A:110:LEU:HB3	1:A:130:ILE:HD12	2.00	0.43
1:D:137:ARG:HG2	1:D:631:TYR:HE1	1.83	0.43
2:E:908:ALA:CB	2:E:932:GLN:HA	2.47	0.43
2:E:1225:GLY:H	2:E:1247:PRO:HB3	1.83	0.43
2:B:1022:LEU:HD12	2:B:1022:LEU:HA	1.83	0.43
3:F:1633:ARG:NH1	3:F:1644:GLU:OE2	2.51	0.43
4:G:349:GLN:O	4:G:351:ASP:N	2.51	0.43
3:C:1501:LEU:O	3:C:1504:LEU:HB2	2.18	0.43
3:F:1483:MET:HA	3:F:1526:PHE:O	2.19	0.43
5:J:629:CYS:HB3	5:J:630:ARG:H	1.74	0.43
2:E:950:PRO:HB2	2:E:951:LEU:H	1.42	0.43
3:F:1643:PHE:CZ	3:F:1677:LEU:HB2	2.54	0.43
1:A:419:GLN:HE22	1:A:436:ILE:H	1.65	0.43
2:B:1000:VAL:HG11	2:B:1020:PRO:HG2	1.99	0.43
2:E:805:THR:HB	2:E:828:ARG:HA	2.01	0.43
1:D:580:GLN:HG3	2:E:828:ARG:HB3	2.00	0.43
2:B:1061:LYS:HD2	2:B:1074:SER:OG	2.18	0.43
3:F:1501:LEU:O	3:F:1504:LEU:HB2	2.19	0.43
2:E:1046:VAL:HA	2:E:1049:ILE:HD12	2.01	0.43
4:I:368:PRO:HA	4:I:369:PRO:HD3	1.82	0.43
2:B:948:LEU:HD22	2:B:1368:VAL:HG21	1.99	0.43
2:B:1126:ARG:HD3	2:B:1260:LEU:HD13	2.00	0.43
2:E:743:ARG:HG2	2:E:747:ARG:NH1	2.33	0.43
2:B:1269:LEU:HD12	2:B:1311:ALA:HB1	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:392:GLU:HB3	1:D:396:SER:C	2.38	0.43
3:C:1630:LYS:HE3	3:C:1680:GLY:O	2.18	0.43
2:B:1244:THR:C	2:B:1246:ALA:H	2.22	0.43
2:B:724:GLN:NE2	2:B:725:GLN:OE1	2.50	0.43
3:C:1631:VAL:HG12	3:C:1679:PRO:HA	2.01	0.43
5:J:551:ILE:HD12	5:J:551:ILE:HA	1.84	0.43
1:A:262:MET:HG3	1:A:262:MET:H	1.63	0.43
1:A:282:VAL:HG13	1:A:301:SER:HB3	2.01	0.43
2:E:1086:LEU:HD23	2:E:1086:LEU:HA	1.68	0.43
2:E:965:ASP:OD1	2:E:1382:ARG:HD3	2.19	0.43
3:C:1675:LEU:HD21	3:C:1709:ILE:HD12	2.01	0.43
2:B:1130:GLY:CA	1:D:104:ARG:HG3	2.49	0.43
1:D:219:PHE:H	1:D:225:SER:HB2	1.84	0.43
1:A:548:TYR:CZ	1:A:553:PRO:HB3	2.54	0.43
1:A:41:VAL:HG23	1:A:83:ALA:HB3	2.01	0.43
1:D:141:LEU:HD23	1:D:162:ALA:HA	2.01	0.43
3:C:1612:TYR:CE1	3:C:1613:ARG:HG3	2.54	0.43
3:F:1634:GLU:HB2	3:F:1643:PHE:CD1	2.51	0.43
1:A:104:ARG:HD2	1:A:104:ARG:HA	1.60	0.43
3:C:1501:LEU:HA	3:C:1501:LEU:HD23	1.75	0.43
2:E:954:ARG:O	2:E:957:THR:OG1	2.32	0.43
2:E:868:HIS:HB3	2:E:884:ALA:HA	2.01	0.43
1:A:288:ASP:HB2	1:A:292:LYS:HE2	2.00	0.43
2:B:1309:LEU:HA	2:B:1309:LEU:HD23	1.74	0.43
1:D:377:HIS:CE1	1:D:641:ASP:HA	2.54	0.43
2:B:949:ASN:HA	2:B:950:PRO:HD3	1.74	0.42
2:E:1418:GLU:HG2	5:H:580:PHE:CE2	2.54	0.42
1:D:506:TYR:CE1	1:D:520:ARG:HD3	2.54	0.42
3:C:1737:TYR:HA	3:C:1741:GLY:HA2	2.01	0.42
2:E:956:ARG:O	2:E:959:GLU:HG2	2.19	0.42
3:C:1689:ASP:OD1	3:C:1689:ASP:N	2.49	0.42
2:E:1397:LEU:HA	2:E:1397:LEU:HD23	1.75	0.42
2:B:827:LEU:HA	2:B:827:LEU:HD12	1.83	0.42
2:E:756:ARG:O	5:H:630:ARG:HA	2.20	0.42
2:B:1368:VAL:HG12	2:B:1370:VAL:HG22	2.01	0.42
2:E:975:ASN:O	2:E:976:SER:OG	2.30	0.42
2:E:684:GLN:NE2	2:E:767:ILE:H	2.12	0.42
1:A:142:PHE:HE2	1:A:163:LEU:HD12	1.84	0.42
1:A:484:ARG:HG2	1:A:563:GLN:OE1	2.20	0.42
2:E:987:ASP:OD1	2:E:987:ASP:N	2.51	0.42
5:J:458:TRP:CE3	5:J:551:ILE:HD13	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:591:LEU:HD12	2:B:789:VAL:HG21	2.02	0.42
2:B:867:VAL:CG2	2:B:897:VAL:HG11	2.49	0.42
2:B:969:ILE:HG12	3:C:1695:LEU:HA	2.01	0.42
3:C:1608:ASP:N	3:C:1608:ASP:OD1	2.51	0.42
1:A:24:LEU:HB2	1:A:42:GLN:O	2.19	0.42
1:D:159:ARG:NH2	1:D:601:LEU:O	2.37	0.42
2:E:1257:ALA:O	2:E:1300:ARG:HD2	2.19	0.42
2:E:1061:LYS:HD2	2:E:1074:SER:OG	2.18	0.42
1:A:123:ARG:HB3	1:A:127:ILE:HD13	2.01	0.42
5:J:581:LEU:HD23	5:J:581:LEU:HA	1.87	0.42
2:B:760:ILE:CG2	2:B:1410:THR:HG21	2.49	0.42
2:B:684:GLN:NE2	2:B:767:ILE:H	2.13	0.42
2:E:1095:GLY:O	2:E:1097:PRO:HD3	2.20	0.42
2:E:989:LEU:HD11	2:E:1351:ILE:N	2.34	0.42
1:D:151:ASN:ND2	1:D:154:GLN:OE1	2.52	0.42
3:F:1723:GLN:O	3:F:1726:ALA:N	2.50	0.42
5:H:679:ILE:O	5:H:683:ILE:HG13	2.19	0.42
4:I:392:ILE:HD13	4:I:418:TRP:CZ3	2.54	0.42
2:E:1201:SER:HG	2:E:1271:HIS:CE1	2.38	0.42
5:H:513:TRP:O	5:H:515:GLU:N	2.53	0.42
2:E:1273:LEU:HD11	2:E:1315:TYR:HB2	2.01	0.42
1:A:99:LEU:HD23	1:A:99:LEU:HA	1.88	0.42
2:B:840:PRO:HG3	3:C:1544:VAL:HB	2.02	0.42
1:D:338:LEU:HD22	1:D:361:TYR:HE2	1.85	0.42
1:A:613:SER:OG	1:A:615:SER:O	2.38	0.42
1:D:668:SER:OG	1:D:670:PRO:HD3	2.20	0.42
2:B:1326:GLY:HA3	2:B:1346:LEU:O	2.20	0.42
4:G:368:PRO:HA	4:G:369:PRO:HD3	1.92	0.42
2:E:1126:ARG:NH1	2:E:1263:GLU:OE1	2.53	0.42
