



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 10:49 PM UTC

PDB ID : 6JXJ / pdb_00006jxj
Title : Rb⁺-bound E2-A1F state of the gastric proton pump (Tyr799Trp)
Authors : Abe, K.; Irie, K.
Deposited on : 2019-04-23
Resolution : 2.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

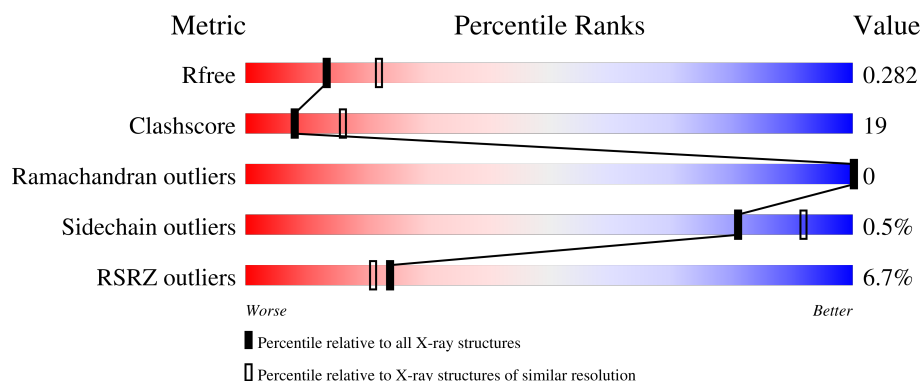
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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

Mol	Chain	Length	Quality of chain
1	A	987	
2	B	289	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 10496 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 Potassium-transporting ATPase alpha chain 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	987	Total	C	N	O	S	0	0	0
			7661	4892	1293	1422	54			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	GLY	-	expression tag	UNP P19156
A	220	CYS	ARG	engineered mutation	UNP P19156
A	593	CYS	SER	engineered mutation	UNP P19156
A	799	TRP	TYR	engineered mutation	UNP P19156
A	1005	SER	GLY	engineered mutation	UNP P19156

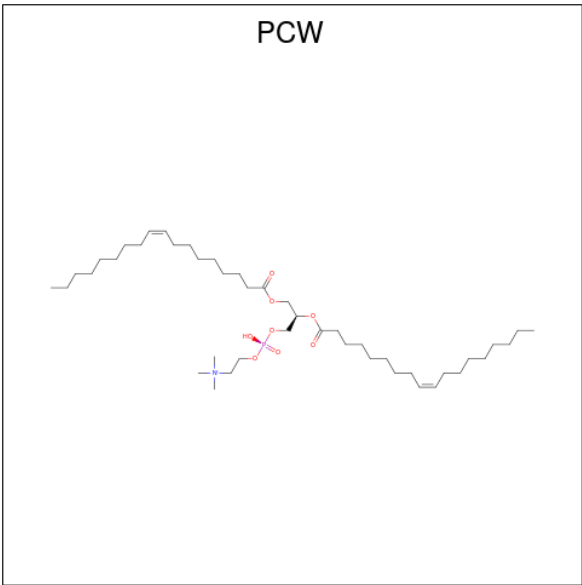
- Molecule 2 is a protein called Potassium-transporting ATPase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	262	Total	C	N	O	S	0	0	0
			2100	1364	348	376	12			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

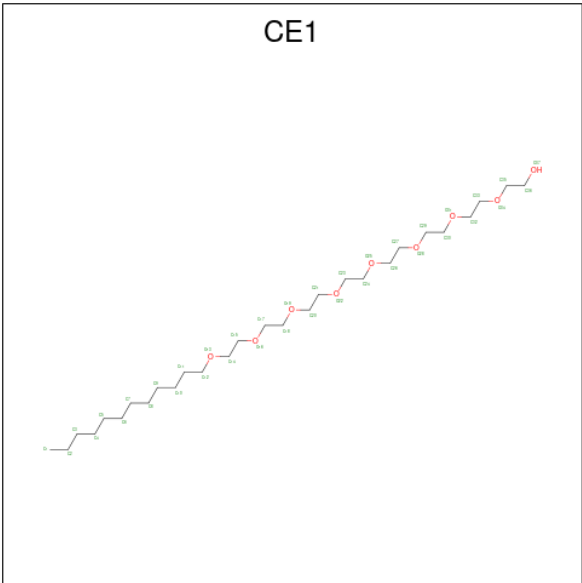
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW) (formula: C₄₄H₈₅NO₈P).



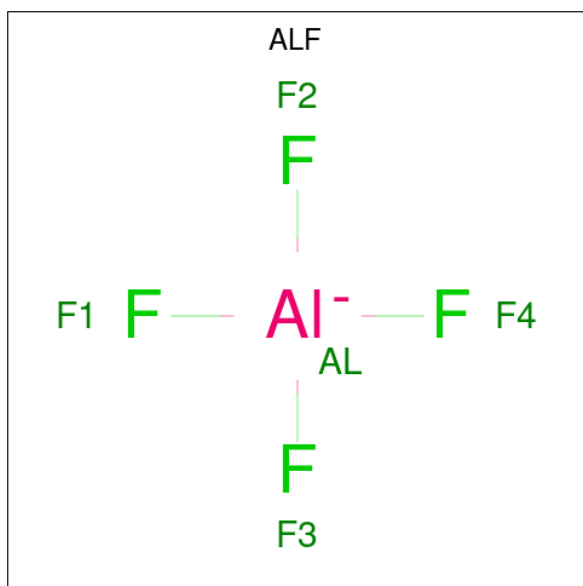
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			46	36	1	8	1		
4	A	1	Total	C	N	O	P	0	0
			47	37	1	8	1		
4	A	1	Total	C	N	O	P	0	0
			54	44	1	8	1		
4	A	1	Total	C	N	O	P	0	0
			54	44	1	8	1		

- Molecule 5 is O-DODECANYL OCTAETHYLENE GLYCOL (CCD ID: CE1) (formula: $C_{28}H_{58}O_9$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			37	28	9		

- Molecule 6 is TETRAFLUOROALUMINATE ION (CCD ID: ALF) (formula: AlF_4).

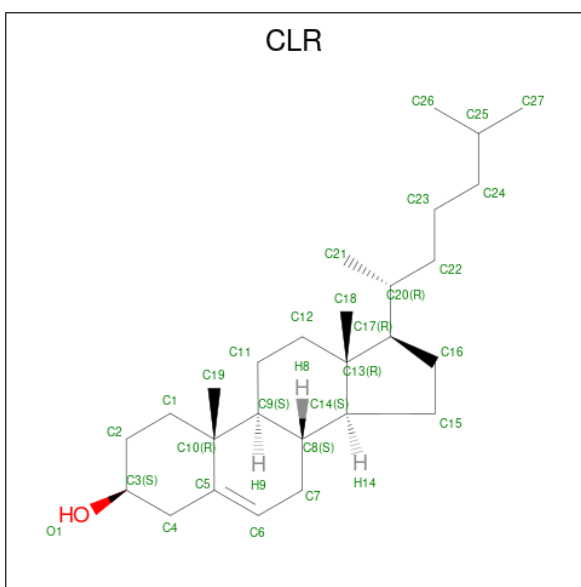


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	Al	F	0	0
			5	1	4		

- Molecule 7 is RUBIDIUM ION (CCD ID: RB) (formula: Rb).

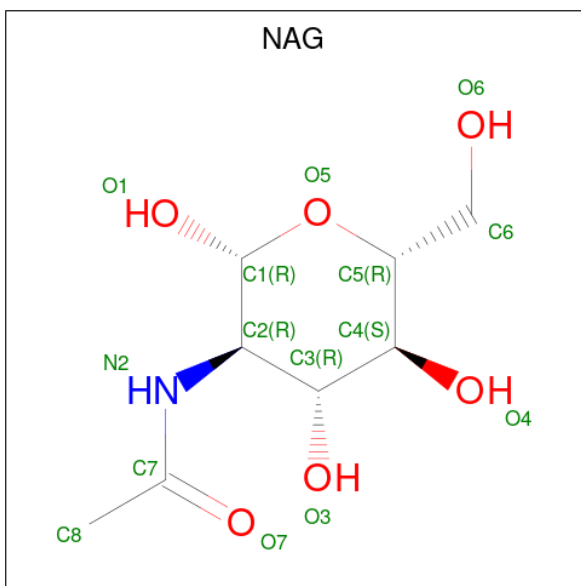
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	7	Total	Rb	0	0
			7	7		
7	B	1	Total	Rb	0	0
			1	1		

- Molecule 8 is CHOLESTEROL (CCD ID: CLR) (formula: $\text{C}_{27}\text{H}_{46}\text{O}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			28	27	1		

