



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 09:21 am BST

PDB ID : 6ADB
Title : Crystal structure of the E148N mutant CLC-ec1 in 20mM bromide
Authors : Lim, H.-H.; Park, K.
Deposited on : 2018-07-31
Resolution : 2.69 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

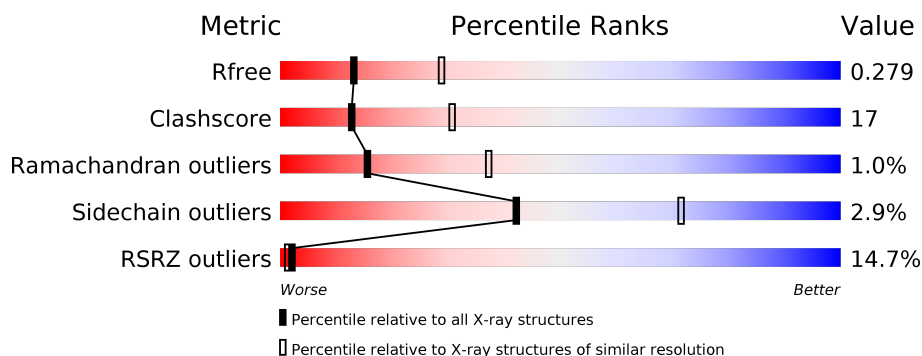
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	473	<div> <div>14%</div> <div> <div>66%</div> <div>27%</div> <div>• 6%</div> </div> </div>
1	B	473	<div> <div>21%</div> <div> <div>61%</div> <div>31%</div> <div>• 7%</div> </div> </div>
2	C	222	<div> <div>10%</div> <div> <div>73%</div> <div>26%</div> <div>•</div> </div> </div>
2	E	222	<div> <div>9%</div> <div> <div>73%</div> <div>23%</div> <div>•</div> </div> </div>
3	D	211	<div> <div>14%</div> <div> <div>61%</div> <div>37%</div> <div>•</div> </div> </div>
3	F	211	<div> <div>10%</div> <div> <div>69%</div> <div>29%</div> <div>•</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	BR	A	501	-	-	X	-
4	BR	A	502	-	-	X	-
4	BR	B	501	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 13247 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 H(+)/Cl(-) exchange transporter ClcA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total	C	N	O	S	0	0	0
			3332	2189	561	562	20			
1	B	442	Total	C	N	O	S	0	0	0
			3314	2179	558	557	20			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	148	ASN	GLU	engineered mutation	UNP P37019
B	148	ASN	GLU	engineered mutation	UNP P37019

- Molecule 2 is a protein called antibody Fab fragment, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	222	Total	C	N	O	S	0	0	0
			1681	1082	275	318	6			
2	E	221	Total	C	N	O	S	0	0	0
			1672	1077	274	315	6			

- Molecule 3 is a protein called antibody Fab fragment, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	211	Total	C	N	O	S	0	0	0
			1621	1008	271	334	8			
3	F	211	Total	C	N	O	S	0	0	0
			1621	1008	271	334	8			

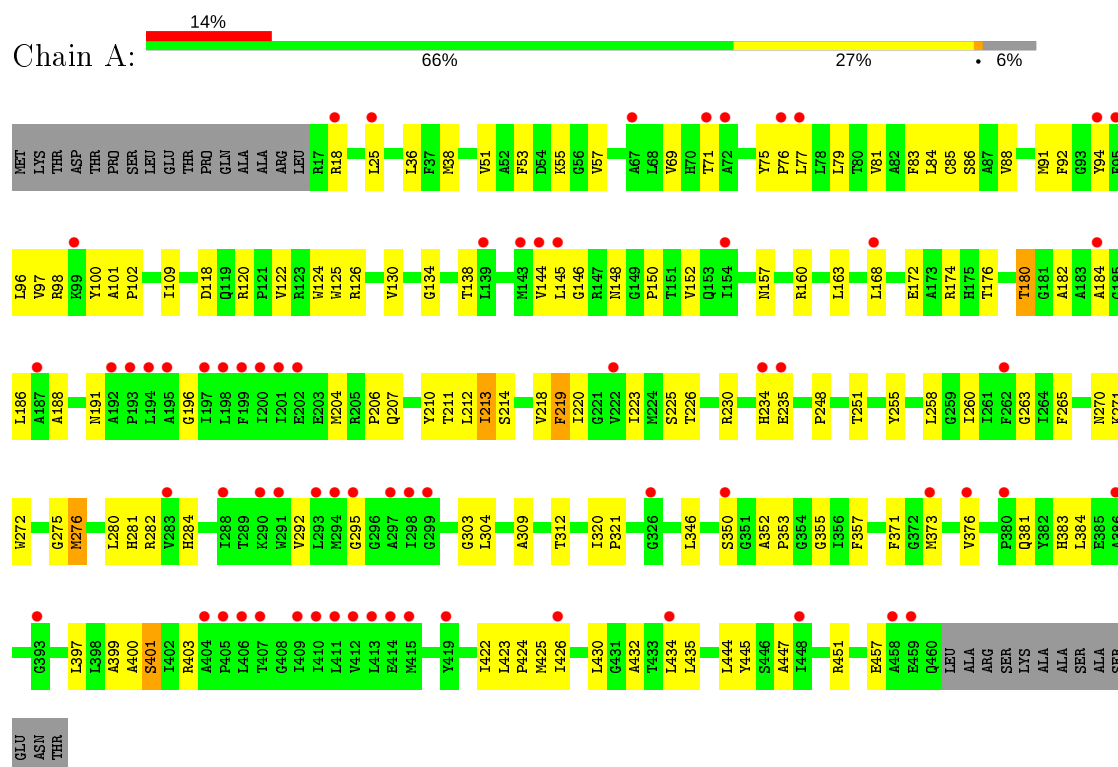
- Molecule 4 is BROMIDE ION (three-letter code: BR) (formula: Br) (labeled as "Ligand of Interest" by author).

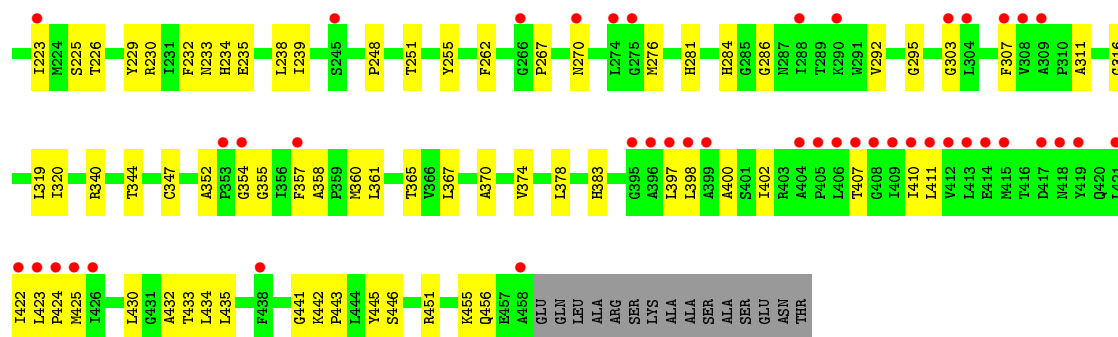
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	3	Total 3	Br 3	0	0
4	A	3	Total 3	Br 3	0	0

3 Residue-property plots

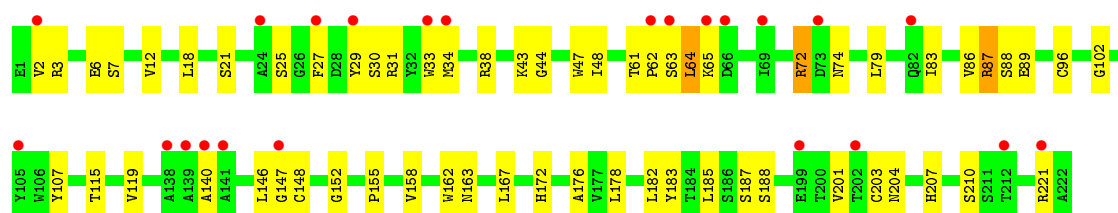
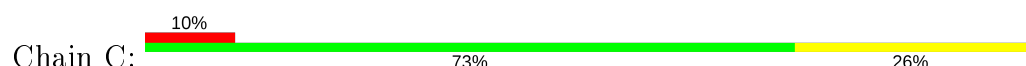
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: H(+)/Cl(-) exchange transporter ClcA

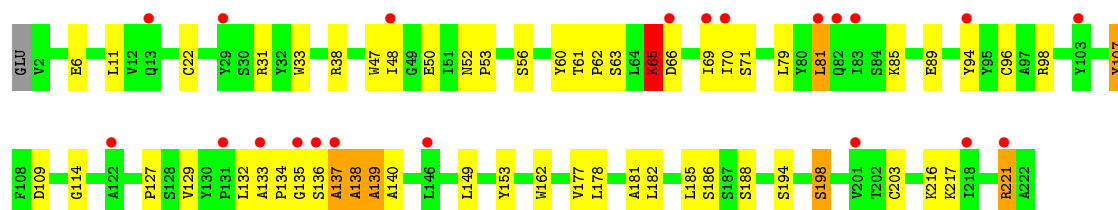




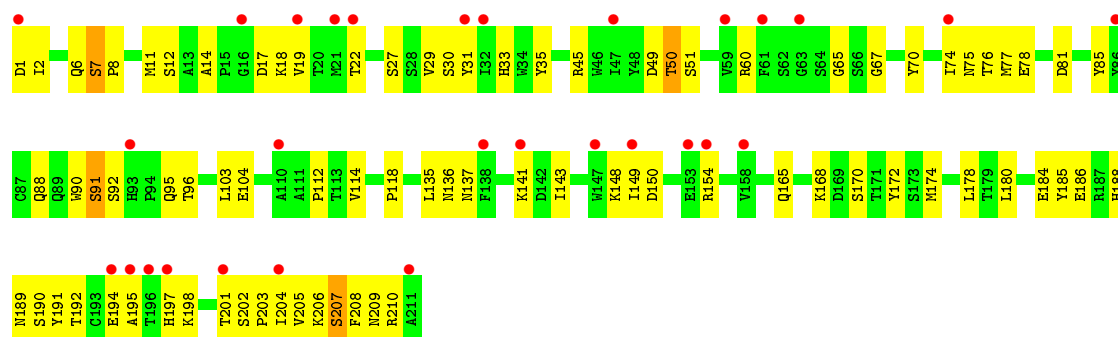
- Molecule 2: antibody Fab fragment, heavy chain