2:E:1258:PRO:HG2	2:E:1261:TRP:CD1	2.54	0.42
2:E:756:ARG:HD3	2:E:756:ARG:HA	1.39	0.42
5:H:575:LEU:HD11	5:H:630:ARG:HD2	2.01	0.42
2:E:1323:GLU:HG2	2:E:1325:ARG:HB2	2.02	0.42
1:D:123:ARG:HD2	1:D:123:ARG:HA	1.74	0.42
2:E:1368:VAL:O	2:E:1370:VAL:N	2.53	0.42
2:E:863:LEU:HD21	2:E:923:VAL:HG11	2.02	0.42
2:E:740:GLU:O	2:E:744:LYS:HG2	2.19	0.42
1:A:61:PRO:HA	1:A:64:ASN:O	2.20	0.42
3:F:1548:LEU:HD13	3:F:1581:THR:HA	2.01	0.42
3:F:1733:PHE:CD2	3:F:1734:LEU:HD23	2.54	0.42
3:F:1549:VAL:CG2	3:F:1578:LEU:HB3	2.50	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:575:LEU:HD23	5:J:581:LEU:HD23	2.01	0.42
4:I:349:GLN:O	4:I:351:ASP:N	2.53	0.42
2:E:1417:TYS:O3	5:H:505:LEU:HB2	2.20	0.42
5:J:476:ASN:OD1	5:J:476:ASN:N	2.53	0.42
1:D:113:HIS:HA	1:D:126:ASN:HA	2.02	0.42
5:J:569:THR:O	5:J:637:LEU:HD12	2.20	0.42
2:B:1337:ASN:OD1	2:B:1359:GLN:NE2	2.53	0.42
5:H:621:LEU:HB2	5:H:624:GLY:H	1.85	0.42
1:A:483:PRO:O	1:A:562:VAL:HG23	2.19	0.42
2:E:848:GLN:HE21	3:F:1548:LEU:CD2	2.23	0.42
2:B:710:LEU:HA	2:B:710:LEU:HD12	1.86	0.42
5:J:457:PRO:HD2	5:J:458:TRP:CZ3	2.55	0.42
2:E:760:ILE:HG13	5:H:466:THR:HA	2.02	0.42
4:I:319:ILE:HG22	4:I:320:LEU:HG	2.02	0.42
2:E:876:CYS:HB3	2:E:902:VAL:HG13	2.02	0.42
3:C:1581:THR:OG1	3:C:1583:CYS:SG	2.78	0.42
1:D:198:PHE:CZ	1:D:200:ASP:HB2	2.55	0.42
2:E:1217:LEU:O	2:E:1230:TRP:HZ3	2.03	0.42
5:H:563:ARG:O	5:H:566:ASP:HB2	2.19	0.42
2:E:1070:LEU:C	2:E:1072:ARG:N	2.73	0.41
2:B:1198:TYR:HA	2:B:1271:HIS:HB2	2.00	0.41
2:B:1267:TYR:CZ	2:B:1307:ILE:HD13	2.55	0.41
4:G:355:ASP:N	4:G:355:ASP:OD1	2.53	0.41
1:D:409:VAL:CG1	1:D:441:ILE:HD13	2.47	0.41
2:B:799:LEU:HA	2:B:800:PRO:HD3	1.91	0.41
5:J:563:ARG:HD3	5:J:563:ARG:HA	1.84	0.41
2:B:1045:ALA:O	2:B:1049:ILE:HG13	2.20	0.41
3:C:1606:LEU:HA	3:C:1606:LEU:HD13	1.73	0.41
1:A:287:LEU:HD23	1:A:287:LEU:HA	1.89	0.41
3:C:1478:VAL:HG11	3:C:1564:ARG:HH12	1.84	0.41
2:E:1295:PHE:HD1	2:E:1296:GLN:N	2.18	0.41
2:B:783:LEU:O	2:B:785:ARG:HG2	2.19	0.41
3:C:1474:ARG:HH21	3:C:1477:LYS:HA	1.84	0.41
4:G:413:GLU:HB2	4:G:419:THR:HG23	2.02	0.41
1:A:164:ASP:OD1	1:A:166:LYS:N	2.51	0.41
2:B:984:ASP:OD1	2:B:1347:ASN:N	2.54	0.41
2:B:1162:GLU:O	2:B:1166:GLN:HB2	2.20	0.41
5:H:568:GLY:HA3	5:H:639:PHE:CE1	2.55	0.41
3:C:1563:GLU:H	3:C:1563:GLU:CD	2.24	0.41
1:A:389:LEU:HD13	1:A:430:GLN:CG	2.50	0.41
5:H:511:GLN:HG3	5:H:512:ALA:N	2.35	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1685:ILE:HA	3:C:1708:TRP:O	2.20	0.41
1:D:276:VAL:HG12	1:D:277:GLN:O	2.20	0.41
5:J:592:ILE:HG23	5:J:618:CYS:O	2.19	0.41
1:A:392:GLU:HB2	1:A:395:GLY:N	2.36	0.41
4:I:370:ASP:HB3	4:I:427:LEU:HD11	2.02	0.41
1:D:282:VAL:HA	1:D:343:ALA:HA	2.03	0.41
1:A:482:PRO:HA	1:A:483:PRO:HD3	1.93	0.41
1:A:204:ILE:HA	1:A:205:PRO:HD2	1.84	0.41
2:B:996:SER:HB3	2:B:1352:ARG:NH2	2.36	0.41
2:E:949:ASN:HA	2:E:950:PRO:HD3	1.73	0.41
2:E:955:GLY:HA2	2:E:958:LEU:HB2	2.02	0.41
2:E:1128:MET:HB2	2:E:1128:MET:HE2	1.95	0.41
1:D:633:LEU:HB3	1:D:664:ARG:HH21	1.85	0.41
3:C:1576:SER:O	3:C:1578:LEU:N	2.54	0.41
3:F:1685:ILE:HG12	3:F:1709:ILE:HG12	2.02	0.41
3:F:1513:SER:OG	3:F:1527:ASP:OD1	2.34	0.41
5:J:474:TYR:O	5:J:550:PRO:HB3	2.20	0.41
2:B:878:ALA:C	2:B:880:GLY:H	2.23	0.41
1:A:279:VAL:HG21	1:A:302:GLN:HG2	2.01	0.41
3:F:1673:CYS:O	3:F:1674:ARG:HG3	2.21	0.41
1:D:164:ASP:OD1	1:D:166:LYS:N	2.53	0.41
2:E:1309:LEU:HA	2:E:1309:LEU:HD23	1.76	0.41
2:B:1323:GLU:HG2	2:B:1325:ARG:HB2	2.03	0.41
5:H:554:PRO:HD2	5:H:676:ILE:HD11	2.03	0.41
2:B:996:SER:HB3	2:B:1352:ARG:HH22	1.86	0.41
1:A:549:HIS:O	1:A:551:ASP:N	2.52	0.41
2:B:1070:LEU:C	2:B:1072:ARG:H	2.24	0.41
5:J:523:TYR:CZ	5:J:525:HIS:HA	2.56	0.41
2:B:814:SER:HB3	2:B:817:LYS:HB2	2.02	0.41
1:D:292:LYS:HB3	1:D:292:LYS:HE2	1.93	0.41
2:B:948:LEU:HB3	2:B:1368:VAL:HG11	2.02	0.41
1:D:604:LEU:HA	1:D:604:LEU:HD23	1.81	0.41
2:B:1295:PHE:HD1	2:B:1296:GLN:H	1.68	0.41
2:B:785:ARG:NH2	2:B:787:GLU:OE2	2.54	0.41
2:B:833:PHE:CE1	2:B:855:LEU:HD22	2.56	0.41
2:E:1370:VAL:HG12	2:E:1373:ASN:H	1.86	0.41
2:E:1191:HIS:HB2	2:E:1264:THR:OG1	2.20	0.41
4:G:427:LEU:HD23	4:G:428:PRO:HD2	2.02	0.41
5:J:513:TRP:O	5:J:515:GLU:N	2.53	0.41
4:I:344:PHE:CG	4:I:359:PRO:HG3	2.55	0.41
1:D:243:VAL:HG22	1:D:345:ILE:HD12	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1716:ARG:HB2	3:F:1716:ARG:HE	1.60	0.41