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

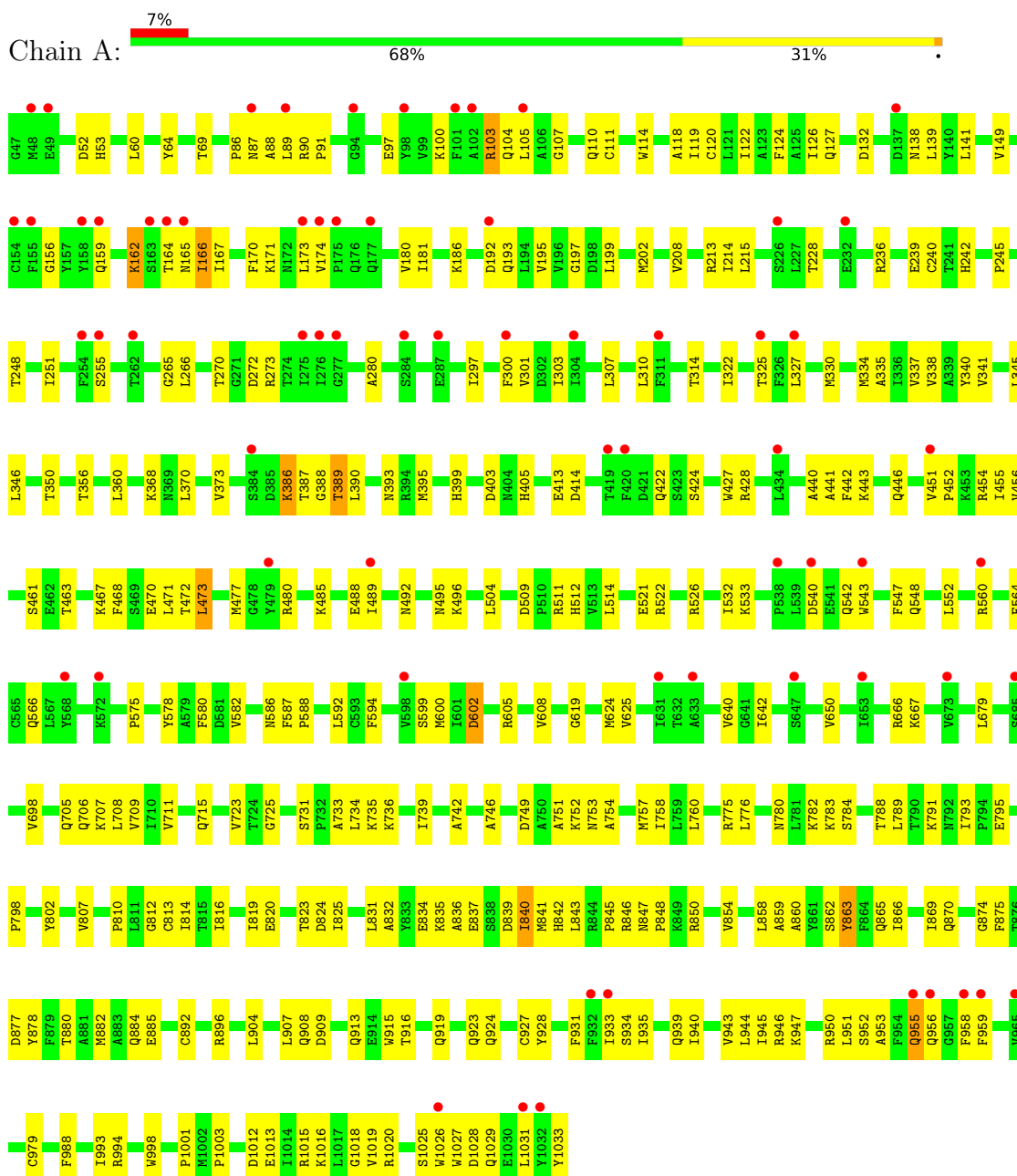
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	289	Total	O	0	0
			289	289		
10	B	82	Total	O	0	0
			82	82		

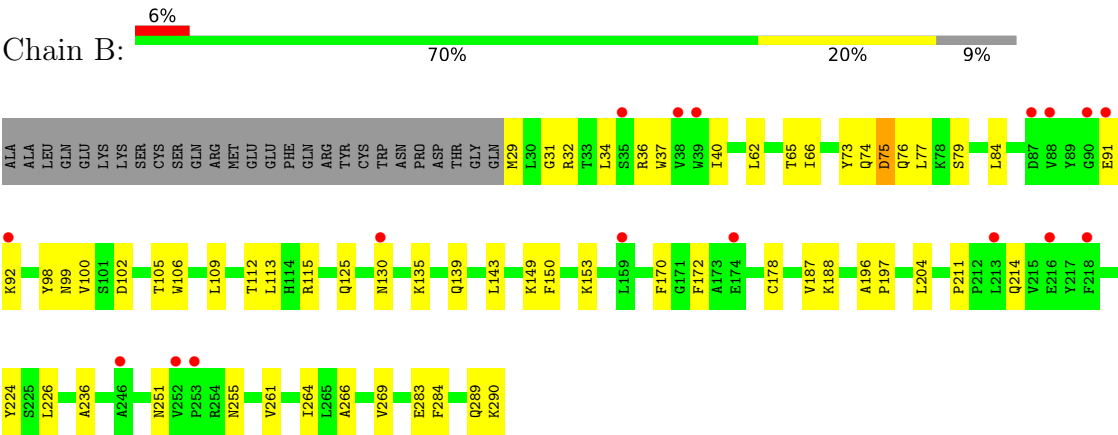
3 Residue-property plots

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

- Molecule 1: Potassium-transporting ATPase alpha chain 1



● Molecule 2: Potassium-transporting ATPase subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	103.23Å 103.23Å 369.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.71 – 2.50 49.71 – 2.50	Depositor EDS
% Data completeness (in resolution range)	76.0 (49.71-2.50) 55.2 (49.71-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.13_2998, PHENIX 1.13_2998	Depositor
R, R_{free}	0.214 , 0.273 (Not available) , 0.282	Depositor DCC
R_{free} test set	3198 reflections (3.98%)	wwPDB-VP
Wilson B-factor (Å ²)	48.5	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	10496	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: RB, NAG, CLR, PCW, CE1, ALF, MG

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	0.47	0/7820	0.71	10/10623 (0.1%)
2	B	0.44	1/2167 (0.0%)	0.63	1/2947 (0.0%)
All	All	0.46	1/9987 (0.0%)	0.69	11/13570 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	31	GLY	CA-C	5.30	1.59	1.51

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	602	ASP	N-CA-C	-8.98	96.76	109.24
1	A	386	LYS	N-CA-C	8.09	119.88	111.14
1	A	166	ILE	N-CA-C	7.88	118.66	110.62
1	A	162	LYS	N-CA-C	7.28	118.85	111.07
1	A	389	THR	N-CA-C	-6.58	101.53	111.34
1	A	840	ILE	N-CA-C	6.29	117.03	110.62
1	A	863	TYR	N-CA-C	5.66	117.25	111.14
1	A	509	ASP	CA-C-N	5.59	127.81	121.04
1	A	509	ASP	C-N-CA	5.59	127.81	121.04
2	B	75	ASP	N-CA-C	5.49	117.26	111.28
1	A	823	THR	N-CA-C	5.12	116.86	111.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7661	0	7686	334	0
2	B	2100	0	2044	68	0
3	A	1	0	0	0	0
4	A	201	0	301	8	0
5	A	37	0	58	2	0
6	A	5	0	0	1	0
7	A	7	0	0	0	0
7	B	1	0	0	0	0
8	B	28	0	46	7	0
9	B	84	0	78	5	0
10	A	289	0	0	98	0
10	B	82	0	0	18	0
All	All	10496	0	10213	396	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 19.