- Molecule 2: antibody Fab fragment, heavy chain

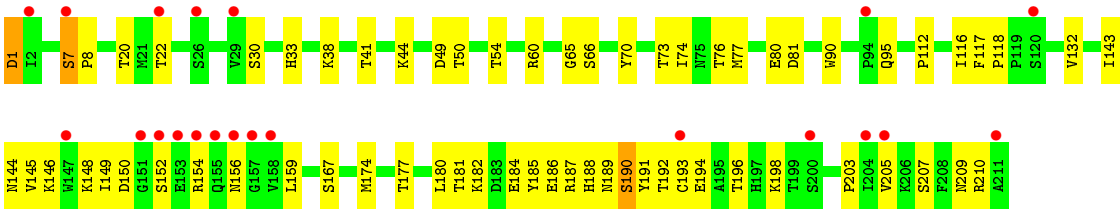


- Molecule 3: antibody Fab fragment, light chain



- Molecule 3: antibody Fab fragment, light chain





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	231.90 Å 97.98 Å 170.79 Å 90.00° 132.02° 90.00°	Depositor
Resolution (Å)	33.96 – 2.69 49.54 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.0 (33.96-2.69) 99.3 (49.54-2.69)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 2.69 Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.237 , 0.278 0.239 , 0.279	Depositor DCC
R_{free} test set	3952 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	77.1	Xtriage
Anisotropy	0.462	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 64.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.006 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	13247	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.49	1/3404 (0.0%)	0.60	0/4620
1	B	0.43	0/3386	0.65	3/4596 (0.1%)
2	C	0.52	1/1730 (0.1%)	0.72	0/2367
2	E	0.50	0/1721	0.68	1/2355 (0.0%)
3	D	0.48	0/1660	0.66	0/2257
3	F	0.48	0/1660	0.67	0/2257
All	All	0.48	2/13561 (0.0%)	0.66	4/18452 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	150	PRO	N-CD	-14.03	1.28	1.47
2	C	148	CYS	CB-SG	-5.54	1.72	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	139	LEU	CA-CB-CG	6.22	129.60	115.30
1	B	212	LEU	CA-CB-CG	-5.34	103.03	115.30
1	B	78	LEU	CB-CG-CD1	-5.06	102.39	111.00
2	E	185	LEU	CA-CB-CG	5.03	126.88	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3332	0	3484	125	0
1	B	3314	0	3470	140	0
2	C	1681	0	1663	40	0
2	E	1672	0	1654	43	0
3	D	1621	0	1546	78	0
3	F	1621	0	1546	57	0
4	A	3	0	0	5	0
4	B	3	0	0	5	0
All	All	13247	0	13363	442	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 17.