1:A:274:LYS:HB2	1:A:274:LYS:HE3	1.79	0.41
2:B:1368:VAL:O	2:B:1370:VAL:N	2.54	0.41
2:E:867:VAL:CG2	2:E:897:VAL:HG11	2.50	0.41
1:D:370:ASP:O	1:D:371:LEU:HD23	2.21	0.41
2:E:950:PRO:HB3	2:E:1370:VAL:CB	2.50	0.41
1:D:110:LEU:HB3	1:D:130:ILE:HD12	2.01	0.41
2:B:747:ARG:C	2:B:749:LYS:H	2.24	0.41
2:E:1287:ALA:O	2:E:1291:ARG:HD3	2.21	0.41
1:D:191:VAL:HG22	1:D:192:TYR:O	2.21	0.41
2:B:1312:LEU:HD22	2:B:1316:TRP:CZ2	2.55	0.41
3:F:1616:PHE:CA	3:F:1621:PRO:HD2	2.48	0.41
1:A:504:HIS:CE1	1:A:522:PRO:HA	2.55	0.41
2:E:1354:LEU:HD13	2:E:1354:LEU:HA	1.76	0.41
3:C:1667:PHE:CE2	3:C:1685:ILE:HG21	2.55	0.41
3:F:1683:TYR:CE2	3:F:1711:GLU:HB3	2.56	0.41
3:F:1686:MET:CG	3:F:1708:TRP:HB3	2.51	0.41
1:A:326:LEU:HD13	1:A:328:MET:SD	2.61	0.41
3:C:1723:GLN:O	3:C:1726:ALA:N	2.53	0.41
1:A:252:ILE:HD13	1:A:262:MET:HG2	2.03	0.41
2:E:720:ALA:O	2:E:723:VAL:HG22	2.21	0.41
4:G:431:GLU:HA	4:G:432:PRO:HD3	1.93	0.41
1:D:145:THR:HG22	1:D:158:TYR:HB3	2.03	0.41
1:D:467:SER:C	1:D:469:GLY:H	2.24	0.41
1:D:146:ASP:HA	2:E:784:TRP:CZ3	2.56	0.41
5:H:521:GLU:H	5:H:521:GLU:CD	2.24	0.41
3:C:1491:LEU:O	3:C:1494:PHE:HB2	2.21	0.41
5:J:575:LEU:HD11	5:J:630:ARG:HD2	2.02	0.41
2:E:1049:ILE:HG13	2:E:1049:ILE:H	1.69	0.41
2:B:1065:SER:HB3	2:B:1106:TRP:CD2	2.56	0.41
4:G:388:TYR:O	4:G:389:LYS:HB2	2.20	0.41
3:F:1491:LEU:O	3:F:1494:PHE:HB2	2.21	0.41
2:E:827:LEU:HA	2:E:827:LEU:HD12	1.80	0.41
1:D:407:ALA:HB2	1:D:446:LEU:HD23	2.02	0.41
2:E:745:LYS:CA	2:E:748:ASP:HB2	2.51	0.40
4:G:413:GLU:HB2	4:G:419:THR:CG2	2.51	0.40
2:E:1101:GLN:HG2	2:E:1156:PHE:CE2	2.56	0.40
1:D:366:PRO:O	1:D:393:MET:HA	2.22	0.40
2:E:719:ARG:HH22	3:F:1507:LEU:HD12	1.86	0.40
2:B:1126:ARG:NH2	3:C:1560:TYR:HB3	2.36	0.40
2:E:1147:ILE:HD13	2:E:1198:TYR:HD2	1.85	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:675:TYR:O	5:H:679:ILE:HG13	2.20	0.40
5:H:482:ALA:HB2	5:H:533:ILE:O	2.21	0.40
1:A:598:LEU:HD23	2:B:788:THR:HG22	2.04	0.40
1:D:346:GLU:HG2	1:D:353:GLU:HG2	2.02	0.40
5:H:678:TRP:O	5:H:682:ILE:HG13	2.21	0.40
1:D:604:LEU:HB3	1:D:605:ASP:H	1.42	0.40
3:C:1614:MET:HE3	3:C:1736:GLU:HG2	2.03	0.40
2:E:1368:VAL:O	2:E:1370:VAL:HG23	2.21	0.40
2:B:839:LEU:HD13	2:B:931:LEU:HD13	2.03	0.40
2:E:1246:ALA:HB1	2:E:1247:PRO:HD2	2.03	0.40
1:A:24:LEU:HD12	1:A:42:GLN:NE2	2.36	0.40
1:A:150:TYR:CE2	1:A:156:VAL:HG12	2.56	0.40
1:A:499:GLY:O	1:A:501:THR:HG22	2.21	0.40
1:A:158:TYR:HE2	1:A:176:VAL:HG21	1.87	0.40
2:E:758:LEU:HA	2:E:758:LEU:HD12	1.90	0.40
3:F:1695:LEU:H	3:F:1695:LEU:HD12	1.86	0.40
5:J:602:TYR:OH	5:J:656:GLY:HA2	2.21	0.40
5:H:457:PRO:HD2	5:H:458:TRP:CZ3	2.56	0.40
2:E:839:LEU:HD13	2:E:931:LEU:HD13	2.02	0.40
2:E:980:VAL:HB	2:E:1356:GLU:HB2	2.04	0.40
2:E:1128:MET:HE1	2:E:1191:HIS:HB3	2.03	0.40
2:B:782:TRP:CD2	2:B:800:PRO:HG2	2.56	0.40
1:A:241:PHE:CE1	1:A:354:GLU:HB2	2.57	0.40
1:A:219:PHE:H	1:A:225:SER:HB2	1.86	0.40
1:A:323:LEU:HA	1:A:326:LEU:HD11	2.04	0.40
3:F:1667:PHE:HD2	3:F:1703:LEU:HD21	1.87	0.40
1:A:282:VAL:HB	1:A:343:ALA:HB2	2.04	0.40
1:A:284:PHE:O	1:A:296:PHE:HB2	2.22	0.40
2:E:877:LEU:HB3	2:E:881:GLY:N	2.37	0.40
4:I:382:GLY:O	4:I:385:VAL:HG12	2.22	0.40
5:H:656:GLY:HA2	5:H:668:VAL:HG23	2.02	0.40
2:E:840:PRO:HG3	3:F:1544:VAL:HB	2.04	0.40
1:D:137:ARG:HB2	1:D:224:GLU:O	2.22	0.40
3:C:1695:LEU:H	3:C:1695:LEU:HD12	1.86	0.40
2:E:1015:MET:HG3	2:E:1085:VAL:HG21	2.03	0.40
1:A:159:ARG:HB3	1:A:199:GLN:HG3	2.03	0.40
1:D:392:GLU:OE1	1:D:397:PRO:HD3	2.22	0.40
2:B:1349:ARG:H	2:B:1349:ARG:HG2	1.66	0.40
2:E:1153:LEU:HA	2:E:1153:LEU:HD23	1.87	0.40
3:C:1731:ASN:O	3:C:1735:GLN:HG2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	649/656 (99%)	541 (83%)	88 (14%)	20 (3%)	5	45
1	D	649/656 (99%)	540 (83%)	89 (14%)	20 (3%)	5	45
2	B	737/767 (96%)	625 (85%)	84 (11%)	28 (4%)	4	39
2	E	737/767 (96%)	630 (86%)	81 (11%)	26 (4%)	4	42
3	C	285/291 (98%)	230 (81%)	41 (14%)	14 (5%)	3	32
3	F	285/291 (98%)	229 (80%)	43 (15%)	13 (5%)	3	34
4	G	143/154 (93%)	122 (85%)	13 (9%)	8 (6%)	2	29
4	I	143/154 (93%)	123 (86%)	12 (8%)	8 (6%)	2	29
5	H	240/242 (99%)	202 (84%)	29 (12%)	9 (4%)	4	39
5	J	240/242 (99%)	203 (85%)	28 (12%)	9 (4%)	4	39
All	All	4108/4220 (97%)	3445 (84%)	508 (12%)	155 (4%)	4	39