All (396) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:GLY:O	10:A:1201:HOH:O	1.63	1.17
1:A:504:LEU:CD1	1:A:511:ARG:O	1.99	1.10
1:A:297:ILE:HA	1:A:300:PHE:CE2	1.94	1.02
1:A:1015:ARG:HA	1:A:1027:TRP:HZ2	1.24	1.01
1:A:310:LEU:O	1:A:314:THR:HG23	1.59	1.01
1:A:839:ASP:O	1:A:843:LEU:CD1	2.08	1.00
1:A:162:LYS:HE2	1:A:164:THR:OG1	1.62	0.99
1:A:88:ALA:HA	1:A:171:LYS:HZ1	1.33	0.94
1:A:489:ILE:HD11	1:A:582:VAL:HG13	1.53	0.90
1:A:933:ILE:HD12	1:A:993:ILE:HD11	1.49	0.90
1:A:440:ALA:O	10:A:1202:HOH:O	1.88	0.90
1:A:489:ILE:HG12	1:A:582:VAL:HG11	1.54	0.89
1:A:489:ILE:HG12	1:A:582:VAL:CG1	2.02	0.89
1:A:468:PHE:O	1:A:472:THR:HG23	1.72	0.87
1:A:955:GLN:NE2	10:A:1209:HOH:O	2.07	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:THR:O	10:A:1203:HOH:O	1.93	0.86
1:A:127:GLN:NE2	10:A:1210:HOH:O	2.08	0.85
1:A:297:ILE:HA	1:A:300:PHE:CD2	2.13	0.84
1:A:807:VAL:HG13	1:A:892:CYS:HB3	1.60	0.84
1:A:863:TYR:OH	10:A:1205:HOH:O	1.97	0.83
1:A:199:LEU:HA	10:A:1218:HOH:O	1.77	0.83
1:A:919:GLN:OE1	10:A:1204:HOH:O	1.97	0.83
1:A:521:GLU:HG3	10:A:1217:HOH:O	1.77	0.82
1:A:504:LEU:HD12	1:A:511:ARG:O	1.76	0.82
1:A:994:ARG:HA	5:A:1106:CE1:H232	1.60	0.82
2:B:187:VAL:HG12	2:B:188:LYS:HG2	1.61	0.81
1:A:496:LYS:HB2	1:A:522:ARG:NH1	1.94	0.81
1:A:489:ILE:CD1	1:A:582:VAL:HG13	2.12	0.80
1:A:988:PHE:O	10:A:1206:HOH:O	1.99	0.80
1:A:88:ALA:HA	1:A:171:LYS:NZ	1.98	0.79
1:A:454:ARG:NH1	10:A:1213:HOH:O	2.14	0.79
1:A:979:CYS:SG	10:A:1370:HOH:O	2.41	0.78
2:B:79:SER:O	10:B:401:HOH:O	2.02	0.78
1:A:1015:ARG:HA	1:A:1027:TRP:CZ2	2.16	0.77
1:A:104:GLN:HE21	1:A:156:GLY:C	1.93	0.76
1:A:489:ILE:CG1	1:A:582:VAL:HG13	2.14	0.76
1:A:813:CYS:SG	10:A:1456:HOH:O	2.43	0.76
1:A:915:TRP:HA	10:A:1204:HOH:O	1.86	0.75
1:A:322:ILE:HG21	4:A:1104:PCW:H412	1.70	0.73
1:A:521:GLU:CG	10:A:1217:HOH:O	2.32	0.73
1:A:522:ARG:NH1	1:A:522:ARG:HB3	2.04	0.73
1:A:489:ILE:CG1	1:A:582:VAL:CG1	2.67	0.73
1:A:64:TYR:O	10:A:1208:HOH:O	2.07	0.72
1:A:300:PHE:CE1	1:A:345:LEU:HD21	2.24	0.72
1:A:303:ILE:HD12	10:A:1470:HOH:O	1.89	0.72
1:A:532:ILE:HG22	1:A:533:LYS:HD2	1.72	0.72
1:A:403:ASP:O	10:A:1207:HOH:O	2.07	0.72
1:A:240:CYS:SG	10:A:1232:HOH:O	2.48	0.71
10:A:1204:HOH:O	2:B:77:LEU:HD21	1.89	0.70
1:A:835:LYS:HE2	1:A:836:ALA:H	1.56	0.70
1:A:338:VAL:HG12	10:A:1257:HOH:O	1.92	0.70
1:A:866:ILE:O	1:A:870:GLN:HG3	1.92	0.70
1:A:485:LYS:HD2	1:A:488:GLU:HB2	1.74	0.69
1:A:819:ILE:O	10:A:1211:HOH:O	2.10	0.69
1:A:667:LYS:NZ	10:A:1224:HOH:O	2.24	0.69
1:A:88:ALA:CA	1:A:171:LYS:HZ1	2.06	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:LEU:H	1:A:171:LYS:NZ	1.90	0.69
1:A:839:ASP:O	1:A:843:LEU:HD13	1.93	0.68
1:A:480:ARG:NH1	10:A:1202:HOH:O	1.92	0.68
2:B:139:GLN:NE2	2:B:150:PHE:O	2.26	0.68
1:A:165:ASN:ND2	10:A:1226:HOH:O	2.26	0.68
1:A:162:LYS:CE	1:A:164:THR:OG1	2.40	0.68
2:B:32:ARG:HH21	8:B:301:CLR:H192	1.58	0.68
1:A:124:PHE:CE2	1:A:139:LEU:HB2	2.29	0.68
1:A:733:ALA:HA	10:A:1235:HOH:O	1.95	0.67
2:B:197:PRO:HB3	2:B:266:ALA:HB2	1.74	0.67
1:A:793:ILE:HG13	1:A:863:TYR:O	1.95	0.67
1:A:104:GLN:NE2	1:A:156:GLY:C	2.53	0.66
2:B:84:LEU:HD21	2:B:284:PHE:CD1	2.31	0.66
1:A:335:ALA:HA	10:A:1456:HOH:O	1.96	0.66
1:A:473:LEU:HD12	1:A:473:LEU:C	2.21	0.66
1:A:104:GLN:OE1	1:A:104:GLN:HA	1.95	0.66
1:A:882:MET:HE2	1:A:882:MET:HA	1.77	0.66
1:A:564:PHE:O	10:A:1212:HOH:O	2.12	0.66
1:A:795:GLU:HB3	1:A:816:ILE:HD13	1.79	0.65
1:A:865:GLN:O	1:A:869:ILE:HG13	1.97	0.65
1:A:725:GLY:N	10:A:1228:HOH:O	2.28	0.65
1:A:89:LEU:H	1:A:171:LYS:HZ3	1.42	0.64
1:A:310:LEU:C	1:A:310:LEU:HD23	2.22	0.64
2:B:255:ASN:HD21	2:B:290:LYS:H	1.45	0.64
1:A:53:HIS:HB2	10:A:1221:HOH:O	1.95	0.64
1:A:162:LYS:HD3	1:A:164:THR:H	1.63	0.64
1:A:199:LEU:HD12	10:A:1218:HOH:O	1.98	0.64
2:B:37:TRP:HZ3	8:B:301:CLR:H193	1.62	0.64
1:A:736:LYS:HB3	10:A:1235:HOH:O	1.97	0.63
1:A:831:LEU:HD22	10:A:1244:HOH:O	1.97	0.63
1:A:858:LEU:HA	1:A:1033:TYR:HB2	1.80	0.63
1:A:642:ILE:O	10:A:1215:HOH:O	2.16	0.63
1:A:492:ASN:HB3	1:A:495:ASN:HB2	1.81	0.63
1:A:341:VAL:HG23	10:A:1339:HOH:O	1.99	0.62
2:B:130:ASN:ND2	10:B:405:HOH:O	2.31	0.62
1:A:504:LEU:HD11	1:A:511:ARG:O	1.96	0.62
1:A:1015:ARG:HD2	1:A:1031:LEU:O	2.00	0.62
1:A:839:ASP:O	1:A:843:LEU:HD12	1.99	0.62
1:A:715:GLN:OE1	1:A:736:LYS:NZ	2.30	0.62
1:A:166:ILE:HD11	1:A:735:LYS:HE2	1.81	0.61
1:A:875:PHE:CD2	4:A:1105:PCW:H431	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:840:ILE:HA	1:A:843:LEU:HD13	1.83	0.61
4:A:1103:PCW:H272	10:B:440:HOH:O	1.99	0.61
1:A:580:PHE:N	10:A:1233:HOH:O	2.34	0.61
1:A:751:ALA:HA	10:A:1345:HOH:O	2.01	0.61
1:A:119:ILE:HG23	1:A:330:MET:HE3	1.83	0.60
1:A:950:ARG:HG2	1:A:951:LEU:HD12	1.82	0.60
1:A:625:VAL:HG12	1:A:707:LYS:HE2	1.83	0.60
2:B:29:MET:SD	2:B:29:MET:N	2.74	0.60
2:B:255:ASN:ND2	2:B:289:GLN:HA	2.16	0.60
1:A:824:ASP:HB2	10:A:1211:HOH:O	2.02	0.60
1:A:880:THR:O	1:A:884:GLN:HG3	2.02	0.59
1:A:266:LEU:HA	10:A:1218:HOH:O	2.01	0.59
1:A:953:ALA:N	1:A:1013:GLU:OE2	2.28	0.59
1:A:90:ARG:HG2	1:A:272:ASP:OD2	2.03	0.58
2:B:255:ASN:HD21	2:B:290:LYS:N	2.01	0.58
1:A:165:ASN:ND2	1:A:167:ILE:HG22	2.18	0.58
1:A:171:LYS:HE3	1:A:174:VAL:HG11	1.84	0.58
1:A:193:GLN:NE2	10:A:1214:HOH:O	2.15	0.58
1:A:297:ILE:HA	1:A:300:PHE:HE2	1.62	0.58
1:A:754:ALA:HB3	10:A:1345:HOH:O	2.01	0.58
1:A:1019:VAL:HG12	1:A:1028:ASP:HA	1.86	0.58
2:B:62:LEU:O	2:B:65:THR:HB	2.04	0.58
1:A:442:PHE:HE2	1:A:470:GLU:HG3	1.68	0.57
1:A:749:ASP:HA	10:A:1222:HOH:O	2.04	0.57
2:B:178:CYS:SG	10:B:455:HOH:O	2.57	0.57
1:A:87:ASN:OD1	1:A:270:THR:HB	2.03	0.57
1:A:105:LEU:O	1:A:110:GLN:HB3	2.04	0.57
1:A:1003:PRO:HB3	4:A:1102:PCW:H221	1.87	0.57
1:A:793:ILE:HD13	10:A:1313:HOH:O	2.05	0.57
2:B:112:THR:HG22	2:B:115:ARG:NH1	2.19	0.57
2:B:211:PRO:O	10:B:403:HOH:O	2.18	0.56
1:A:214:ILE:HD13	1:A:236:ARG:HB3	1.87	0.56
1:A:181:ILE:HD12	1:A:199:LEU:HD23	1.87	0.56
1:A:734:LEU:HD21	10:A:1228:HOH:O	2.06	0.56
1:A:950:ARG:NH1	10:A:1239:HOH:O	2.39	0.56
1:A:213:ARG:NH1	1:A:214:ILE:O	2.38	0.56
1:A:788:THR:HG22	10:A:1379:HOH:O	2.04	0.56