All (442) 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)
3:D:194:GLU:HG2	3:D:205:VAL:HG12	1.16	1.11
2:E:133:ALA:O	2:E:221:ARG:NH1	1.88	1.05
3:D:60:ARG:NH1	3:D:81:ASP:OD1	1.89	1.05
3:D:95:GLN:N	3:D:95:GLN:OE1	1.94	1.00
3:F:95:GLN:H	3:F:95:GLN:CD	1.66	0.99
3:D:6:GLN:NE2	3:D:85:TYR:O	1.98	0.96
3:F:95:GLN:OE1	3:F:95:GLN:N	1.99	0.94
3:D:194:GLU:CG	3:D:205:VAL:HG12	2.00	0.90
1:A:146:GLY:HA3	4:A:501:BR:BR	2.27	0.89
1:B:18:ARG:H	1:B:18:ARG:HD3	1.36	0.89
1:B:320:ILE:HG23	1:B:365:THR:HG21	1.54	0.88
2:E:47:TRP:CD2	3:F:95:GLN:NE2	2.42	0.88
1:B:59:TRP:CE2	1:B:63:GLN:NE2	2.41	0.88
3:D:60:ARG:NH1	3:D:78:GLU:HB2	1.91	0.86
3:D:104:GLU:OE2	3:D:172:TYR:OH	1.95	0.84
3:F:192:THR:HG22	3:F:207:SER:HB3	1.60	0.84
1:A:98:ARG:HH22	1:A:102:PRO:HB3	1.44	0.82
3:D:114:VAL:HG22	3:D:135:LEU:HD22	1.63	0.81
1:A:206:PRO:HG2	1:A:211:THR:HG21	1.63	0.81
1:A:125:TRP:CD1	1:A:126:ARG:HG3	2.16	0.80
3:D:60:ARG:HB2	3:D:74:ILE:CD1	2.11	0.80
1:A:38:MET:HG3	1:A:168:LEU:HD11	1.62	0.80
1:A:101:ALA:HB3	1:A:130:VAL:HG11	1.63	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:PHE:HB3	1:B:430:LEU:HD21	1.64	0.79
3:D:60:ARG:HH12	3:D:78:GLU:HB2	1.50	0.77
2:E:70:ILE:HG13	2:E:81:LEU:HD12	1.68	0.76
1:A:124:TRP:HA	1:A:157:ASN:HD22	1.51	0.75
2:E:135:GLY:HA2	2:E:221:ARG:HD2	1.67	0.75
3:F:185:TYR:O	3:F:191:TYR:OH	2.05	0.75
1:A:176:THR:HG22	1:A:213:ILE:HA	1.67	0.75
2:E:134:PRO:C	2:E:221:ARG:NH1	2.40	0.75
1:A:126:ARG:O	1:A:130:VAL:HG12	1.87	0.75
2:E:135:GLY:O	2:E:137:ALA:N	2.20	0.75
2:E:134:PRO:C	2:E:221:ARG:HH11	1.90	0.74
1:A:430:LEU:HD11	1:B:219:PHE:CD1	2.22	0.74
3:F:194:GLU:HG2	3:F:205:VAL:HG13	1.69	0.74
3:D:31:TYR:HA	3:D:50:THR:HG23	1.70	0.74
2:C:30:SER:O	2:C:31:ARG:HB2	1.88	0.73
3:D:60:ARG:HD2	3:D:74:ILE:HD11	1.71	0.73
3:F:192:THR:HG22	3:F:207:SER:CB	2.18	0.73
1:A:207:GLN:NE2	1:B:28:ARG:HH11	1.86	0.73
1:B:206:PRO:HG2	1:B:211:THR:HG21	1.71	0.73
2:E:89:GLU:N	2:E:89:GLU:OE2	2.22	0.72
1:B:145:LEU:HD11	1:B:347:CYS:HB3	1.72	0.72
1:A:18:ARG:NH2	1:B:456:GLN:CD	2.44	0.71
1:B:72:ALA:HA	1:B:78:LEU:HD22	1.72	0.71
2:C:221:ARG:HH12	3:D:118:PRO:HD2	1.56	0.71
1:A:422:ILE:HA	1:A:425:MET:HE2	1.73	0.71
1:A:83:PHE:HD1	1:A:84:LEU:HD12	1.55	0.70
3:D:29:VAL:O	3:D:70:TYR:OH	2.07	0.70
1:B:150:PRO:HD3	1:B:354:GLY:HA2	1.73	0.70
1:B:229:TYR:OH	1:B:238:LEU:HD11	1.91	0.70
2:C:163:ASN:HD22	2:C:167:LEU:HD13	1.56	0.70
3:F:186:GLU:O	3:F:210:ARG:NH2	2.25	0.69
1:B:38:MET:HA	1:B:41:VAL:HG13	1.74	0.69
3:D:104:GLU:HB2	3:D:165:GLN:OE1	1.92	0.69
3:D:60:ARG:HB2	3:D:74:ILE:HD12	1.74	0.69
1:A:18:ARG:NH2	1:B:456:GLN:OE1	2.25	0.69
3:F:7:SER:HB3	3:F:22:THR:OG1	1.92	0.69
1:B:68:LEU:HD13	1:B:307:PHE:HD1	1.59	0.68
1:A:148:ASN:O	1:A:152:VAL:HG22	1.95	0.67
1:A:426:ILE:HG23	1:B:219:PHE:CE2	2.30	0.67
1:A:191:ASN:HD21	1:A:230:ARG:NH1	1.92	0.67
1:B:374:VAL:HG12	1:B:378:LEU:HD11	1.77	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:88:SER:HA	2:C:119:VAL:HG13	1.76	0.66
1:A:98:ARG:NH2	1:A:102:PRO:HB3	2.10	0.66
3:D:60:ARG:HB2	3:D:74:ILE:HD11	1.76	0.66
3:D:19:VAL:HB	3:D:74:ILE:CG2	2.25	0.66
3:F:192:THR:CG2	3:F:207:SER:HB3	2.26	0.66
3:F:132:VAL:HG22	3:F:177:THR:HG23	1.77	0.66
1:B:184:ALA:HB1	1:B:225:SER:HB2	1.78	0.65
1:B:124:TRP:HA	1:B:157:ASN:HD22	1.61	0.65
1:B:239:ILE:HD11	1:B:320:ILE:CG2	2.26	0.65
2:E:47:TRP:CE3	3:F:95:GLN:NE2	2.64	0.65
2:E:98:ARG:NH1	2:E:109:ASP:OD2	2.28	0.65
1:A:210:TYR:HB3	1:B:209:ARG:HH11	1.61	0.65
3:D:154:ARG:HH12	3:D:180:LEU:HD21	1.62	0.65
3:D:192:THR:HG22	3:D:207:SER:HB2	1.79	0.65
2:E:134:PRO:O	2:E:221:ARG:NH1	2.31	0.64
1:B:98:ARG:NH2	1:B:102:PRO:HB3	2.12	0.64
2:C:38:ARG:HD3	2:C:48:ILE:HD11	1.80	0.64
2:C:34:MET:HB3	2:C:79:LEU:HD22	1.79	0.64
1:A:376:VAL:HG12	1:A:384:LEU:HB2	1.79	0.64
2:C:64:LEU:HD12	2:C:65:LYS:H	1.61	0.64
1:A:430:LEU:HD21	1:B:219:PHE:HB3	1.80	0.64
1:A:184:ALA:HB1	1:A:225:SER:HB2	1.80	0.64
1:B:20:GLN:O	1:B:24:GLN:HG3	1.98	0.64
1:B:360:MET:HE3	1:B:398:LEU:HD23	1.78	0.64
3:F:145:VAL:HG11	3:F:174:MET:HE1	1.80	0.63
3:F:146:LYS:HB3	3:F:194:GLU:HB2	1.81	0.63
1:B:20:GLN:OE1	1:B:24:GLN:NE2	2.32	0.63
1:A:75:TYR:CE2	1:A:79:LEU:HD11	2.34	0.62
2:E:149:LEU:HD12	2:E:186:SER:OG	2.00	0.62
3:D:31:TYR:HB3	3:D:49:ASP:HA	1.82	0.62
2:C:207:HIS:HD2	2:C:210:SER:OG	1.83	0.62
1:B:17:ARG:O	1:B:20:GLN:HG3	2.00	0.62
1:B:59:TRP:CD2	1:B:63:GLN:NE2	2.62	0.61
1:A:255:TYR:CD1	1:A:424:PRO:HB3	2.36	0.61
1:B:74:ASN:HB3	1:B:77:LEU:HB3	1.82	0.61
1:A:271:LYS:NZ	1:A:275:GLY:HA3	2.16	0.61
2:E:85:LYS:HD2	2:E:85:LYS:N	2.15	0.61
1:A:447:ALA:O	1:A:451:ARG:HG3	2.00	0.61
1:B:112:ILE:HG23	1:B:178:LEU:HD21	1.83	0.61
2:C:87:ARG:HH11	2:C:89:GLU:HB3	1.66	0.61
3:D:185:TYR:CZ	3:D:210:ARG:HD3	2.36	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:THR:HG22	1:B:218:VAL:HA	1.81	0.60
1:B:146:GLY:HA3	4:B:501:BR:BR	2.56	0.60
1:A:118:ASP:CG	1:A:174:ARG:HH21	2.03	0.60
2:E:47:TRP:CE2	3:F:95:GLN:NE2	2.69	0.60
1:A:100:TYR:O	1:A:126:ARG:NH1	2.34	0.60
1:B:219:PHE:O	1:B:223:ILE:HD12	2.01	0.60
1:B:125:TRP:CD1	1:B:126:ARG:HG3	2.37	0.60
3:F:148:LYS:HB2	3:F:192:THR:OG1	2.02	0.60
1:A:94:TYR:CZ	1:A:352:ALA:HB2	2.37	0.59
3:D:75:ASN:O	3:D:76:THR:HG22	2.02	0.59
1:A:172:GLU:O	1:A:176:THR:HG23	2.02	0.59
2:C:2:VAL:HG23	2:C:27:PHE:CD1	2.37	0.59
3:F:180:LEU:HD22	3:F:184:GLU:HG2	1.83	0.59
1:A:276:MET:O	1:A:280:LEU:HD12	2.03	0.59
1:B:41:VAL:O	1:B:45:LEU:HG	2.03	0.59
2:C:7:SER:HA	2:C:115:THR:HG21	1.84	0.59
1:A:36:LEU:HD13	1:B:434:LEU:HD21	1.85	0.58
3:D:19:VAL:HG11	3:D:103:LEU:CD1	2.33	0.58
3:D:35:TYR:OH	3:D:88:GLN:OE1	2.15	0.58
2:C:146:LEU:HD12	2:C:201:VAL:HG11	1.84	0.58
3:D:7:SER:HB3	3:D:22:THR:HB	1.85	0.58
1:A:207:GLN:HE21	1:B:28:ARG:HD2	1.66	0.58
1:B:144:VAL:HG23	1:B:144:VAL:O	2.02	0.58
1:B:150:PRO:CD	1:B:354:GLY:HA2	2.33	0.58
1:B:145:LEU:CD1	1:B:347:CYS:HB3	2.33	0.58
1:A:423:LEU:HD13	1:B:230:ARG:CZ	2.34	0.58
1:B:234:HIS:CE1	1:B:235:GLU:HG3	2.39	0.58
1:B:59:TRP:CZ2	1:B:63:GLN:NE2	2.71	0.58
3:D:19:VAL:HB	3:D:74:ILE:HG22	1.85	0.58
3:D:17:ASP:OD1	3:D:18:LYS:N	2.37	0.57
1:A:75:TYR:O	1:A:79:LEU:HD12	2.03	0.57
1:B:239:ILE:HD11	1:B:320:ILE:HG21	1.86	0.57
2:E:85:LYS:HD2	2:E:85:LYS:H	1.67	0.57
1:A:434:LEU:HD11	1:B:220:ILE:HD11	1.87	0.57
1:B:248:PRO:O	1:B:251:THR:HB	2.05	0.57
1:A:146:GLY:CA	4:A:501:BR:BR	3.06	0.57
1:B:66:GLY:O	1:B:69:VAL:HG12	2.04	0.57
2:C:12:VAL:HG11	2:C:18:LEU:HD23	1.86	0.57
1:A:176:THR:HG22	1:A:214:SER:H	1.69	0.57
1:B:358:ALA:HA	1:B:361:LEU:HD12	1.86	0.57
2:C:162:TRP:CZ3	2:C:203:CYS:HB3	2.40	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:178:LEU:HB2	2:C:183:TYR:CE2	2.39	0.57
1:A:207:GLN:HE21	1:B:28:ARG:HH11	1.48	0.57