All (155) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	394	SER
2	B	878	ALA
2	B	950	PRO
2	B	1132	LEU
2	B	1204	LYS
2	B	1250	PRO
3	C	1462	GLN
3	C	1483	MET
3	C	1610	ASP
1	D	348	PRO
1	D	394	SER
2	E	878	ALA
2	E	950	PRO
2	E	1132	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	E	1204	LYS
2	E	1250	PRO
3	F	1462	GLN
3	F	1483	MET
3	F	1610	ASP
4	G	320	LEU
4	G	336	GLN
4	G	405	VAL
4	I	320	LEU
4	I	336	GLN
4	I	405	VAL
1	A	259	LEU
1	A	260	ASP
1	A	331	THR
1	A	348	PRO
1	A	453	PRO
1	A	668	SER
2	B	919	PHE
2	B	1062	ALA
2	B	1248	ARG
2	B	1347	ASN
3	C	1478	VAL
3	C	1622	ARG
3	C	1674	ARG
3	C	1692	THR
1	D	259	LEU
1	D	260	ASP
1	D	331	THR
1	D	453	PRO
1	D	668	SER
2	E	919	PHE
2	E	1248	ARG
3	F	1478	VAL
3	F	1506	SER
3	F	1608	ASP
3	F	1622	ARG
3	F	1674	ARG
3	F	1692	THR
5	H	447	GLY
5	H	609	ARG
5	J	447	GLY
5	J	514	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	J	609	ARG
1	A	128	GLN
1	A	184	LEU
1	A	350	GLY
1	A	550	GLY
1	A	582	ARG
2	B	724	GLN
2	B	972	GLY
2	B	974	PHE
2	B	1010	CYS
2	B	1128	MET
2	B	1159	GLU
2	B	1348	ASN
2	B	1353	GLY
3	C	1506	SER
3	C	1598	GLN
3	C	1608	ASP
3	C	1609	GLU
1	D	128	GLN
1	D	184	LEU
1	D	350	GLY
1	D	550	GLY
1	D	582	ARG
2	E	724	GLN
2	E	972	GLY
2	E	974	PHE
2	E	1010	CYS
2	E	1062	ALA
2	E	1128	MET
2	E	1159	GLU
2	E	1279	ALA
2	E	1347	ASN
3	F	1577	ARG
3	F	1598	GLN
3	F	1609	GLU
4	G	350	LYS
4	G	354	TRP
5	H	487	GLU
5	H	492	ALA
5	H	514	SER
4	I	350	LYS
5	J	492	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	J	608	PRO
1	A	256	PRO
1	A	665	LYS
2	B	1247	PRO
2	B	1361	SER
3	C	1564	ARG
3	C	1577	ARG
1	D	152	PRO
1	D	223	LEU
1	D	256	PRO
1	D	665	LYS
2	E	1070	LEU
2	E	1247	PRO
2	E	1348	ASN
2	E	1353	GLY
2	E	1361	SER
3	F	1564	ARG
5	H	493	SER
5	H	605	PRO
5	H	608	PRO
4	I	354	TRP
5	J	487	GLU
5	J	493	SER
5	J	605	PRO
5	J	613	THR
1	A	152	PRO
1	A	223	LEU
2	B	748	ASP
2	B	757	ALA
2	B	1070	LEU
2	B	1162	GLU
2	B	1293	GLY
2	B	1369	LYS
1	D	127	ILE
1	D	614	LYS
2	E	1162	GLU
2	E	1293	GLY
2	E	1369	LYS
4	G	355	ASP
4	I	355	ASP
1	A	526	LEU
1	A	614	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	1245	PRO
2	B	1279	ALA
1	D	526	LEU
2	E	1032	GLU
2	E	1245	PRO
4	G	313	PRO
5	H	613	THR
4	I	313	PRO
1	D	515	ILE
1	A	515	ILE
1	A	127	ILE
2	B	1009	GLY
3	C	1572	ALA
4	G	383	PRO
4	I	383	PRO