1:A:839:ASP:O	1:A:843:LEU:HD11	2.03	0.56
1:A:124:PHE:CD2	1:A:139:LEU:HB2	2.42	0.55
1:A:1027:TRP:CZ3	1:A:1031:LEU:HD12	2.41	0.55
1:A:548:GLN:OE1	10:A:1217:HOH:O	2.18	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:PRO:HA	1:A:248:THR:HG22	1.87	0.55
1:A:746:ALA:HB3	10:A:1201:HOH:O	2.07	0.55
1:A:775:ARG:HB3	1:A:840:ILE:HD11	1.88	0.55
2:B:196:ALA:HA	2:B:226:LEU:HD21	1.88	0.55
1:A:1003:PRO:HG3	4:A:1102:PCW:H162	1.88	0.55
1:A:300:PHE:HE1	1:A:345:LEU:HD21	1.71	0.55
1:A:389:THR:HG23	10:A:1282:HOH:O	2.07	0.55
4:A:1102:PCW:H51	10:B:461:HOH:O	2.05	0.55
1:A:904:LEU:HD21	1:A:907:LEU:HD13	1.89	0.55
2:B:100:VAL:HG21	10:B:402:HOH:O	2.07	0.55
1:A:265:GLY:O	10:A:1218:HOH:O	2.18	0.54
1:A:547:PHE:HE1	10:A:1217:HOH:O	1.90	0.54
2:B:112:THR:HG22	2:B:115:ARG:HH12	1.72	0.54
1:A:88:ALA:CA	1:A:171:LYS:NZ	2.68	0.54
1:A:162:LYS:O	1:A:164:THR:HG23	2.07	0.54
1:A:841:MET:SD	10:A:1301:HOH:O	2.59	0.54
1:A:504:LEU:HD13	1:A:511:ARG:O	1.98	0.54
1:A:945:ILE:HB	1:A:1012:ASP:OD2	2.08	0.54
2:B:29:MET:HE1	2:B:34:LEU:HD22	1.88	0.54
1:A:228:THR:O	10:A:1219:HOH:O	2.19	0.54
1:A:452:PRO:O	1:A:467:LYS:NZ	2.40	0.54
1:A:213:ARG:HA	1:A:251:ILE:HD13	1.88	0.54
1:A:386:LYS:HA	1:A:390:LEU:HD12	1.89	0.53
1:A:885:GLU:OE1	2:B:73:TYR:HB2	2.07	0.53
2:B:91:GLU:O	2:B:92:LYS:HB2	2.08	0.53
2:B:100:VAL:HG23	2:B:289:GLN:O	2.08	0.53
2:B:204:LEU:HB2	2:B:261:VAL:HG23	1.90	0.53
2:B:211:PRO:HB2	10:B:441:HOH:O	2.09	0.53
10:A:1204:HOH:O	2:B:77:LEU:CD2	2.51	0.53
1:A:202:MET:HE3	1:A:208:VAL:HG22	1.90	0.53
1:A:489:ILE:CD1	1:A:582:VAL:CG1	2.84	0.53
1:A:780:ASN:ND2	1:A:832:ALA:O	2.40	0.53
1:A:114:TRP:CZ2	1:A:149:VAL:HG11	2.45	0.52
1:A:370:LEU:O	1:A:373:VAL:HG12	2.08	0.52
1:A:489:ILE:HD11	1:A:582:VAL:CG1	2.35	0.52
1:A:522:ARG:HB3	1:A:522:ARG:CZ	2.40	0.52
1:A:952:SER:HB2	1:A:1020:ARG:NH2	2.25	0.52
1:A:52:ASP:OD2	1:A:64:TYR:OH	2.20	0.52
2:B:40:ILE:HD13	8:B:301:CLR:H191	1.92	0.52
2:B:289:GLN:HB3	9:B:302:NAG:H82	1.92	0.52
1:A:480:ARG:NH2	10:A:1202:HOH:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:860:ALA:HB1	8:B:301:CLR:H6	1.91	0.52
2:B:29:MET:HB3	2:B:32:ARG:O	2.10	0.52
2:B:125:GLN:O	2:B:153:LYS:HE3	2.10	0.52
1:A:776:LEU:HD23	10:A:1408:HOH:O	2.10	0.52
2:B:170:PHE:HB2	10:B:437:HOH:O	2.09	0.52
1:A:608:VAL:HG12	1:A:640:VAL:CG2	2.40	0.51
4:A:1105:PCW:H71	10:B:413:HOH:O	2.10	0.51
1:A:602:ASP:HB3	10:A:1271:HOH:O	2.10	0.51
1:A:723:VAL:HG12	10:A:1228:HOH:O	2.09	0.51
1:A:859:ALA:O	1:A:863:TYR:HB2	2.10	0.51
1:A:340:TYR:HB3	10:A:1339:HOH:O	2.10	0.51
2:B:99:ASN:HA	2:B:289:GLN:HB2	1.92	0.51
1:A:395:MET:O	10:A:1220:HOH:O	2.19	0.51
1:A:736:LYS:HG3	1:A:736:LYS:O	2.09	0.51
1:A:605:ARG:HB2	1:A:608:VAL:HG23	1.93	0.51
1:A:846:ARG:O	1:A:846:ARG:HG3	2.11	0.51
1:A:162:LYS:HE2	1:A:164:THR:HG1	1.72	0.51
1:A:526:ARG:O	1:A:592:LEU:HD12	2.11	0.51
1:A:994:ARG:NH1	2:B:75:ASP:OD2	2.43	0.50
4:A:1103:PCW:H382	4:A:1105:PCW:H382	1.94	0.50
1:A:118:ALA:O	1:A:122:ILE:HG13	2.11	0.50
1:A:934:SER:HA	1:A:1001:PRO:HG3	1.93	0.50
1:A:297:ILE:CA	1:A:300:PHE:CE2	2.81	0.50
1:A:807:VAL:HG12	1:A:878:TYR:OH	2.12	0.50
1:A:909:ASP:C	1:A:909:ASP:OD1	2.54	0.50
1:A:731:SER:HA	10:A:1345:HOH:O	2.11	0.50
1:A:784:SER:HA	1:A:831:LEU:HD12	1.94	0.50
1:A:843:LEU:HD12	1:A:843:LEU:N	2.27	0.50
1:A:863:TYR:HA	10:A:1229:HOH:O	2.12	0.50
1:A:1015:ARG:NH1	1:A:1033:TYR:HE1	2.10	0.49
1:A:860:ALA:HB2	8:B:301:CLR:H3	1.93	0.49
1:A:1026:TRP:HD1	2:B:36:ARG:HH11	1.59	0.49
1:A:1025:SER:O	1:A:1029:GLN:HG2	2.13	0.49
2:B:62:LEU:O	2:B:66:ILE:HG12	2.12	0.49
1:A:126:ILE:HD12	1:A:327:LEU:HD11	1.93	0.49
1:A:812:GLY:N	10:A:1216:HOH:O	2.17	0.49
1:A:814:ILE:HB	10:A:1411:HOH:O	2.11	0.49
1:A:951:LEU:HD23	1:A:956:GLN:NE2	2.28	0.49
1:A:742:ALA:HB3	1:A:758:ILE:HD13	1.94	0.49
1:A:854:VAL:HG13	1:A:858:LEU:HD22	1.95	0.49
2:B:125:GLN:HB3	2:B:153:LYS:HG2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:ILE:HG21	10:A:1203:HOH:O	2.13	0.48
1:A:240:CYS:HA	10:A:1221:HOH:O	2.13	0.48
2:B:130:ASN:ND2	9:B:303:NAG:O5	2.46	0.48
1:A:325:THR:HG21	10:A:1461:HOH:O	2.13	0.48
2:B:32:ARG:NH2	8:B:301:CLR:H22	2.27	0.48
2:B:106:TRP:HB2	10:B:424:HOH:O	2.13	0.48
1:A:303:ILE:HD13	10:A:1355:HOH:O	2.13	0.48
1:A:512:HIS:CE1	10:A:1419:HOH:O	2.65	0.48
1:A:877:ASP:HB3	10:A:1310:HOH:O	2.13	0.48
1:A:916:THR:HG23	1:A:919:GLN:OE1	2.13	0.48
1:A:994:ARG:HH12	2:B:75:ASP:CG	2.22	0.48
1:A:405:HIS:HB2	10:A:1207:HOH:O	2.12	0.48
1:A:443:LYS:HD2	1:A:455:ILE:HG13	1.95	0.48
1:A:775:ARG:NH1	1:A:843:LEU:O	2.46	0.48
1:A:783:LYS:HB3	10:A:1244:HOH:O	2.14	0.48
1:A:802:TYR:CE1	1:A:896:ARG:HD3	2.48	0.48
1:A:913:GLN:HG2	2:B:187:VAL:HG23	1.95	0.48
2:B:135:LYS:NZ	10:B:409:HOH:O	2.47	0.48
1:A:239:GLU:HG2	10:A:1412:HOH:O	2.14	0.47
1:A:753:ASN:HA	10:A:1333:HOH:O	2.14	0.47
1:A:619:GLY:HA3	1:A:845:PRO:HD3	1.96	0.47
1:A:919:GLN:NE2	10:B:401:HOH:O	2.47	0.47
1:A:998:TRP:O	1:A:1001:PRO:HD2	2.14	0.47
2:B:37:TRP:CZ3	8:B:301:CLR:H193	2.47	0.47
2:B:226:LEU:HD22	10:B:469:HOH:O	2.13	0.47
2:B:264:ILE:HB	2:B:269:VAL:HG11	1.96	0.47
1:A:816:ILE:HG21	10:A:1257:HOH:O	2.14	0.47
1:A:885:GLU:OE2	2:B:75:ASP:HB2	2.14	0.47
1:A:504:LEU:CD1	1:A:511:ARG:C	2.81	0.47
1:A:1026:TRP:HD1	2:B:36:ARG:NH1	2.13	0.47
1:A:835:LYS:HE2	1:A:836:ALA:N	2.28	0.47
9:B:302:NAG:O6	10:B:404:HOH:O	2.21	0.47
1:A:180:VAL:HG13	10:A:1421:HOH:O	2.14	0.47
1:A:908:GLN:HA	1:A:913:GLN:O	2.14	0.47
1:A:998:TRP:CD2	5:A:1106:CE1:H152	2.50	0.46
2:B:130:ASN:HD21	9:B:303:NAG:C1	2.27	0.46
2:B:255:ASN:N	2:B:255:ASN:HD22	2.11	0.46
2:B:214:GLN:H	2:B:251:ASN:HB2	1.81	0.46
1:A:831:LEU:HD21	1:A:943:VAL:HG22	1.96	0.46
1:A:935:ILE:HG23	10:A:1223:HOH:O	2.13	0.46
1:A:126:ILE:CD1	1:A:327:LEU:HD11	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:VAL:HG22	10:A:1248:HOH:O	2.14	0.46
1:A:297:ILE:HG23	1:A:300:PHE:CZ	2.51	0.46
1:A:923:GLN:HB2	2:B:76:GLN:HG3	1.98	0.46
1:A:798:PRO:HB2	10:A:1342:HOH:O	2.16	0.46
1:A:820:GLU:O	1:A:825:ILE:HD11	2.15	0.46
1:A:846:ARG:NH1	1:A:848:PRO:HA	2.30	0.46
1:A:441:ALA:HA	1:A:477:MET:HE3	1.98	0.46