1:B:38:MET:O	1:B:42:VAL:HG23	2.05	0.57
3:D:7:SER:HB3	3:D:8:PRO:HD3	1.87	0.57
1:A:276:MET:HG3	1:A:280:LEU:CD1	2.34	0.56
1:B:267:PRO:HB3	1:B:441:GLY:HA3	1.86	0.56
1:A:346:LEU:O	1:A:350:SER:HB3	2.05	0.56
1:B:110:PRO:HG2	4:B:503:BR:BR	2.61	0.56
1:B:68:LEU:HA	1:B:78:LEU:HD11	1.88	0.56
1:A:138:THR:HG21	1:A:353:PRO:O	2.06	0.56
1:A:92:PHE:O	1:A:96:LEU:HD12	2.06	0.56
1:B:357:PHE:HE2	1:B:411:LEU:HD22	1.71	0.56
1:B:198:LEU:HG	1:B:410:ILE:HD12	1.88	0.55
1:A:191:ASN:ND2	1:A:230:ARG:NH1	2.54	0.55
1:B:123:ARG:HE	1:B:126:ARG:HD2	1.70	0.55
1:A:400:ALA:HB2	1:A:432:ALA:HB1	1.89	0.55
1:A:381:GLN:N	1:A:381:GLN:OE1	2.27	0.55
1:B:176:THR:O	1:B:180:THR:HG23	2.07	0.55
1:B:402:ILE:N	1:B:402:ILE:HD12	2.22	0.55
3:F:148:LYS:HA	3:F:152:SER:O	2.08	0.54
1:A:430:LEU:HD22	1:B:223:ILE:HD11	1.88	0.54
3:D:1:ASP:N	3:D:1:ASP:OD2	2.36	0.54
3:F:144:ASN:HB2	3:F:196:THR:OG1	2.06	0.54
1:A:92:PHE:CZ	1:A:96:LEU:HD11	2.43	0.54
3:F:38:LYS:O	3:F:41:THR:HB	2.07	0.54
1:A:77:LEU:O	1:A:81:VAL:HG23	2.07	0.54
1:B:132:PHE:O	1:B:136:LEU:HG	2.08	0.54
2:E:149:LEU:HD13	3:F:132:VAL:HG21	1.89	0.54
3:F:192:THR:CB	3:F:207:SER:HB3	2.38	0.54
1:B:94:TYR:CZ	1:B:352:ALA:HB2	2.43	0.53
3:F:182:LYS:O	3:F:186:GLU:HG3	2.08	0.53
1:A:176:THR:CG2	1:A:214:SER:H	2.21	0.53
3:F:181:THR:HG23	3:F:184:GLU:H	1.73	0.53
2:C:43:LYS:CD	2:C:44:GLY:H	2.22	0.53
3:F:145:VAL:HA	3:F:194:GLU:O	2.08	0.53
1:B:47:GLY:O	1:B:51:VAL:HG23	2.08	0.53
1:B:255:TYR:CD1	1:B:424:PRO:HB3	2.44	0.53
3:D:60:ARG:NH1	3:D:78:GLU:CB	2.69	0.53
2:E:22:CYS:HB3	2:E:79:LEU:HB3	1.90	0.53
1:A:355:GLY:HA3	4:A:501:BR:BR	2.64	0.52
1:B:109:ILE:HB	1:B:110:PRO:HD3	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:162:TRP:CZ3	2:E:203:CYS:HB3	2.44	0.52
1:A:281:HIS:HA	1:A:284:HIS:CE1	2.44	0.52
1:A:220:ILE:HD11	1:B:434:LEU:HD11	1.92	0.52
3:F:44:LYS:NZ	3:F:54:THR:HG21	2.25	0.52
1:A:191:ASN:OD1	1:A:230:ARG:NH1	2.43	0.52
1:A:251:THR:HG22	1:A:255:TYR:HE1	1.73	0.52
2:C:43:LYS:HD2	2:C:44:GLY:H	1.74	0.52
1:A:191:ASN:HD21	1:A:230:ARG:HH11	1.57	0.52
3:F:60:ARG:NH2	3:F:81:ASP:OD2	2.42	0.52
3:D:141:LYS:HD3	3:D:172:TYR:CZ	2.45	0.52
3:D:60:ARG:CD	3:D:74:ILE:HD11	2.40	0.52
1:A:94:TYR:CE1	1:A:295:GLY:HA3	2.45	0.52
2:C:87:ARG:O	2:C:119:VAL:HG11	2.10	0.52
3:F:30:SER:HA	3:F:70:TYR:OH	2.10	0.52
3:D:14:ALA:O	3:D:17:ASP:HB3	2.10	0.51
2:E:127:PRO:HB3	2:E:153:TYR:HB3	1.93	0.51
2:C:152:GLY:HA2	2:C:182:LEU:HB3	1.91	0.51
2:C:162:TRP:CH2	2:C:203:CYS:HB3	2.45	0.51
1:B:144:VAL:CG2	1:B:344:THR:HA	2.40	0.51
2:C:176:ALA:HB2	2:C:185:LEU:HD23	1.93	0.51
3:D:148:LYS:HB2	3:D:192:THR:OG1	2.10	0.51
1:B:148:ASN:HB3	4:B:501:BR:BR	2.65	0.51
1:B:281:HIS:HA	1:B:284:HIS:CE1	2.46	0.51
1:B:400:ALA:HB2	1:B:432:ALA:HB1	1.92	0.51
3:D:180:LEU:HD23	3:D:184:GLU:OE1	2.09	0.51
1:B:451:ARG:O	1:B:455:LYS:HE2	2.11	0.51
2:C:12:VAL:O	2:C:119:VAL:HA	2.12	0.50
2:C:72:ARG:HD3	2:C:74:ASN:OD1	2.11	0.50
3:D:197:HIS:CG	3:D:198:LYS:H	2.29	0.50
1:A:191:ASN:ND2	1:A:230:ARG:HH11	2.10	0.50
1:B:145:LEU:HD23	1:B:354:GLY:C	2.32	0.50
1:B:144:VAL:HG21	1:B:344:THR:HA	1.94	0.50
2:C:47:TRP:CE2	3:D:95:GLN:NE2	2.80	0.50
1:B:20:GLN:HA	1:B:23:ARG:NH1	2.27	0.50
2:E:47:TRP:HZ2	2:E:50:GLU:HG2	1.77	0.50
1:A:122:VAL:HB	1:A:160:ARG:HG2	1.93	0.49
1:A:260:ILE:HG23	1:A:435:LEU:HG	1.93	0.49
3:D:31:TYR:HA	3:D:50:THR:CG2	2.39	0.49
2:E:38:ARG:HD3	2:E:48:ILE:HD11	1.94	0.49
2:E:137:ALA:O	2:E:139:ALA:N	2.42	0.49
1:A:180:THR:HB	1:A:218:VAL:HA	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:ASP:CG	1:B:174:ARG:HH21	2.12	0.49
2:C:155:PRO:O	2:C:207:HIS:HE1	1.95	0.49
3:D:136:ASN:HB3	3:D:137:ASN:HD22	1.78	0.49
3:F:186:GLU:C	3:F:188:HIS:H	2.16	0.49
1:B:148:ASN:HD21	1:B:186:LEU:HD12	1.77	0.49
3:D:2:ILE:HD12	3:D:27:SER:HB2	1.95	0.49
1:B:77:LEU:O	1:B:81:VAL:HG12	2.13	0.49
1:B:61:GLN:OE1	1:B:64:ARG:NH2	2.46	0.49
3:D:191:TYR:HB2	3:D:208:PHE:CE2	2.47	0.49
1:A:109:ILE:HG12	1:A:152:VAL:HG21	1.94	0.49
3:F:80:GLU:HA	3:F:167:SER:O	2.13	0.49
1:A:83:PHE:CD1	1:A:84:LEU:HD12	2.42	0.49
1:A:18:ARG:NH2	1:B:456:GLN:NE2	2.61	0.48
1:A:270:ASN:ND2	1:A:444:LEU:HD13	2.28	0.48
1:A:144:VAL:O	1:A:145:LEU:HG	2.14	0.48
3:D:74:ILE:HG12	3:D:81:ASP:OD2	2.12	0.48
1:A:234:HIS:HD1	1:A:235:GLU:HG3	1.78	0.48
1:A:186:LEU:HD22	1:A:196:GLY:HA2	1.96	0.48
3:D:30:SER:H	3:D:91:SER:HB3	1.78	0.48
3:F:20:THR:HG23	3:F:73:THR:OG1	2.13	0.48
2:E:177:VAL:HG11	3:F:159:LEU:HD13	1.95	0.48
1:A:97:VAL:HA	1:A:130:VAL:HG21	1.95	0.48
3:F:95:GLN:CD	3:F:95:GLN:N	2.45	0.48
1:B:355:GLY:HA3	4:B:501:BR:BR	2.69	0.48
3:D:186:GLU:O	3:D:210:ARG:NH2	2.47	0.48
1:A:152:VAL:HG12	1:A:182:ALA:O	2.14	0.48
1:B:152:VAL:HG13	1:B:182:ALA:HB1	1.95	0.48
1:A:188:ALA:HB2	1:A:225:SER:OG	2.13	0.47
1:A:226:THR:HG21	1:B:423:LEU:HD11	1.95	0.47
2:C:86:VAL:HG12	2:C:119:VAL:HG21	1.96	0.47
3:D:7:SER:CB	3:D:8:PRO:HD3	2.43	0.47
3:F:154:ARG:HE	3:F:156:ASN:HB2	1.79	0.47
3:F:66:SER:HA	3:F:70:TYR:CZ	2.48	0.47
1:A:25:LEU:HD23	1:B:208:PHE:HE1	1.79	0.47
2:C:107:TYR:HB3	3:D:33:HIS:CE1	2.49	0.47
2:E:132:LEU:HD11	2:E:149:LEU:HB2	1.95	0.47
3:F:150:ASP:HA	3:F:190:SER:HB3	1.97	0.47
3:D:2:ILE:O	3:D:96:THR:HG21	2.14	0.47
1:B:422:ILE:HA	1:B:425:MET:HE3	1.96	0.47
1:B:71:THR:HB	1:B:77:LEU:HD23	1.95	0.47
2:E:107:TYR:HB3	3:F:33:HIS:CD2	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:66:ASP:HB3	2:E:69:ILE:HD11	1.96	0.47
1:A:109:ILE:HG23	1:A:204:MET:SD	2.55	0.47
1:B:38:MET:HE1	1:B:166:PHE:CD2	2.49	0.47
1:B:51:VAL:HG11	1:B:232:PHE:HB2	1.97	0.47
1:A:148:ASN:HD21	1:A:186:LEU:HD12	1.80	0.47
3:D:104:GLU:OE1	3:D:141:LYS:HE2	2.15	0.47
2:E:70:ILE:CG1	2:E:81:LEU:HD12	2.43	0.47
1:A:251:THR:HG22	1:A:255:TYR:CE1	2.49	0.46
1:A:399:ALA:O	1:A:403:ARG:HA	2.16	0.46
1:B:397:LEU:HA	1:B:397:LEU:HD23	1.72	0.46
1:B:430:LEU:HA	1:B:433:THR:HG22	1.98	0.46
1:B:68:LEU:HD13	1:B:307:PHE:CD1	2.44	0.46
2:C:18:LEU:HD11	2:C:83:ILE:HD12	1.97	0.46
3:D:112:PRO:HG3	3:D:143:ILE:HD11	1.96	0.46
1:B:212:LEU:HD23	1:B:212:LEU:HA	1.64	0.46
1:B:53:PHE:O	1:B:57:VAL:HG23	2.16	0.46
2:C:87:ARG:HH11	2:C:89:GLU:CB	2.28	0.46
1:B:91:MET:HG2	1:B:292:VAL:O	2.14	0.46
3:D:60:ARG:NH1	3:D:78:GLU:HG2	2.31	0.46
1:A:422:ILE:HA	1:A:422:ILE:HD12	1.79	0.46
1:B:118:ASP:OD1	1:B:174:ARG:NH2	2.29	0.46
1:B:374:VAL:HG12	1:B:378:LEU:CD1	2.45	0.46
1:A:91:MET:HG2	1:A:292:VAL:O	2.16	0.46
1:B:360:MET:HE1	1:B:402:ILE:HD11	1.97	0.46
1:B:445:TYR:OH	4:B:502:BR:BR	2.77	0.46
3:D:77:MET:HE2	3:D:103:LEU:HD21	1.98	0.46
1:B:229:TYR:O	1:B:233:ASN:HB2	2.16	0.46
1:B:360:MET:SD	1:B:402:ILE:HD11	2.56	0.46
3:D:90:TRP:CG	3:D:95:GLN:HB3	2.51	0.46
1:A:160:ARG:NE	1:A:163:LEU:HD23	2.31	0.45
3:F:49:ASP:O	3:F:50:THR:HB	2.17	0.45