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	557/562 (99%)	504 (90%)	53 (10%)	11	46
1	D	557/562 (99%)	505 (91%)	52 (9%)	11	48
2	B	615/639 (96%)	558 (91%)	57 (9%)	11	48
2	E	615/639 (96%)	561 (91%)	54 (9%)	12	50
3	C	246/249 (99%)	222 (90%)	24 (10%)	10	44
3	F	246/249 (99%)	225 (92%)	21 (8%)	13	52
4	G	124/131 (95%)	119 (96%)	5 (4%)	38	75
4	I	124/131 (95%)	119 (96%)	5 (4%)	38	75
5	H	193/193 (100%)	179 (93%)	14 (7%)	17	58
5	J	193/193 (100%)	179 (93%)	14 (7%)	17	58
All	All	3470/3548 (98%)	3171 (91%)	299 (9%)	13	52

All (299) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	ARG
1	A	43	LEU
1	A	46	VAL
1	A	73	ASP
1	A	77	SER
1	A	78	SER
1	A	81	ASP
1	A	93	ASP
1	A	103	LEU
1	A	109	GLN
1	A	126	ASN
1	A	143	LEU
1	A	155	ARG
1	A	175	THR
1	A	176	VAL
1	A	180	ASN
1	A	182	HIS
1	A	188	LYS
1	A	209	GLU
1	A	212	THR
1	A	240	ASN
1	A	258	HIS
1	A	282	VAL
1	A	283	ARG
1	A	294	THR
1	A	299	LEU
1	A	306	VAL
1	A	326	LEU
1	A	338	LEU
1	A	339	TYR
1	A	347	SER
1	A	358	THR
1	A	360	TRP
1	A	385	LEU
1	A	386	LEU
1	A	392	GLU
1	A	405	VAL
1	A	420	ASP
1	A	431	VAL
1	A	501	THR
1	A	527	THR
1	A	536	HIS
1	A	540	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	548	TYR
1	A	562	VAL
1	A	608	LEU
1	A	616	HIS
1	A	629	ASN
1	A	642	SER
1	A	654	PHE
1	A	659	GLN
1	A	663	SER
1	A	666	ARG
2	B	701	ARG
2	B	712	MET
2	B	713	MET
2	B	723	VAL
2	B	742	LEU
2	B	748	ASP
2	B	754	LEU
2	B	756	ARG
2	B	761	LEU
2	B	762	GLN
2	B	772	ILE
2	B	793	GLN
2	B	796	THR
2	B	806	TRP
2	B	809	HIS
2	B	813	LEU
2	B	814	SER
2	B	841	MET
2	B	844	ARG
2	B	849	LEU
2	B	867	VAL
2	B	876	CYS
2	B	877	LEU
2	B	899	PHE
2	B	911	LEU
2	B	963	ASN
2	B	974	PHE
2	B	977	TYR
2	B	984	ASP
2	B	988	THR
2	B	995	LEU
2	B	1008	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	1013	GLN
2	B	1018	LEU
2	B	1022	LEU
2	B	1036	THR
2	B	1043	ASP
2	B	1046	VAL
2	B	1050	GLN
2	B	1074	SER
2	B	1107	LEU
2	B	1108	LEU
2	B	1125	ASP
2	B	1210	LEU
2	B	1238	SER
2	B	1262	ILE
2	B	1295	PHE
2	B	1296	GLN
2	B	1303	GLN
2	B	1304	ASP
2	B	1313	SER
2	B	1322	THR
2	B	1329	VAL
2	B	1344	LEU
2	B	1369	LYS
2	B	1390	LYS
2	B	1403	VAL
3	C	1458	VAL
3	C	1504	LEU
3	C	1506	SER
3	C	1512	VAL
3	C	1527	ASP
3	C	1541	VAL
3	C	1553	SER
3	C	1557	TYR
3	C	1558	ASP
3	C	1559	TYR
3	C	1576	SER
3	C	1577	ARG
3	C	1581	THR
3	C	1607	GLN
3	C	1632	LEU
3	C	1653	PHE
3	C	1654	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	C	1668	LEU
3	C	1674	ARG
3	C	1676	ARG
3	C	1677	LEU
3	C	1689	ASP
3	C	1718	CYS
3	C	1723	GLN
1	D	22	ARG
1	D	43	LEU
1	D	46	VAL
1	D	73	ASP
1	D	77	SER
1	D	78	SER
1	D	81	ASP
1	D	103	LEU
1	D	111	VAL
1	D	126	ASN
1	D	137	ARG
1	D	143	LEU
1	D	155	ARG
1	D	157	ARG
1	D	175	THR
1	D	176	VAL
1	D	180	ASN
1	D	182	HIS
1	D	188	LYS
1	D	209	GLU
1	D	212	THR
1	D	240	ASN
1	D	258	HIS
1	D	282	VAL
1	D	283	ARG
1	D	294	THR
1	D	299	LEU
1	D	306	VAL
1	D	326	LEU
1	D	338	LEU
1	D	347	SER
1	D	358	THR
1	D	360	TRP
1	D	385	LEU
1	D	386	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	392	GLU
1	D	405	VAL
1	D	420	ASP
1	D	431	VAL
1	D	501	THR
1	D	527	THR
1	D	536	HIS
1	D	540	SER
1	D	548	TYR
1	D	562	VAL
1	D	608	LEU
1	D	616	HIS
1	D	629	ASN
1	D	642	SER
1	D	654	PHE
1	D	659	GLN
1	D	666	ARG
2	E	701	ARG
2	E	712	MET
2	E	713	MET
2	E	756	ARG
2	E	761	LEU
2	E	762	GLN
2	E	772	ILE
2	E	793	GLN
2	E	806	TRP
2	E	809	HIS
2	E	813	LEU
2	E	841	MET
2	E	844	ARG
2	E	849	LEU
2	E	867	VAL
2	E	876	CYS
2	E	877	LEU
2	E	899	PHE
2	E	911	LEU
2	E	921	PHE
2	E	963	ASN
2	E	974	PHE
2	E	977	TYR
2	E	984	ASP
2	E	988	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	E	995	LEU
2	E	1008	ARG
2	E	1013	GLN
2	E	1018	LEU
2	E	1022	LEU
2	E	1036	THR
2	E	1043	ASP
2	E	1046	VAL
2	E	1050	GLN
2	E	1107	LEU
2	E	1108	LEU
2	E	1125	ASP
2	E	1155	VAL
2	E	1210	LEU
2	E	1238	SER
2	E	1262	ILE
2	E	1269	LEU
2	E	1291	ARG
2	E	1295	PHE
2	E	1296	GLN
2	E	1303	GLN
2	E	1304	ASP
2	E	1305	THR
2	E	1313	SER
2	E	1322	THR
2	E	1329	VAL
2	E	1369	LYS
2	E	1390	LYS
2	E	1403	VAL
3	F	1458	VAL
3	F	1504	LEU
3	F	1512	VAL
3	F	1527	ASP
3	F	1553	SER
3	F	1557	TYR
3	F	1558	ASP
3	F	1559	TYR
3	F	1576	SER
3	F	1577	ARG
3	F	1581	THR
3	F	1607	GLN
3	F	1632	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	F	1653	PHE
3	F	1654	THR
3	F	1668	LEU
3	F	1674	ARG
3	F	1676	ARG
3	F	1677	LEU
3	F	1689	ASP
3	F	1718	CYS
4	G	304	MET
4	G	338	HIS
4	G	392	ILE
4	G	415	ASP
4	G	419	THR
5	H	460	VAL
5	H	463	LEU
5	H	487	GLU
5	H	490	HIS
5	H	524	THR
5	H	543	VAL
5	H	549	THR
5	H	552	CYS
5	H	555	ARG
5	H	566	ASP
5	H	583	ARG
5	H	602	TYR
5	H	628	SER
5	H	660	CYS
4	I	304	MET
4	I	338	HIS
4	I	392	ILE
4	I	415	ASP
4	I	419	THR
5	J	463	LEU
5	J	487	GLU
5	J	490	HIS
5	J	524	THR
5	J	543	VAL
5	J	549	THR
5	J	552	CYS
5	J	555	ARG
5	J	566	ASP
5	J	583	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	J	602	TYR
5	J	628	SER
5	J	660	CYS
5	J	668	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	GLN
2	B	684	GLN
2	B	688	ASN
2	B	848	GLN
2	B	949	ASN
3	C	1700	GLN
2	E	684	GLN
2	E	848	GLN
2	E	949	ASN
2	E	1296	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are 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	TYS	B	1417	2	15,16,17	1.13	2 (13%)	16,22,24	1.38	1 (6%)
2	TYS	B	1420	-	15,16,17	0.93	1 (6%)	16,22,24	0.88	1 (6%)
2	TYS	E	1417	2	15,16,17	1.02	1 (6%)	16,22,24	1.64	4 (25%)
2	TYS	E	1420	-	15,16,17	0.91	2 (13%)	16,22,24	0.91	1 (6%)