1:A:933:ILE:HD12	1:A:993:ILE:CD1	2.34	0.45
1:A:107:GLY:O	1:A:111:CYS:SG	2.71	0.45
1:A:181:ILE:HG12	1:A:186:LYS:HB2	1.98	0.45
1:A:862:SER:OG	1:A:946:ARG:NH2	2.49	0.45
1:A:958:PHE:HB2	1:A:959:PHE:CD2	2.52	0.45
1:A:120:CYS:HB3	1:A:138:ASN:O	2.17	0.45
1:A:127:GLN:O	1:A:132:ASP:HB3	2.16	0.45
1:A:909:ASP:OD2	1:A:913:GLN:HB2	2.16	0.45
2:B:196:ALA:HB1	2:B:224:TYR:O	2.16	0.45
1:A:735:LYS:HD3	1:A:735:LYS:HA	1.79	0.45
1:A:197:GLY:HA3	10:A:1208:HOH:O	2.16	0.45
1:A:913:GLN:OE1	2:B:74:GLN:NE2	2.49	0.45
1:A:940:ILE:O	1:A:944:LEU:HG	2.17	0.45
1:A:297:ILE:HG12	1:A:300:PHE:HE2	1.81	0.45
1:A:424:SER:HB3	1:A:427:TRP:HB3	1.98	0.45
1:A:514:LEU:HD22	1:A:592:LEU:HD21	1.97	0.45
1:A:547:PHE:CD1	1:A:547:PHE:C	2.95	0.45
2:B:109:LEU:HB2	10:B:424:HOH:O	2.17	0.45
2:B:102:ASP:HB3	2:B:105:THR:HG23	1.98	0.45
1:A:165:ASN:ND2	1:A:167:ILE:CG2	2.80	0.45
1:A:248:THR:OG1	10:A:1221:HOH:O	2.21	0.45
1:A:356:THR:HG22	1:A:373:VAL:HG22	1.99	0.45
1:A:173:LEU:O	1:A:255:SER:HB2	2.17	0.44
1:A:422:GLN:HB3	1:A:427:TRP:NE1	2.32	0.44
1:A:504:LEU:HD11	1:A:511:ARG:C	2.42	0.44
1:A:791:LYS:O	1:A:795:GLU:HG3	2.17	0.44
1:A:958:PHE:HB2	1:A:959:PHE:CE2	2.52	0.44
1:A:994:ARG:CZ	2:B:73:TYR:CD2	3.00	0.44
1:A:114:TRP:CE2	1:A:149:VAL:HG11	2.53	0.44
1:A:575:PRO:HD2	1:A:578:TYR:HD1	1.81	0.44
1:A:442:PHE:CD1	1:A:456:VAL:HG12	2.53	0.44
1:A:834:GLU:OE2	1:A:947:LYS:HE3	2.16	0.44
1:A:679:LEU:HB3	1:A:706:GLN:NE2	2.33	0.44
1:A:789:LEU:HD23	10:A:1379:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:824:ASP:OD2	1:A:939:GLN:HG3	2.18	0.44
1:A:708:LEU:HG	10:A:1235:HOH:O	2.17	0.44
1:A:839:ASP:OD2	1:A:842:HIS:ND1	2.51	0.44
1:A:820:GLU:HA	10:A:1211:HOH:O	2.17	0.44
9:B:306:NAG:H4	10:B:470:HOH:O	2.16	0.44
1:A:387:THR:HB	6:A:1107:ALF:F3	2.08	0.44
2:B:113:LEU:HD23	2:B:113:LEU:HA	1.76	0.44
1:A:171:LYS:HD2	1:A:174:VAL:HG21	1.99	0.44
1:A:307:LEU:HD23	1:A:307:LEU:HA	1.84	0.44
1:A:521:GLU:HG2	10:A:1217:HOH:O	2.06	0.44
1:A:560:ARG:O	1:A:599:SER:HA	2.18	0.43
1:A:456:VAL:CG2	1:A:463:THR:HG23	2.48	0.43
1:A:782:LYS:HB3	1:A:782:LYS:HE3	1.71	0.43
1:A:1018:GLY:HA3	1:A:1027:TRP:NE1	2.32	0.43
1:A:443:LYS:O	1:A:446:GLN:HG3	2.19	0.43
1:A:775:ARG:CB	1:A:840:ILE:HD11	2.48	0.43
1:A:300:PHE:HE1	1:A:345:LEU:CD2	2.31	0.43
1:A:399:HIS:HB2	1:A:599:SER:OG	2.18	0.43
1:A:442:PHE:CE2	1:A:470:GLU:HG3	2.50	0.43
1:A:837:GLU:HB3	1:A:951:LEU:HD13	2.01	0.43
2:B:98:TYR:CZ	2:B:172:PHE:HD1	2.37	0.43
1:A:103:ARG:HA	1:A:103:ARG:HD2	1.80	0.43
1:A:522:ARG:HB3	1:A:522:ARG:HH11	1.77	0.43
1:A:587:PHE:HB2	1:A:588:PRO:HD2	2.00	0.43
1:A:924:GLN:O	1:A:927:CYS:HB2	2.19	0.43
1:A:994:ARG:NH1	2:B:75:ASP:CG	2.77	0.43
1:A:97:GLU:O	1:A:100:LYS:HB2	2.19	0.43
1:A:242:HIS:N	10:A:1232:HOH:O	2.31	0.43
1:A:428:ARG:HB3	10:A:1445:HOH:O	2.19	0.43
1:A:566:GLN:NE2	10:A:1258:HOH:O	2.51	0.43
2:B:98:TYR:CD2	2:B:106:TRP:HB3	2.54	0.43
1:A:89:LEU:N	1:A:171:LYS:NZ	2.64	0.43
1:A:91:PRO:HA	1:A:167:ILE:HD13	2.01	0.43
1:A:265:GLY:C	10:A:1218:HOH:O	2.62	0.43
2:B:236:ALA:N	10:B:406:HOH:O	2.38	0.43
1:A:166:ILE:CD1	1:A:735:LYS:HE2	2.47	0.42
2:B:204:LEU:HB2	2:B:261:VAL:CG2	2.49	0.42
1:A:87:ASN:HB3	1:A:192:ASP:HA	2.01	0.42
1:A:451:VAL:HG11	1:A:471:LEU:HG	2.01	0.42
1:A:578:TYR:HE2	1:A:586:ASN:ND2	2.17	0.42
1:A:760:LEU:HA	1:A:760:LEU:HD23	1.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1016:LYS:O	1:A:1020:ARG:HG3	2.19	0.42
1:A:461:SER:OG	1:A:560:ARG:NH2	2.53	0.42
1:A:580:PHE:HA	1:A:586:ASN:HD21	1.84	0.42
1:A:952:SER:H	1:A:955:GLN:NE2	2.18	0.42
1:A:1016:LYS:O	1:A:1019:VAL:HG22	2.19	0.42
1:A:1026:TRP:CD1	2:B:36:ARG:HH11	2.36	0.42
2:B:261:VAL:HG13	2:B:283:GLU:HG2	2.02	0.42
1:A:337:VAL:HA	10:A:1339:HOH:O	2.19	0.42
1:A:532:ILE:HD12	1:A:543:TRP:CH2	2.54	0.42
1:A:86:PRO:HD2	1:A:90:ARG:HH12	1.84	0.42
1:A:141:LEU:HD12	1:A:141:LEU:HA	1.85	0.42
1:A:608:VAL:HG12	1:A:640:VAL:HG21	2.02	0.42
1:A:60:LEU:HD23	1:A:60:LEU:HA	1.93	0.42
1:A:297:ILE:HG23	1:A:300:PHE:CE2	2.54	0.42
1:A:504:LEU:HB3	10:A:1317:HOH:O	2.19	0.42
1:A:789:LEU:HD22	1:A:863:TYR:OH	2.20	0.42
1:A:368:LYS:NZ	1:A:752:LYS:O	2.52	0.42
1:A:793:ILE:HD13	1:A:793:ILE:HA	1.85	0.42
1:A:835:LYS:HE2	1:A:835:LYS:CA	2.50	0.42
1:A:882:MET:HE1	1:A:923:GLN:CG	2.50	0.42
1:A:810:PRO:O	1:A:928:TYR:HA	2.20	0.41
2:B:37:TRP:HE3	2:B:40:ILE:HD11	1.84	0.41
1:A:156:GLY:O	1:A:159:GLN:HG2	2.20	0.41
1:A:456:VAL:HG22	1:A:463:THR:HG23	2.01	0.41
1:A:705:GLN:O	1:A:709:VAL:HG23	2.19	0.41
1:A:215:LEU:HD23	1:A:215:LEU:HA	1.85	0.41
1:A:540:ASP:OD1	1:A:542:GLN:N	2.54	0.41
1:A:739:ILE:HD11	1:A:757:MET:HE3	2.02	0.41
1:A:742:ALA:HB2	10:A:1338:HOH:O	2.19	0.41
1:A:360:LEU:HD12	1:A:373:VAL:HG23	2.03	0.41
1:A:548:GLN:O	1:A:552:LEU:HG	2.20	0.41
1:A:170:PHE:CD2	1:A:280:ALA:HB2	2.55	0.41
1:A:393:ASN:O	1:A:393:ASN:CG	2.63	0.41
1:A:874:GLY:HA2	10:A:1310:HOH:O	2.20	0.41
1:A:90:ARG:HG3	10:A:1487:HOH:O	2.20	0.41
1:A:310:LEU:C	1:A:310:LEU:CD2	2.92	0.41
1:A:346:LEU:O	1:A:350:THR:HG23	2.20	0.41
2:B:139:GLN:HB2	2:B:149:LYS:HD3	2.03	0.41
1:A:734:LEU:HD23	1:A:734:LEU:HA	1.85	0.41
1:A:273:ARG:HD2	10:A:1367:HOH:O	2.21	0.40
1:A:707:LYS:O	1:A:711:VAL:HG23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:GLN:NE2	1:A:156:GLY:HA3	2.36	0.40
1:A:512:HIS:ND1	1:A:580:PHE:HE2	2.19	0.40
1:A:624:MET:HB3	1:A:698:VAL:HG13	2.04	0.40
1:A:847:ASN:CG	1:A:850:ARG:HG2	2.46	0.40
1:A:360:LEU:HD11	10:A:1354:HOH:O	2.21	0.40
1:A:560:ARG:HH21	1:A:600:MET:HE2	1.86	0.40
2:B:143:LEU:HB2	2:B:150:PHE:HE2	1.86	0.40
1:A:334:MET:HE2	10:A:1269:HOH:O	2.21	0.40
1:A:547:PHE:HE2	1:A:594:PHE:CE2	2.39	0.40
1:A:650:VAL:HG11	1:A:666:ARG:HD3	2.03	0.40
1:A:749:ASP:OD1	10:A:1222:HOH:O	2.22	0.40
1:A:413:GLU:HG2	1:A:414:ASP:N	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	200/987 (20%)	197 (98%)	3 (2%)	0	100	100
2	B	260/289 (90%)	254 (98%)	6 (2%)	0	100	100
All	All	460/1276 (36%)	451 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	834/834 (100%)	829 (99%)	5 (1%)	78	91
2	B	229/253 (90%)	229 (100%)	0	100	100
All	All	1063/1087 (98%)	1058 (100%)	5 (0%)	81	92