1:A:397:LEU:HD23	1:A:397:LEU:HA	1.68	0.45
1:B:116:LEU:HG	1:B:178:LEU:HD22	1.98	0.45
3:D:198:LYS:HD2	3:D:198:LYS:HA	1.86	0.45
1:A:212:LEU:HD12	1:A:212:LEU:HA	1.71	0.45
1:B:443:PRO:HB2	1:B:446:SER:HB2	1.97	0.45
1:B:120:ARG:HB3	1:B:120:ARG:HE	1.42	0.45
1:B:199:PHE:CD1	1:B:407:THR:HG21	2.52	0.45
1:A:276:MET:HG3	1:A:280:LEU:HD12	1.99	0.45
1:A:53:PHE:O	1:A:57:VAL:HG23	2.16	0.45
1:A:223:ILE:HD11	1:B:430:LEU:HD22	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:61:THR:O	2:C:63:SER:N	2.49	0.45
3:D:149:ILE:HD11	3:D:178:LEU:HD21	1.99	0.45
3:D:76:THR:HG23	3:D:76:THR:O	2.17	0.45
3:F:65:GLY:HA3	3:F:70:TYR:HA	1.98	0.45
1:B:78:LEU:HA	1:B:78:LEU:HD12	1.55	0.45
1:B:19:ARG:O	1:B:23:ARG:HG2	2.17	0.45
1:B:434:LEU:HD23	1:B:434:LEU:HA	1.65	0.45
2:E:194:SER:O	2:E:198:SER:HB3	2.16	0.45
1:A:51:VAL:O	1:A:55:LYS:HG2	2.17	0.45
1:B:206:PRO:CG	1:B:211:THR:HG21	2.45	0.45
1:A:226:THR:CG2	1:B:423:LEU:HD11	2.47	0.44
1:A:255:TYR:CG	1:A:424:PRO:HB3	2.53	0.44
1:A:120:ARG:HE	1:A:120:ARG:HB3	1.56	0.44
1:A:219:PHE:CG	1:B:430:LEU:HD11	2.52	0.44
1:B:75:TYR:O	1:B:79:LEU:HG	2.17	0.44
3:D:150:ASP:HA	3:D:190:SER:OG	2.17	0.44
1:B:284:HIS:C	1:B:286:GLY:H	2.21	0.44
2:E:129:VAL:O	2:E:216:LYS:HE3	2.17	0.44
3:F:196:THR:HG22	3:F:203:PRO:HB3	1.99	0.44
1:B:360:MET:HB2	1:B:360:MET:HE2	1.81	0.44
3:D:35:TYR:CD2	3:D:45:ARG:HA	2.52	0.44
1:A:373:MET:HA	1:A:376:VAL:HG22	2.00	0.44
1:A:430:LEU:CD2	1:B:223:ILE:HD11	2.48	0.44
1:B:86:SER:OG	1:B:303:GLY:HA3	2.17	0.44
3:F:117:PHE:HA	3:F:118:PRO:HD3	1.88	0.44
3:F:1:ASP:OD1	3:F:1:ASP:N	2.45	0.44
2:E:60:TYR:CE2	2:E:70:ILE:HD12	2.52	0.44
1:A:86:SER:OG	1:A:303:GLY:HA3	2.17	0.44
2:C:3:ARG:HB2	2:C:25:SER:OG	2.17	0.44
3:F:112:PRO:HG3	3:F:143:ILE:HD11	1.99	0.44
3:F:60:ARG:HD2	3:F:81:ASP:OD1	2.17	0.44
1:A:69:VAL:C	1:A:71:THR:H	2.21	0.44
3:D:194:GLU:HG2	3:D:205:VAL:CG1	2.11	0.44
2:E:6:GLU:CD	2:E:114:GLY:H	2.20	0.44
2:E:11:LEU:HD12	2:E:11:LEU:HA	1.81	0.44
1:A:276:MET:HG3	1:A:280:LEU:HD11	2.00	0.43
2:C:172:HIS:HE1	3:D:136:ASN:CG	2.21	0.43
3:D:19:VAL:HG11	3:D:103:LEU:HD13	1.99	0.43
1:B:42:VAL:O	1:B:46:VAL:HG23	2.18	0.43
1:A:265:PHE:CD2	1:A:397:LEU:HD21	2.53	0.43
1:B:94:TYR:CE1	1:B:295:GLY:HA3	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:30:SER:HB3	3:D:31:TYR:CD2	2.52	0.43
3:D:49:ASP:O	3:D:51:SER:N	2.50	0.43
1:B:383:HIS:HD2	2:E:33:TRP:CE3	2.35	0.43
1:A:204:MET:HE3	1:A:204:MET:HB3	1.78	0.43
1:A:423:LEU:HD11	1:B:226:THR:HG21	1.99	0.43
3:D:65:GLY:HA3	3:D:70:TYR:HA	1.99	0.43
1:A:376:VAL:HG12	1:A:384:LEU:CB	2.48	0.43
2:C:158:VAL:HG12	2:C:207:HIS:HB2	2.00	0.43
3:D:165:GLN:HE21	3:D:170:SER:HB3	1.84	0.43
1:A:271:LYS:HZ2	1:A:275:GLY:HA3	1.83	0.43
1:B:238:LEU:HD12	1:B:238:LEU:N	2.33	0.43
2:C:6:GLU:HA	2:C:21:SER:O	2.18	0.43
2:E:133:ALA:C	2:E:221:ARG:NH1	2.67	0.43
1:A:88:VAL:HA	1:A:91:MET:HE2	2.01	0.43
1:A:210:TYR:HB2	1:B:209:ARG:HD2	2.00	0.43
3:D:60:ARG:C	3:D:74:ILE:HD12	2.39	0.43
3:F:44:LYS:HZ1	3:F:54:THR:HG21	1.83	0.43
3:F:77:MET:HB3	3:F:77:MET:HE2	1.85	0.43
1:A:81:VAL:O	1:A:85:CYS:HB2	2.19	0.43
1:B:370:ALA:O	1:B:374:VAL:HG23	2.18	0.42
2:C:221:ARG:HH12	3:D:118:PRO:CD	2.29	0.42
3:D:165:GLN:NE2	3:D:170:SER:HB3	2.34	0.42
3:D:30:SER:H	3:D:91:SER:CB	2.31	0.42
3:D:90:TRP:CZ2	3:D:95:GLN:NE2	2.87	0.42
1:B:98:ARG:HH21	1:B:102:PRO:HB3	1.83	0.42
1:B:234:HIS:CE1	2:C:102:GLY:O	2.72	0.42
1:B:441:GLY:C	1:B:442:LYS:HG3	2.39	0.42
1:A:445:TYR:OH	4:A:502:BR:BR	2.84	0.42
3:F:149:ILE:HG12	3:F:191:TYR:CD2	2.54	0.42
3:F:60:ARG:HG3	3:F:74:ILE:HG23	2.01	0.42
1:A:191:ASN:CG	1:A:230:ARG:HH11	2.22	0.42
1:B:184:ALA:HB1	1:B:225:SER:CB	2.47	0.42
3:F:182:LYS:HZ1	3:F:186:GLU:CD	2.23	0.42
1:B:383:HIS:CE1	3:F:90:TRP:CZ2	3.07	0.42
2:C:38:ARG:CD	2:C:48:ILE:HD11	2.49	0.42
3:D:60:ARG:NH1	3:D:78:GLU:CG	2.83	0.42
2:E:138:ALA:O	2:E:140:ALA:N	2.51	0.42
1:A:234:HIS:O	1:A:235:GLU:HB2	2.19	0.42
1:A:18:ARG:HH22	1:B:456:GLN:NE2	2.18	0.42
2:E:94:TYR:O	2:E:114:GLY:HA2	2.20	0.42
1:A:248:PRO:O	1:A:251:THR:HB	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:LEU:O	1:A:401:SER:HB2	2.19	0.42
1:B:311:ALA:O	1:B:340:ARG:HD2	2.19	0.42
1:B:360:MET:CE	1:B:402:ILE:HD11	2.49	0.42
3:D:192:THR:HG22	3:D:207:SER:CB	2.49	0.42
1:A:219:PHE:O	1:A:223:ILE:HG13	2.20	0.42
3:D:12:SER:HA	3:D:104:GLU:O	2.19	0.42
2:E:52:ASN:HD21	2:E:56:SER:HB3	1.84	0.42
3:D:202:SER:HA	3:D:203:PRO:HD2	1.94	0.42
3:F:159:LEU:HA	3:F:159:LEU:HD23	1.77	0.42
3:D:150:ASP:OD1	3:D:188:HIS:HB3	2.20	0.41
3:D:195:ALA:HB3	3:D:204:ILE:HG23	2.02	0.41
3:F:7:SER:OG	3:F:8:PRO:CD	2.68	0.41
1:A:309:ALA:O	1:A:312:THR:OG1	2.32	0.41
1:A:383:HIS:HD2	2:C:33:TRP:CE3	2.38	0.41
1:B:78:LEU:HA	1:B:81:VAL:HG12	2.02	0.41
2:C:163:ASN:ND2	2:C:167:LEU:HD22	2.35	0.41
2:C:147:GLY:HA2	2:C:187:SER:O	2.20	0.41
2:E:61:THR:O	2:E:63:SER:N	2.53	0.41
1:A:357:PHE:HB2	4:A:502:BR:BR	2.76	0.41
1:A:75:TYR:CZ	1:A:79:LEU:HD11	2.55	0.41
1:A:403:ARG:NH2	1:B:29:ASP:OD2	2.46	0.41
1:B:68:LEU:HD21	1:B:82:ALA:HB2	2.01	0.41
1:B:88:VAL:HA	1:B:91:MET:HE2	2.01	0.41
3:D:189:ASN:O	3:D:209:ASN:HA	2.21	0.41
3:F:196:THR:CG2	3:F:203:PRO:HB3	2.51	0.41
1:A:263:GLY:HA3	1:A:435:LEU:HB2	2.02	0.41
1:A:75:TYR:HB3	1:A:76:PRO:HD3	2.03	0.41
1:A:94:TYR:OH	1:A:352:ALA:HB2	2.21	0.41
1:B:316:GLY:O	1:B:319:LEU:HG	2.20	0.41
2:E:178:LEU:HD11	2:E:181:ALA:HA	2.02	0.41
3:F:184:GLU:HA	3:F:187:ARG:HG2	2.03	0.41
3:F:189:ASN:ND2	3:F:209:ASN:OD1	2.54	0.41
3:F:7:SER:HB2	3:F:8:PRO:HD3	2.03	0.41
1:B:103:GLU:O	1:B:111:GLU:HG3	2.21	0.41
2:E:133:ALA:O	2:E:221:ARG:CZ	2.63	0.41
1:A:130:VAL:O	1:A:134:GLY:N	2.46	0.41
1:A:258:LEU:HD13	1:A:371:PHE:CG	2.55	0.41
1:B:262:PHE:CZ	1:B:367:LEU:HD23	2.56	0.41
2:E:178:LEU:HD12	2:E:182:LEU:O	2.21	0.41
1:A:118:ASP:OD2	1:A:174:ARG:NH2	2.53	0.41
1:B:358:ALA:O	1:B:361:LEU:HB2	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:116:ILE:HD12	3:F:193:CYS:SG	2.61	0.41
1:B:422:ILE:HA	1:B:425:MET:CE	2.51	0.40
3:D:19:VAL:HG21	3:D:77:MET:SD	2.61	0.40
2:E:65:LYS:H	2:E:65:LYS:CD	2.35	0.40
1:A:272:TRP:CD1	1:A:272:TRP:N	2.89	0.40
1:A:320:ILE:HB	1:A:321:PRO:HD3	2.02	0.40
1:B:435:LEU:HD13	1:B:435:LEU:HA	1.90	0.40
2:E:31:ARG:H	2:E:53:PRO:HB3	1.85	0.40
1:B:239:ILE:HD11	1:B:320:ILE:CB	2.50	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	442/473 (93%)	417 (94%)	23 (5%)	2 (0%)	29	54
1	B	440/473 (93%)	418 (95%)	20 (4%)	2 (0%)	29	54
2	C	220/222 (99%)	203 (92%)	14 (6%)	3 (1%)	11	28
2	E	219/222 (99%)	201 (92%)	12 (6%)	6 (3%)	5	12
3	D	209/211 (99%)	193 (92%)	13 (6%)	3 (1%)	11	28
3	F	209/211 (99%)	198 (95%)	9 (4%)	2 (1%)	15	37
All	All	1739/1812 (96%)	1630 (94%)	91 (5%)	18 (1%)	15	37