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	TYS	B	1417	2	-	0/9/11/13	0/1/1/1
2	TYS	B	1420	-	-	0/9/11/13	0/1/1/1
2	TYS	E	1417	2	-	0/9/11/13	0/1/1/1
2	TYS	E	1420	-	-	0/9/11/13	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1420	TYS	OH-CZ	-2.02	1.39	1.42
2	E	1417	TYS	OH-S	2.09	1.67	1.63
2	B	1417	TYS	CE1-CD1	2.21	1.42	1.38
2	E	1420	TYS	OH-S	2.51	1.68	1.63
2	B	1420	TYS	OH-S	2.62	1.68	1.63
2	B	1417	TYS	OH-S	2.72	1.68	1.63

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1417	TYS	OH-CZ-CE2	-2.69	113.42	118.74
2	E	1417	TYS	CZ-OH-S	-2.29	114.61	118.52
2	E	1420	TYS	OH-CZ-CE2	2.18	123.05	118.74
2	B	1420	TYS	OH-CZ-CE2	2.28	123.24	118.74
2	E	1417	TYS	CG-CB-CA	2.33	119.48	114.21
2	B	1417	TYS	OH-CZ-CE1	3.72	126.09	118.74
2	E	1417	TYS	OH-CZ-CE1	4.22	127.08	118.74