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	ARG
1	A	301	VAL
1	A	473	LEU
1	A	931	PHE
1	A	955	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	GLN
1	A	165	ASN
1	A	172	ASN
1	A	188	GLN
1	A	193	GLN
1	A	369	ASN
1	A	407	HIS
1	A	415	GLN
1	A	663	GLN
1	A	865	GLN
1	A	870	GLN
1	A	986	ASN
2	B	255	ASN
2	B	268	HIS
2	B	275	HIS

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 9 are monoatomic - leaving 13 for Mogul analysis.

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$
8	CLR	B	301	-	31,31,31	0.66	0	48,48,48	1.38	7 (14%)
4	PCW	A	1105	-	53,53,53	0.96	2 (3%)	59,61,61	1.00	2 (3%)
9	NAG	B	303	-	14,14,15	0.78	1 (7%)	17,19,21	0.85	1 (5%)
9	NAG	B	307	2	14,14,15	0.88	1 (7%)	17,19,21	0.48	0
9	NAG	B	305	2	14,14,15	0.44	0	17,19,21	0.56	0
9	NAG	B	304	2	14,14,15	0.35	0	17,19,21	0.61	0
9	NAG	B	302	2	14,14,15	0.82	1 (7%)	17,19,21	0.69	1 (5%)
5	CE1	A	1106	-	36,36,36	0.52	0	35,35,35	0.54	0
4	PCW	A	1103	-	46,46,53	1.11	2 (4%)	52,54,61	0.87	3 (5%)
6	ALF	A	1107	-	4,4,4	1.42	0	-	-	-
4	PCW	A	1104	-	53,53,53	0.99	2 (3%)	59,61,61	0.99	4 (6%)
9	NAG	B	306	2	14,14,15	2.29	1 (7%)	17,19,21	2.47	5 (29%)
4	PCW	A	1102	-	45,45,53	1.07	2 (4%)	51,53,61	0.96	3 (5%)

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
8	CLR	B	301	-	-	5/10/68/68	0/4/4/4
4	PCW	A	1105	-	-	9/57/57/57	-
9	NAG	B	303	-	-	2/6/23/26	0/1/1/1
9	NAG	B	307	2	-	2/6/23/26	0/1/1/1
9	NAG	B	304	2	-	0/6/23/26	0/1/1/1
9	NAG	B	302	2	-	2/6/23/26	0/1/1/1
5	CE1	A	1106	-	-	13/34/34/34	-
4	PCW	A	1103	-	-	14/50/50/57	-
9	NAG	B	305	2	-	2/6/23/26	0/1/1/1
4	PCW	A	1104	-	-	27/57/57/57	-
9	NAG	B	306	2	-	2/6/23/26	0/1/1/1
4	PCW	A	1102	-	-	22/49/49/57	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	306	NAG	O5-C1	8.22	1.57	1.43
4	A	1103	PCW	O3-C11	4.66	1.46	1.33
4	A	1102	PCW	O2-C31	4.61	1.47	1.34
4	A	1103	PCW	O2-C31	4.57	1.47	1.34
4	A	1104	PCW	O2-C31	4.43	1.46	1.34
4	A	1104	PCW	O3-C11	4.38	1.46	1.33
4	A	1105	PCW	O3-C11	4.37	1.46	1.33
4	A	1102	PCW	O3-C11	4.26	1.45	1.33
4	A	1105	PCW	O2-C31	4.21	1.46	1.34
9	B	307	NAG	C1-C2	2.87	1.56	1.52
9	B	303	NAG	O5-C1	2.61	1.48	1.43
9	B	302	NAG	O5-C1	2.38	1.47	1.43