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	64	LEU
3	D	50	THR
2	E	65	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	E	136	SER
3	F	7	SER
1	B	210	TYR
3	D	67	GLY
2	E	138	ALA
1	A	457	GLU
2	E	139	ALA
1	B	29	ASP
2	C	62	PRO
2	C	140	ALA
3	D	7	SER
2	E	137	ALA
2	E	62	PRO
3	F	76	THR
1	A	213	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	335/358 (94%)	329 (98%)	6 (2%)	59	83
1	B	333/358 (93%)	325 (98%)	8 (2%)	49	77
2	C	182/182 (100%)	176 (97%)	6 (3%)	38	67
2	E	181/182 (100%)	172 (95%)	9 (5%)	24	51
3	D	185/185 (100%)	177 (96%)	8 (4%)	29	57
3	F	185/185 (100%)	182 (98%)	3 (2%)	62	85
All	All	1401/1450 (97%)	1361 (97%)	40 (3%)	42	71

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	180	THR
1	A	219	PHE
1	A	276	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	282	ARG
1	A	304	LEU
1	A	401	SER
1	B	18	ARG
1	B	23	ARG
1	B	160	ARG
1	B	168	LEU
1	B	205	ARG
1	B	219	PHE
1	B	270	ASN
1	B	276	MET
2	C	29	TYR
2	C	72	ARG
2	C	87	ARG
2	C	96	CYS
2	C	188	SER
2	C	204	ASN
3	D	11	MET
3	D	91	SER
3	D	92	SER
3	D	168	LYS
3	D	174	MET
3	D	201	THR
3	D	206	LYS
3	D	207	SER
2	E	65	LYS
2	E	71	SER
2	E	81	LEU
2	E	96	CYS
2	E	107	TYR
2	E	188	SER
2	E	198	SER
2	E	217	LYS
2	E	221	ARG
3	F	1	ASP
3	F	190	SER
3	F	198	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	157	ASN
1	A	207	GLN
1	A	270	ASN
1	B	24	GLN
1	B	157	ASN
1	B	234	HIS
1	B	270	ASN
1	B	284	HIS
2	C	39	GLN
2	C	163	ASN
2	C	172	HIS
2	C	207	HIS
3	D	136	ASN
3	D	137	ASN
3	F	36	GLN
3	F	136	ASN
3	F	189	ASN
3	F	209	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