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1420	TYS	1	0
2	E	1417	TYS	1	0
2	E	1420	TYS	1	0

5.5 Carbohydrates ⓘ

18 carbohydrates are 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$
6	NAG	A	701	1,6	14,14,15	0.95	1 (7%)	15,19,21	1.70	5 (33%)
6	NAG	A	702	6	14,14,15	0.59	0	15,19,21	1.13	1 (6%)
6	BMA	A	703	6	11,11,12	0.54	0	14,15,17	0.92	1 (7%)
6	NAG	B	1501	2,6	14,14,15	1.11	0	15,19,21	3.38	8 (53%)
6	NAG	B	1502	6	14,14,15	1.11	1 (7%)	15,19,21	3.48	8 (53%)
6	BMA	B	1503	6	11,11,12	1.28	2 (18%)	14,15,17	2.02	6 (42%)
6	NAG	B	1504	2,6	14,14,15	0.56	0	15,19,21	0.85	0
6	NAG	B	1505	6	14,14,15	0.52	0	15,19,21	0.80	0
6	BMA	B	1506	6	11,11,12	0.59	0	14,15,17	0.69	0
6	NAG	D	701	1,6	14,14,15	0.91	1 (7%)	15,19,21	1.74	4 (26%)
6	NAG	D	702	6	14,14,15	0.58	0	15,19,21	1.06	1 (6%)
6	BMA	D	703	6	11,11,12	0.55	0	14,15,17	0.77	0
6	NAG	E	1501	2,6	14,14,15	1.59	3 (21%)	15,19,21	4.03	11 (73%)
6	NAG	E	1502	6	14,14,15	1.19	1 (7%)	15,19,21	3.84	7 (46%)
6	BMA	E	1503	6	11,11,12	1.35	2 (18%)	14,15,17	3.21	6 (42%)
6	NAG	E	1504	2,6	14,14,15	0.57	0	15,19,21	1.00	0
6	NAG	E	1505	6	14,14,15	0.52	0	15,19,21	0.78	0
6	BMA	E	1506	6	11,11,12	0.59	0	14,15,17	0.71	0

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
6	NAG	A	701	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	702	6	-	0/6/23/26	0/1/1/1
6	BMA	A	703	6	-	0/2/19/22	0/1/1/1
6	NAG	B	1501	2,6	-	0/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	B	1502	6	-	0/6/23/26	0/1/1/1
6	BMA	B	1503	6	-	0/2/19/22	0/1/1/1
6	NAG	B	1504	2,6	-	0/6/23/26	0/1/1/1
6	NAG	B	1505	6	-	0/6/23/26	0/1/1/1
6	BMA	B	1506	6	-	0/2/19/22	0/1/1/1
6	NAG	D	701	1,6	-	0/6/23/26	0/1/1/1
6	NAG	D	702	6	-	0/6/23/26	0/1/1/1
6	BMA	D	703	6	-	0/2/19/22	0/1/1/1
6	NAG	E	1501	2,6	-	0/6/23/26	0/1/1/1
6	NAG	E	1502	6	-	0/6/23/26	0/1/1/1
6	BMA	E	1503	6	-	0/2/19/22	0/1/1/1
6	NAG	E	1504	2,6	-	0/6/23/26	0/1/1/1
6	NAG	E	1505	6	-	0/6/23/26	0/1/1/1
6	BMA	E	1506	6	-	0/2/19/22	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	1502	NAG	O5-C1	-2.76	1.39	1.43
6	A	701	NAG	O5-C1	-2.68	1.39	1.43
6	E	1501	NAG	O5-C1	-2.59	1.39	1.43
6	D	701	NAG	O5-C1	-2.42	1.39	1.43
6	B	1502	NAG	O5-C1	-2.39	1.39	1.43
6	E	1501	NAG	C4-C5	2.20	1.57	1.53
6	B	1503	BMA	C1-C2	2.30	1.57	1.52
6	E	1503	BMA	C2-C3	2.76	1.56	1.52
6	B	1503	BMA	C2-C3	3.12	1.56	1.52
6	E	1503	BMA	C1-C2	3.20	1.59	1.52
6	E	1501	NAG	C1-C2	3.41	1.57	1.52

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	1501	NAG	C2-N2-C7	-8.83	111.69	123.04
6	B	1501	NAG	C2-N2-C7	-8.53	112.08	123.04
6	B	1502	NAG	C2-N2-C7	-6.13	115.16	123.04
6	E	1501	NAG	O3-C3-C4	-5.05	98.96	110.34
6	B	1502	NAG	O3-C3-C2	-4.54	100.13	109.11
6	E	1502	NAG	O3-C3-C2	-4.37	100.45	109.11
6	B	1501	NAG	O3-C3-C4	-4.04	101.24	110.34
6	E	1502	NAG	C2-N2-C7	-3.87	118.07	123.04
6	B	1501	NAG	O3-C3-C2	-3.77	101.64	109.11