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	306	NAG	C1-O5-C5	8.01	122.92	112.19
4	A	1104	PCW	O2-C31-C32	3.86	119.83	111.48
4	A	1102	PCW	O2-C31-C32	3.79	119.67	111.48
4	A	1105	PCW	O2-C31-C32	3.75	119.60	111.48
8	B	301	CLR	C8-C7-C6	-3.60	107.78	112.76
9	B	306	NAG	C2-N2-C7	3.52	127.61	122.90
8	B	301	CLR	C1-C2-C3	3.36	114.93	110.48
8	B	301	CLR	C9-C10-C5	3.28	114.45	109.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	303	NAG	C1-O5-C5	3.11	116.35	112.19
4	A	1104	PCW	O3-C11-C12	3.11	121.31	111.83
4	A	1103	PCW	O2-C31-C32	3.07	118.11	111.48
4	A	1105	PCW	O3-C11-C12	2.88	120.61	111.83
4	A	1102	PCW	O3-C11-C12	2.58	119.69	111.83
9	B	306	NAG	C3-C4-C5	-2.50	105.70	110.23
8	B	301	CLR	C1-C10-C5	-2.37	104.66	108.74
8	B	301	CLR	C3-C4-C5	-2.35	108.31	112.05
8	B	301	CLR	C15-C14-C13	2.33	106.58	103.84
9	B	306	NAG	C1-C2-N2	-2.32	106.78	110.43
9	B	306	NAG	O3-C3-C2	-2.28	104.66	109.40
9	B	302	NAG	C1-O5-C5	2.27	115.22	112.19
4	A	1103	PCW	O3-C11-C12	2.25	118.70	111.83
4	A	1104	PCW	O3-C11-O11	-2.20	118.13	123.63
4	A	1103	PCW	C3-C2-C1	-2.18	106.70	111.78
8	B	301	CLR	C19-C10-C9	-2.15	109.24	111.66
4	A	1102	PCW	O3-C11-O11	-2.11	118.35	123.63
4	A	1104	PCW	C3-C2-C1	-2.08	106.94	111.78

There are no chirality outliers.

All (100) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1102	PCW	C4-O4P-P-O2P
4	A	1103	PCW	O2-C2-C3-O3
4	A	1104	PCW	C2-C1-O3P-P
4	A	1104	PCW	O4P-C4-C5-N
4	A	1104	PCW	C32-C31-O2-C2
4	A	1104	PCW	C1-O3P-P-O1P
4	A	1104	PCW	C1-O3P-P-O2P
4	A	1104	PCW	C1-O3P-P-O4P
4	A	1104	PCW	C4-O4P-P-O2P
4	A	1104	PCW	C4-O4P-P-O3P
4	A	1104	PCW	O31-C31-O2-C2
9	B	303	NAG	O5-C5-C6-O6
9	B	306	NAG	O5-C5-C6-O6
9	B	302	NAG	O5-C5-C6-O6
9	B	303	NAG	C4-C5-C6-O6
9	B	302	NAG	C4-C5-C6-O6
9	B	307	NAG	O5-C5-C6-O6
9	B	307	NAG	C4-C5-C6-O6
9	B	306	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
8	B	301	CLR	C17-C20-C22-C23
5	A	1106	CE1	O22-C23-C24-O25
8	B	301	CLR	C21-C20-C22-C23
8	B	301	CLR	C23-C24-C25-C27
8	B	301	CLR	C20-C22-C23-C24
4	A	1103	PCW	C12-C11-O3-C3
4	A	1103	PCW	C23-C24-C25-C26
5	A	1106	CE1	O16-C17-C18-O19
4	A	1105	PCW	C33-C34-C35-C36
4	A	1104	PCW	C31-C32-C33-C34
4	A	1102	PCW	C12-C13-C14-C15
4	A	1103	PCW	O11-C11-O3-C3
4	A	1102	PCW	C32-C31-O2-C2
4	A	1104	PCW	C40-C41-C42-C43
9	B	305	NAG	C4-C5-C6-O6
4	A	1104	PCW	C34-C35-C36-C37
4	A	1102	PCW	C21-C22-C23-C24
4	A	1102	PCW	C33-C34-C35-C36
8	B	301	CLR	C23-C24-C25-C26
5	A	1106	CE1	C3-C4-C5-C6
4	A	1104	PCW	C14-C15-C16-C17
4	A	1104	PCW	C32-C33-C34-C35
4	A	1102	PCW	O31-C31-O2-C2
4	A	1103	PCW	C1-C2-C3-O3
5	A	1106	CE1	C11-C10-C9-C8
4	A	1105	PCW	C20-C21-C22-C23
4	A	1102	PCW	C32-C33-C34-C35
4	A	1103	PCW	C20-C21-C22-C23
4	A	1104	PCW	C36-C37-C38-C39
4	A	1104	PCW	C21-C22-C23-C24
4	A	1105	PCW	C12-C11-O3-C3
9	B	305	NAG	O5-C5-C6-O6
4	A	1105	PCW	C34-C35-C36-C37
4	A	1102	PCW	C1-C2-C3-O3
4	A	1105	PCW	C43-C44-C45-C46
4	A	1102	PCW	C14-C15-C16-C17
4	A	1103	PCW	O3P-C1-C2-O2
4	A	1103	PCW	C36-C37-C38-C39
4	A	1103	PCW	C2-C1-O3P-P
4	A	1102	PCW	O2-C2-C3-O3
5	A	1106	CE1	C32-C33-O34-C35
4	A	1104	PCW	C15-C16-C17-C18

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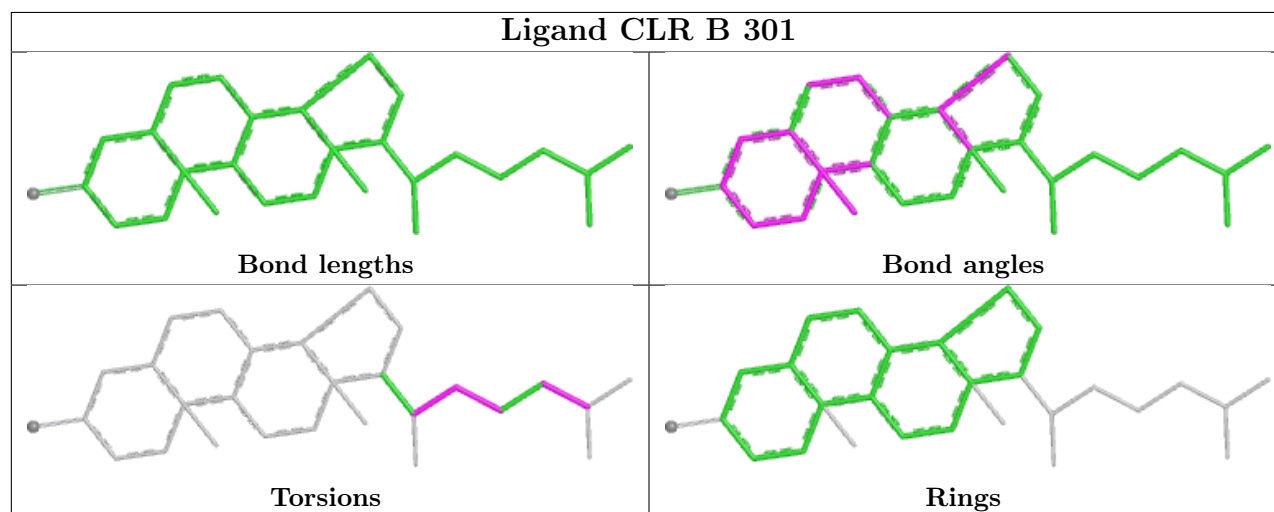
Mol	Chain	Res	Type	Atoms
4	A	1103	PCW	O3P-C1-C2-C3
4	A	1102	PCW	C23-C24-C25-C26
4	A	1102	PCW	C34-C35-C36-C37
5	A	1106	CE1	C2-C3-C4-C5
4	A	1105	PCW	O11-C11-O3-C3
5	A	1106	CE1	C24-C23-O22-C21
5	A	1106	CE1	O13-C14-C15-O16
4	A	1102	PCW	O4P-C4-C5-N
4	A	1103	PCW	O4P-C4-C5-N
4	A	1102	PCW	C20-C21-C22-C23
5	A	1106	CE1	C10-C11-C12-O13
5	A	1106	CE1	C27-C26-O25-C24
4	A	1102	PCW	C25-C26-C27-C28
5	A	1106	CE1	C20-C21-O22-C23
4	A	1102	PCW	C1-O3P-P-O2P
4	A	1103	PCW	C4-O4P-P-O3P
4	A	1105	PCW	C4-O4P-P-O2P
4	A	1103	PCW	C32-C33-C34-C35
4	A	1104	PCW	O3P-C1-C2-O2
4	A	1104	PCW	C43-C44-C45-C46
4	A	1102	PCW	C3-C2-O2-C31
4	A	1104	PCW	C1-C2-O2-C31
4	A	1102	PCW	C24-C25-C26-C27
4	A	1105	PCW	C45-C46-C47-C48
4	A	1102	PCW	C35-C36-C37-C38
4	A	1102	PCW	C37-C38-C39-C40
4	A	1104	PCW	O2-C31-C32-C33
4	A	1104	PCW	C17-C18-C19-C20
4	A	1102	PCW	C1-C2-O2-C31
4	A	1102	PCW	C17-C18-C19-C20
4	A	1105	PCW	C19-C20-C21-C22
4	A	1104	PCW	O3P-C1-C2-C3
4	A	1104	PCW	O11-C11-O3-C3
4	A	1104	PCW	C12-C11-O3-C3
4	A	1104	PCW	C35-C36-C37-C38
5	A	1106	CE1	O31-C32-C33-O34
4	A	1104	PCW	C3-C2-O2-C31
4	A	1103	PCW	O2-C31-C32-C33
5	A	1106	CE1	C23-C24-O25-C26