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	444/473 (93%)	0.91	66 (14%) 2 1	62, 88, 119, 166	0
1	B	442/473 (93%)	1.11	97 (21%) 0 0	65, 91, 134, 173	0
2	C	222/222 (100%)	0.64	23 (10%) 6 4	53, 80, 125, 179	0
2	E	221/222 (99%)	0.36	21 (9%) 8 6	55, 80, 120, 165	0
3	D	211/211 (100%)	0.69	29 (13%) 3 2	61, 91, 111, 132	0
3	F	211/211 (100%)	0.58	21 (9%) 7 5	54, 74, 117, 148	0
All	All	1751/1812 (96%)	0.79	257 (14%) 2 1	53, 86, 122, 179	0

All (257) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	140	ALA	11.9
2	C	139	ALA	8.2
1	B	73	ASP	6.1
3	D	110	ALA	5.9
1	A	283	VAL	5.7
2	C	65	LYS	5.6
1	B	410	ILE	5.5
1	A	72	ALA	5.5
1	B	72	ALA	5.5
1	A	235	GLU	5.4
3	F	156	ASN	5.3
2	E	135	GLY	5.3
1	B	104	ALA	5.2
1	B	70	HIS	5.1
1	B	66	GLY	5.1
3	F	147	TRP	5.0
2	C	147	GLY	4.8
3	F	158	VAL	4.8
2	C	29	TYR	4.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	307	PHE	4.7
1	B	69	VAL	4.7
2	E	221	ARG	4.6
2	E	136	SER	4.6
1	B	67	ALA	4.6
1	B	409	ILE	4.5
1	A	407	THR	4.5
1	B	33	LEU	4.5
1	B	198	LEU	4.4
1	B	354	GLY	4.4
2	E	201	VAL	4.3
1	B	71	THR	4.3
1	B	34	ALA	4.3
1	B	95	PHE	4.3
1	B	195	ALA	4.3
3	D	196	THR	4.3
1	A	77	LEU	4.2
1	B	426	ILE	4.2
2	C	63	SER	4.2
1	B	139	LEU	4.2
1	A	18	ARG	4.1
1	B	127	VAL	4.1
3	D	16	GLY	4.1
1	B	353	PRO	4.1
1	A	143	MET	4.1
3	F	153	GLU	4.1
1	B	166	PHE	4.0
1	A	410	ILE	4.0
1	A	291	TRP	4.0
1	B	200	ILE	3.9
3	F	155	GLN	3.9
3	D	195	ALA	3.9
1	A	406	LEU	3.8
1	B	412	VAL	3.8
2	C	62	PRO	3.7
1	B	199	PHE	3.7
1	B	197	ILE	3.7
1	A	195	ALA	3.6
1	B	407	THR	3.6
2	C	105	TYR	3.6
1	B	145	LEU	3.6
1	A	290	LYS	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	458	ALA	3.6
1	B	275	GLY	3.6
3	F	205	VAL	3.5
3	D	61	PHE	3.5
1	B	419	TYR	3.5
1	B	398	LEU	3.5
2	C	199	GLU	3.5
2	C	141	ALA	3.4
1	B	422	ILE	3.4
3	F	7	SER	3.4
1	B	177	LEU	3.4
1	B	303	GLY	3.4
3	D	1	ASP	3.4
1	B	405	PRO	3.4
1	A	298	ILE	3.4
1	B	78	LEU	3.4
1	A	145	LEU	3.4
1	B	162	VAL	3.4
2	C	2	VAL	3.3
1	B	65	MET	3.3
1	B	404	ALA	3.3
1	B	274	LEU	3.3
1	B	408	GLY	3.3
1	A	412	VAL	3.2
1	A	414	GLU	3.2
3	D	138	PHE	3.2
1	A	139	LEU	3.2
1	B	68	LEU	3.2
1	B	406	LEU	3.2
1	B	396	ALA	3.2
3	F	211	ALA	3.2
3	F	204	ILE	3.2
1	B	399	ALA	3.2
1	B	168	LEU	3.2
1	B	215	ILE	3.1
3	F	154	ARG	3.1
3	F	193	CYS	3.1
1	A	288	ILE	3.1
1	B	193	PRO	3.1
1	B	38	MET	3.1
1	A	197	ILE	3.1
1	A	415	MET	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	202	GLU	3.0
1	B	411	LEU	3.0
2	C	66	ASP	3.0
3	D	201	THR	3.0
1	A	411	LEU	3.0
2	C	69	ILE	3.0
1	B	75	TYR	3.0
3	D	149	ILE	3.0
3	D	154	ARG	3.0
1	A	413	LEU	3.0
1	B	397	LEU	2.9
3	D	59	VAL	2.9
1	B	213	ILE	2.9
1	B	266	GLY	2.9
1	B	415	MET	2.9
3	D	93	HIS	2.9
1	A	193	PRO	2.9
1	B	74	ASN	2.9
1	A	299	GLY	2.8
3	F	157	GLY	2.8
1	B	438	PHE	2.8
2	E	81	LEU	2.8
1	A	144	VAL	2.8
1	A	426	ILE	2.8
2	C	138	ALA	2.8
1	B	35	ILE	2.8
1	B	288	ILE	2.8
1	B	423	LEU	2.8
2	E	83	ILE	2.7
1	A	184	ALA	2.7
1	B	309	ALA	2.7
1	B	143	MET	2.7
2	E	66	ASP	2.7
1	B	126	ARG	2.7
3	D	63	GLY	2.7
1	A	71	THR	2.7
1	B	210	TYR	2.7
1	B	159	GLY	2.7
2	E	131	PRO	2.7
3	D	211	ALA	2.7
1	B	425	MET	2.7
1	B	201	ILE	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	297	ALA	2.6
1	B	223	ILE	2.6
1	B	163	LEU	2.6
1	A	194	LEU	2.6
1	A	293	LEU	2.6
1	B	304	LEU	2.6
2	C	73	ASP	2.6
1	A	409	ILE	2.6
1	A	262	PHE	2.6
1	A	448	ILE	2.6
1	B	192	ALA	2.6
2	C	221	ARG	2.6
2	C	34	MET	2.6
2	E	218	ILE	2.6
1	B	196	GLY	2.6
1	B	414	GLU	2.5
1	A	25	LEU	2.5
1	B	413	LEU	2.5
3	D	158	VAL	2.5
2	C	24	ALA	2.5
1	A	94	TYR	2.5
2	E	48	ILE	2.5
1	A	76	PRO	2.5
1	A	386	ALA	2.5
2	E	29	TYR	2.5
1	A	192	ALA	2.4
2	C	202	THR	2.4
1	A	154	ILE	2.4
2	E	94	TYR	2.4
1	A	393	GLY	2.4
1	B	194	LEU	2.4
2	E	122	ALA	2.4
1	A	200	ILE	2.4
1	B	204	MET	2.4
1	B	424	PRO	2.4
1	A	404	ALA	2.4
1	A	458	ALA	2.4
1	A	199	PHE	2.4
1	A	222	VAL	2.4
2	C	33	TRP	2.4
2	E	103	TYR	2.4
3	D	86	TYR	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
3	D	74	ILE	2.4
3	D	204	ILE	2.4
2	C	82	GLN	2.3
1	A	234	HIS	2.3
3	F	200	SER	2.3
2	E	13	GLN	2.3
1	A	419	TYR	2.3
2	E	133	ALA	2.3
1	B	165	ILE	2.3
2	E	70	ILE	2.3
3	F	2	ILE	2.3
1	B	357	PHE	2.3
1	B	220	ILE	2.3
3	D	32	ILE	2.3
3	D	147	TRP	2.3
1	A	294	MET	2.3
1	B	18	ARG	2.3
1	A	67	ALA	2.3
3	D	153	GLU	2.3
3	F	94	PRO	2.3
3	D	21	MET	2.3
1	A	95	PHE	2.3
1	B	209	ARG	2.3
1	B	418	ASN	2.2
1	B	308	VAL	2.2
3	D	47	ILE	2.2
3	F	29	VAL	2.2
3	F	26	SER	2.2
1	A	198	LEU	2.2
2	E	146	LEU	2.2
1	A	187	ALA	2.2
3	D	22	THR	2.2
1	B	141	GLY	2.2
1	B	395	GLY	2.2
3	D	19	VAL	2.2
1	B	421	LEU	2.2
1	A	99	LYS	2.2
1	A	376	VAL	2.2
1	B	157	ASN	2.2
3	F	151	GLY	2.2
1	B	100	TYR	2.2
3	F	152	SER	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	380	PRO	2.2
1	B	290	LYS	2.1
3	D	141	LYS	2.1
3	F	22	THR	2.1
1	B	36	LEU	2.1
1	A	459	GLU	2.1
2	E	82	GLN	2.1
1	A	434	LEU	2.1
1	B	417	ASP	2.1
2	E	137	ALA	2.1
1	A	350	SER	2.1
3	F	120	SER	2.1
1	A	201	ILE	2.1
1	B	94	TYR	2.1
1	A	168	LEU	2.1
2	C	212	THR	2.1
1	B	245	SER	2.1
1	A	295	GLY	2.1
1	A	373	MET	2.1
2	C	27	PHE	2.1
3	D	31	TYR	2.0
1	B	270	ASN	2.0
1	B	138	THR	2.0
2	E	69	ILE	2.0
1	A	405	PRO	2.0
1	A	326	GLY	2.0
3	D	194	GLU	2.0
3	D	197	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

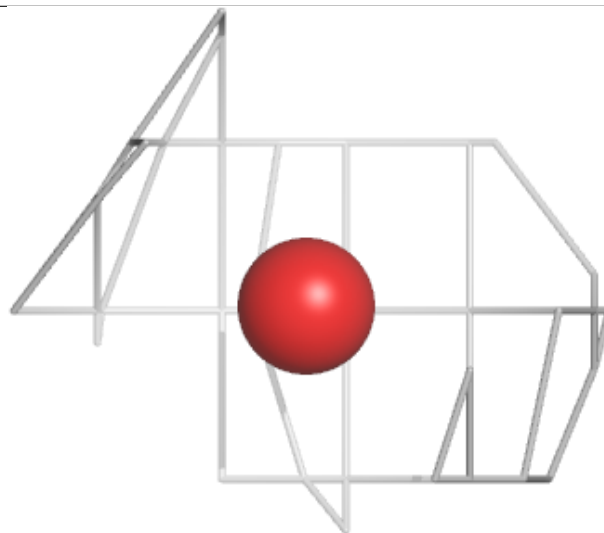
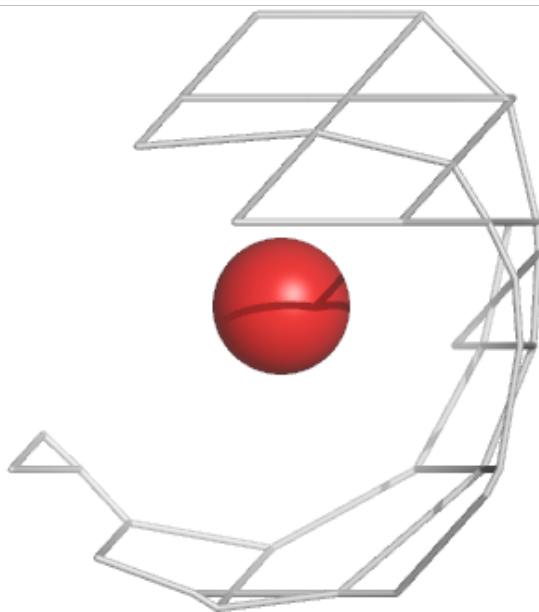
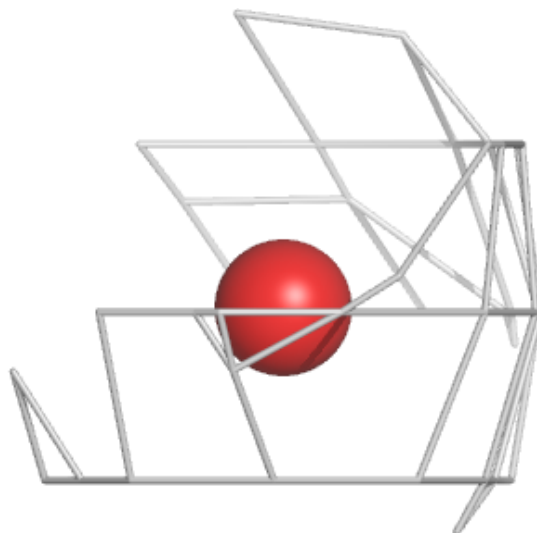
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BR	B	503	1/1	0.85	0.19	161,161,161,161	0
4	BR	B	501	1/1	0.92	0.19	118,118,118,118	0
4	BR	B	502	1/1	0.92	0.20	141,141,141,141	0
4	BR	A	503	1/1	0.92	0.30	168,168,168,168	0
4	BR	A	501	1/1	0.96	0.23	125,125,125,125	0
4	BR	A	502	1/1	0.96	0.24	123,123,123,123	0

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

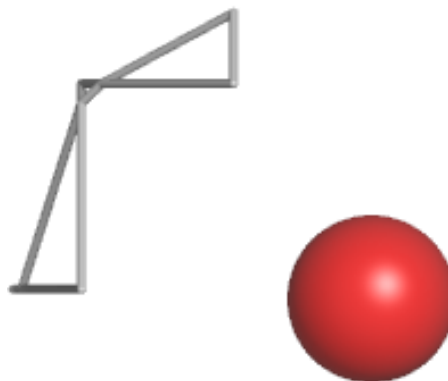
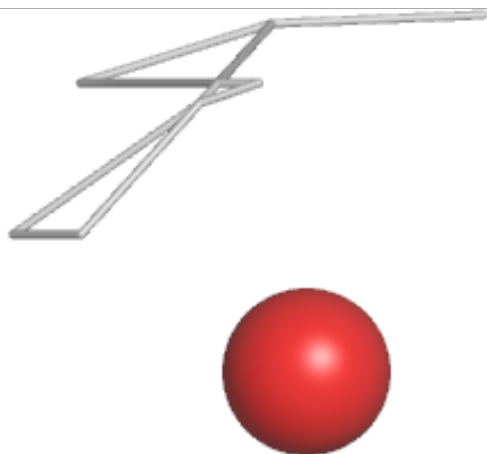
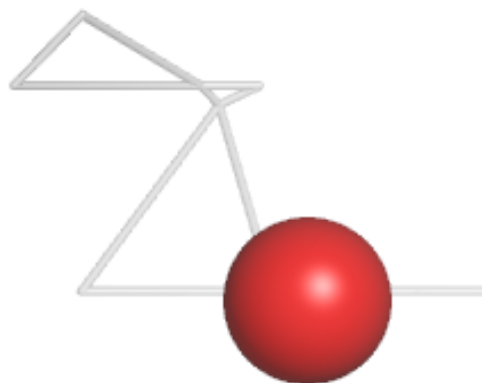
Electron density around BR B 503:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