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	1502	NAG	O3-C3-C4	-3.73	101.93	110.34
6	E	1501	NAG	C3-C4-C5	-3.68	103.79	110.20
6	E	1502	NAG	O5-C5-C6	-3.53	99.71	107.35
6	B	1502	NAG	O3-C3-C4	-3.31	102.89	110.34
6	E	1501	NAG	O7-C7-C8	-3.29	116.02	122.06
6	E	1501	NAG	O4-C4-C3	-3.14	103.26	110.34
6	E	1501	NAG	C3-C2-N2	-3.09	103.16	110.56
6	B	1501	NAG	O7-C7-C8	-3.06	116.45	122.06
6	B	1502	NAG	O5-C5-C6	-2.97	100.91	107.35
6	D	701	NAG	O4-C4-C3	-2.86	103.91	110.34
6	D	701	NAG	O5-C5-C6	-2.80	101.28	107.35
6	A	701	NAG	O5-C5-C6	-2.73	101.45	107.35
6	E	1501	NAG	O7-C7-N2	-2.72	116.31	121.86
6	A	701	NAG	O4-C4-C3	-2.60	104.49	110.34
6	A	703	BMA	O5-C1-C2	-2.48	106.83	110.86
6	E	1501	NAG	O3-C3-C2	-2.41	104.35	109.11
6	E	1503	BMA	C6-C5-C4	-2.21	107.56	113.02
6	B	1501	NAG	O4-C4-C3	-2.19	105.42	110.34
6	A	701	NAG	O3-C3-C4	-2.09	105.63	110.34
6	B	1502	NAG	O7-C7-N2	-2.02	117.74	121.86
6	B	1503	BMA	C6-C5-C4	-2.02	108.04	113.02
6	B	1503	BMA	C1-C2-C3	2.03	111.94	109.54
6	E	1503	BMA	O2-C2-C3	2.33	114.80	110.12
6	E	1503	BMA	C2-C3-C4	2.36	115.05	111.04
6	B	1503	BMA	O2-C2-C1	2.44	114.10	109.21
6	D	702	NAG	C4-C3-C2	2.50	115.11	111.23
6	E	1503	BMA	O5-C1-C2	2.60	115.07	110.86
6	D	701	NAG	C3-C4-C5	2.60	114.73	110.20
6	A	701	NAG	C3-C4-C5	2.65	114.81	110.20
6	A	702	NAG	C4-C3-C2	2.67	115.39	111.23
6	B	1503	BMA	O2-C2-C3	2.92	115.99	110.12
6	B	1501	NAG	C1-O5-C5	3.10	116.18	112.25
6	D	701	NAG	C4-C3-C2	3.17	116.16	111.23
6	E	1502	NAG	C8-C7-N2	3.21	122.26	116.11
6	B	1503	BMA	C2-C3-C4	3.23	116.52	111.04
6	A	701	NAG	C4-C3-C2	3.25	116.28	111.23
6	E	1503	BMA	O2-C2-C1	3.73	116.68	109.21
6	B	1502	NAG	C8-C7-N2	3.76	123.29	116.11
6	E	1501	NAG	C4-C3-C2	3.90	117.29	111.23
6	B	1503	BMA	C1-O5-C5	3.99	117.31	112.25
6	B	1501	NAG	C4-C3-C2	4.31	117.93	111.23
6	B	1501	NAG	C8-C7-N2	4.36	124.44	116.11

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	1501	NAG	C1-O5-C5	5.37	119.06	112.25
6	B	1502	NAG	C4-C3-C2	5.86	120.35	111.23
6	E	1501	NAG	C8-C7-N2	6.04	127.66	116.11
6	B	1502	NAG	C1-O5-C5	6.74	120.81	112.25
6	E	1502	NAG	C4-C3-C2	7.55	122.96	111.23
6	E	1502	NAG	C1-O5-C5	9.00	123.67	112.25
6	E	1503	BMA	C1-O5-C5	9.82	124.71	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1504	NAG	2	0
6	E	1504	NAG	2	0

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	651/656 (99%)	-0.39	1 (0%) 95 91	68, 116, 172, 203	0
1	D	651/656 (99%)	-0.39	2 (0%) 94 89	54, 103, 169, 213	0
2	B	738/767 (96%)	-0.34	7 (0%) 85 74	51, 109, 185, 245	0
2	E	738/767 (96%)	-0.25	12 (1%) 74 59	66, 114, 202, 290	0
3	C	287/291 (98%)	-0.48	0 100 100	52, 89, 137, 180	0
3	F	287/291 (98%)	-0.37	0 100 100	59, 92, 150, 193	0
4	G	145/154 (94%)	-0.54	0 100 100	89, 123, 167, 197	0
4	I	145/154 (94%)	-0.31	1 (0%) 89 80	86, 123, 186, 204	0
5	H	242/242 (100%)	-0.01	3 (1%) 81 67	117, 178, 222, 247	0
5	J	242/242 (100%)	-0.29	2 (0%) 87 77	77, 129, 183, 202	0
All	All	4126/4220 (97%)	-0.33	28 (0%) 89 80	51, 112, 190, 290	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	1128	MET	3.9
2	B	1236	SER	3.8
2	B	1238	SER	3.7
2	E	1246	ALA	3.7
2	B	1246	ALA	3.6
5	H	625	GLY	3.3
2	B	1237	GLN	3.1
2	E	1235	GLY	2.9
2	E	1236	SER	2.8
2	E	1131	GLY	2.8
5	H	445	ILE	2.7
5	J	445	ILE	2.7
5	J	611	SER	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	E	1130	GLY	2.6
2	B	1241	VAL	2.6
5	H	626	LYS	2.6
2	E	1129	GLN	2.5
2	B	1235	GLY	2.5
2	E	1239	ASN	2.4
1	A	583	ASN	2.3
2	E	1238	SER	2.2
2	E	1371	GLY	2.2
1	D	332	ASP	2.2
2	E	1234	THR	2.1
1	D	670	PRO	2.1
2	B	1240	ALA	2.1
2	E	831	ARG	2.1
4	I	398	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	TYS	E	1420	16/17	0.64	0.30	-	173,250,270,277	4
2	TYS	B	1417	16/17	0.72	0.33	-	114,210,238,244	4
2	TYS	E	1417	16/17	0.69	0.47	-	132,258,279,279	4
2	TYS	B	1420	16/17	0.73	0.35	-	209,229,236,239	4

6.3 Carbohydrates [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
6	NAG	B	1504	14/15	0.85	0.32	0.80	227,232,239,241	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	NAG	E	1504	14/15	0.83	0.26	-0.64	186,197,224,226	0
6	NAG	A	701	14/15	0.77	0.31	-	174,184,212,218	0
6	NAG	B	1501	14/15	0.93	0.31	-	214,224,238,245	0
6	BMA	A	703	11/12	0.85	0.19	-	159,171,177,179	0
6	BMA	E	1503	11/12	0.72	0.32	-	205,219,235,236	0
6	NAG	B	1505	14/15	0.75	0.30	-	209,215,234,239	0
6	NAG	B	1502	14/15	0.86	0.30	-	216,226,228,229	0
6	NAG	A	702	14/15	0.79	0.24	-	170,179,185,188	0
6	NAG	E	1502	14/15	0.82	0.30	-	213,218,243,245	0
6	BMA	D	703	11/12	0.77	0.25	-	233,241,247,252	0
6	NAG	E	1505	14/15	0.82	0.22	-	187,199,207,210	0
6	BMA	E	1506	11/12	0.78	0.20	-	182,195,199,203	0
6	BMA	B	1506	11/12	0.80	0.27	-	192,201,204,205	0
6	NAG	E	1501	14/15	0.91	0.22	-	197,205,224,225	0
6	BMA	B	1503	11/12	0.71	0.23	-	218,228,232,232	0
6	NAG	D	701	14/15	0.80	0.33	-	167,208,231,234	0
6	NAG	D	702	14/15	0.82	0.35	-	214,228,238,244	0

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.