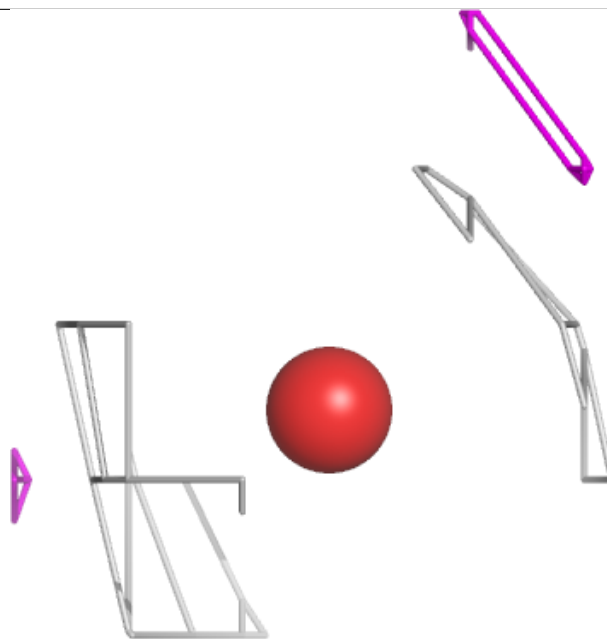
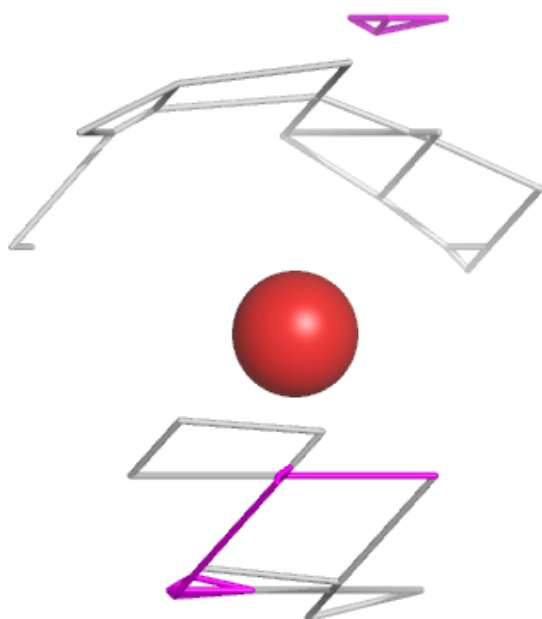
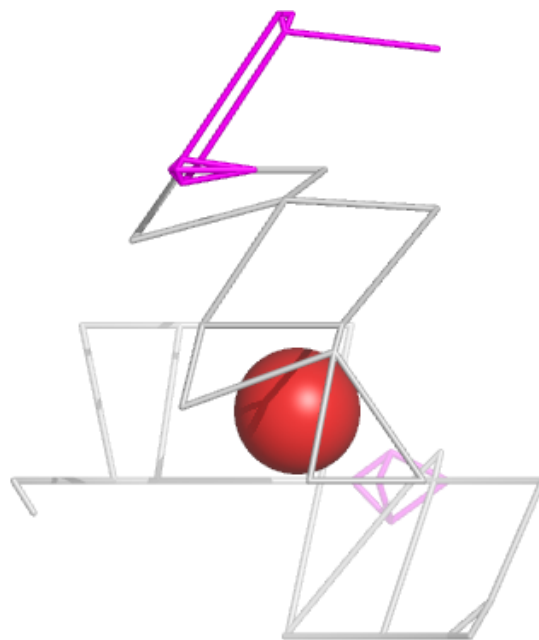
Electron density around BR B 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



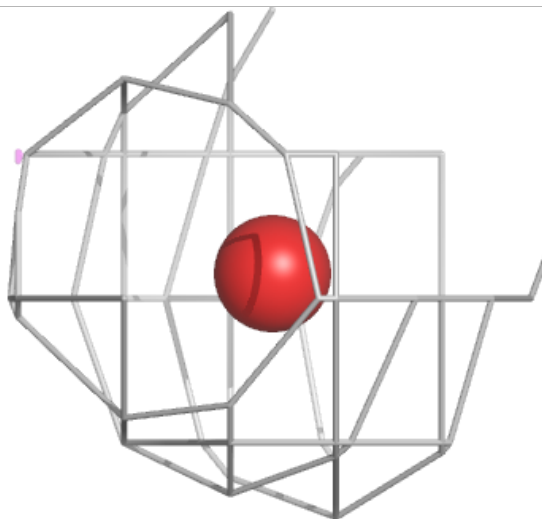
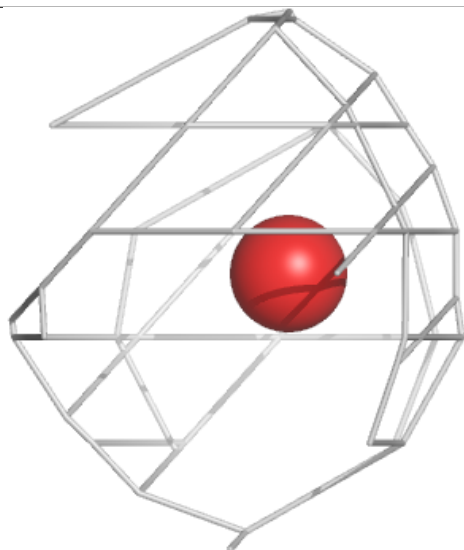
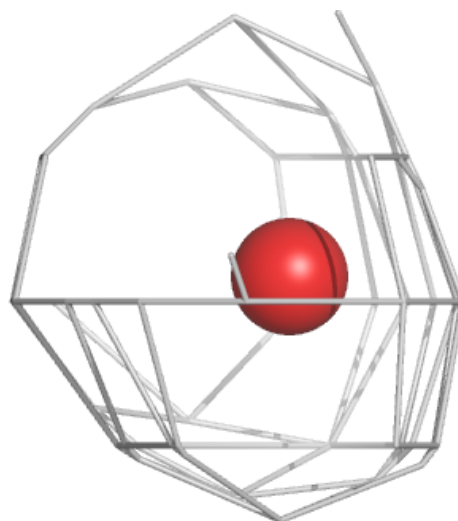
Electron density around BR B 502:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



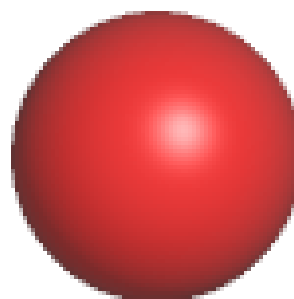
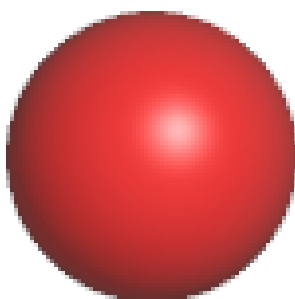
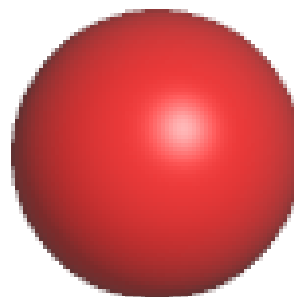
Electron density around BR A 503:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



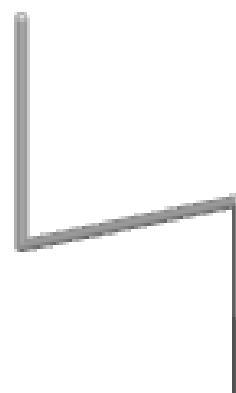
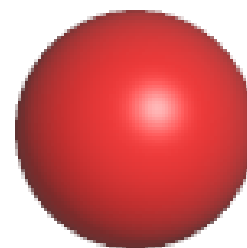
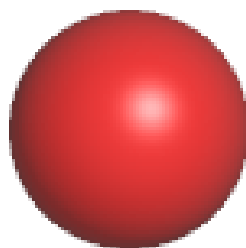
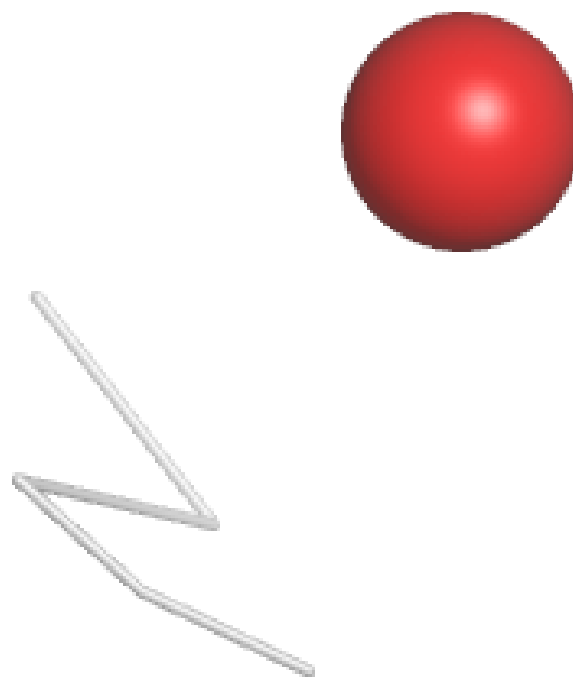
Electron density around BR A 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around BR A 502:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.