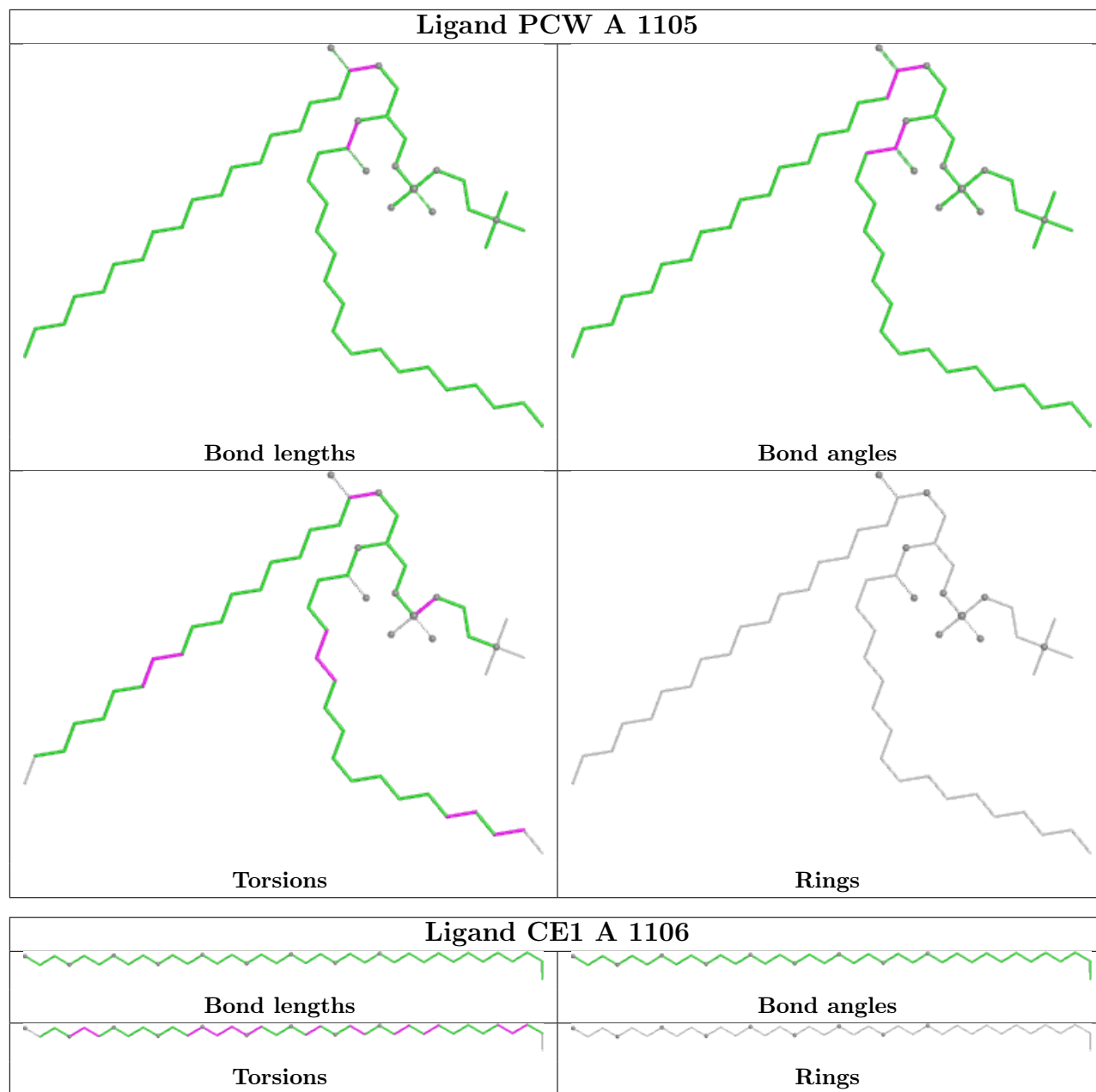
There are no ring outliers.

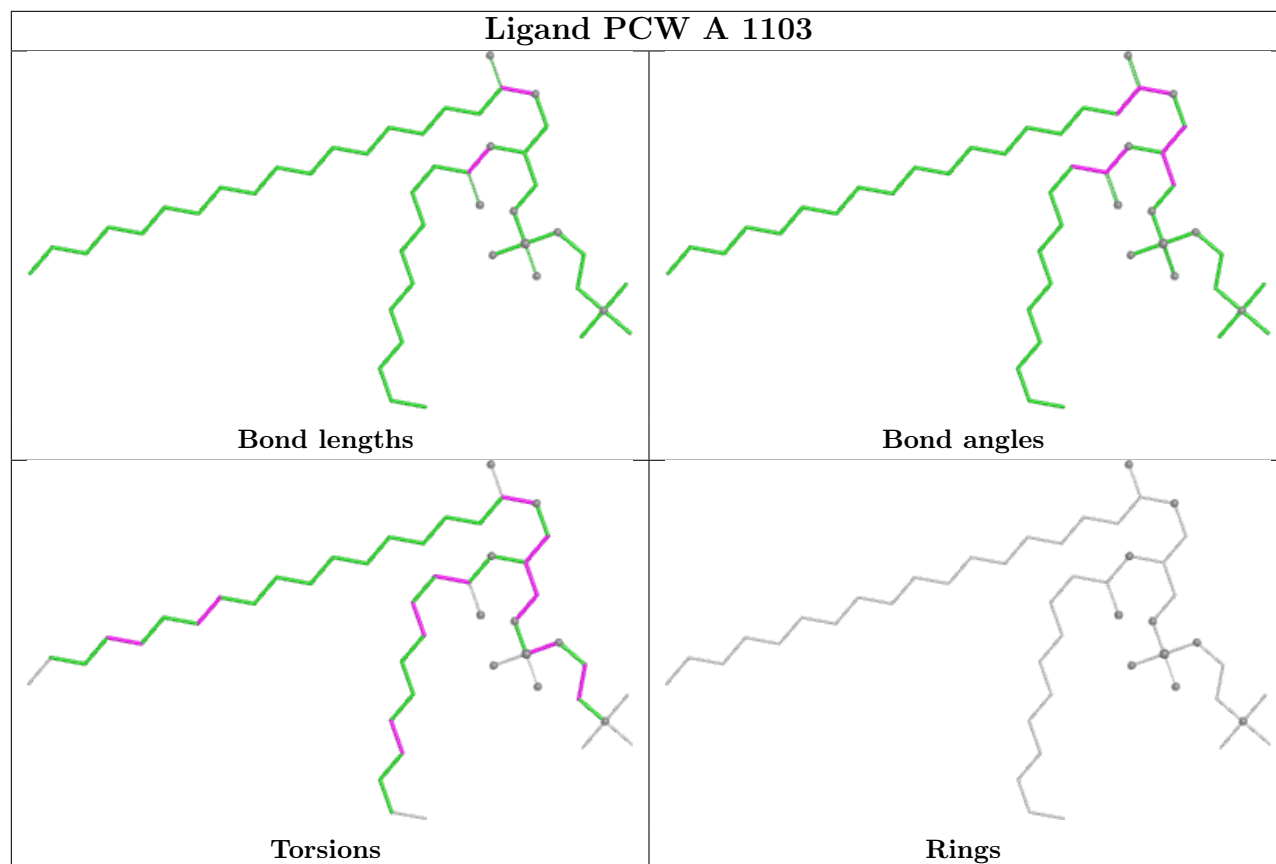
10 monomers are involved in 23 short contacts:

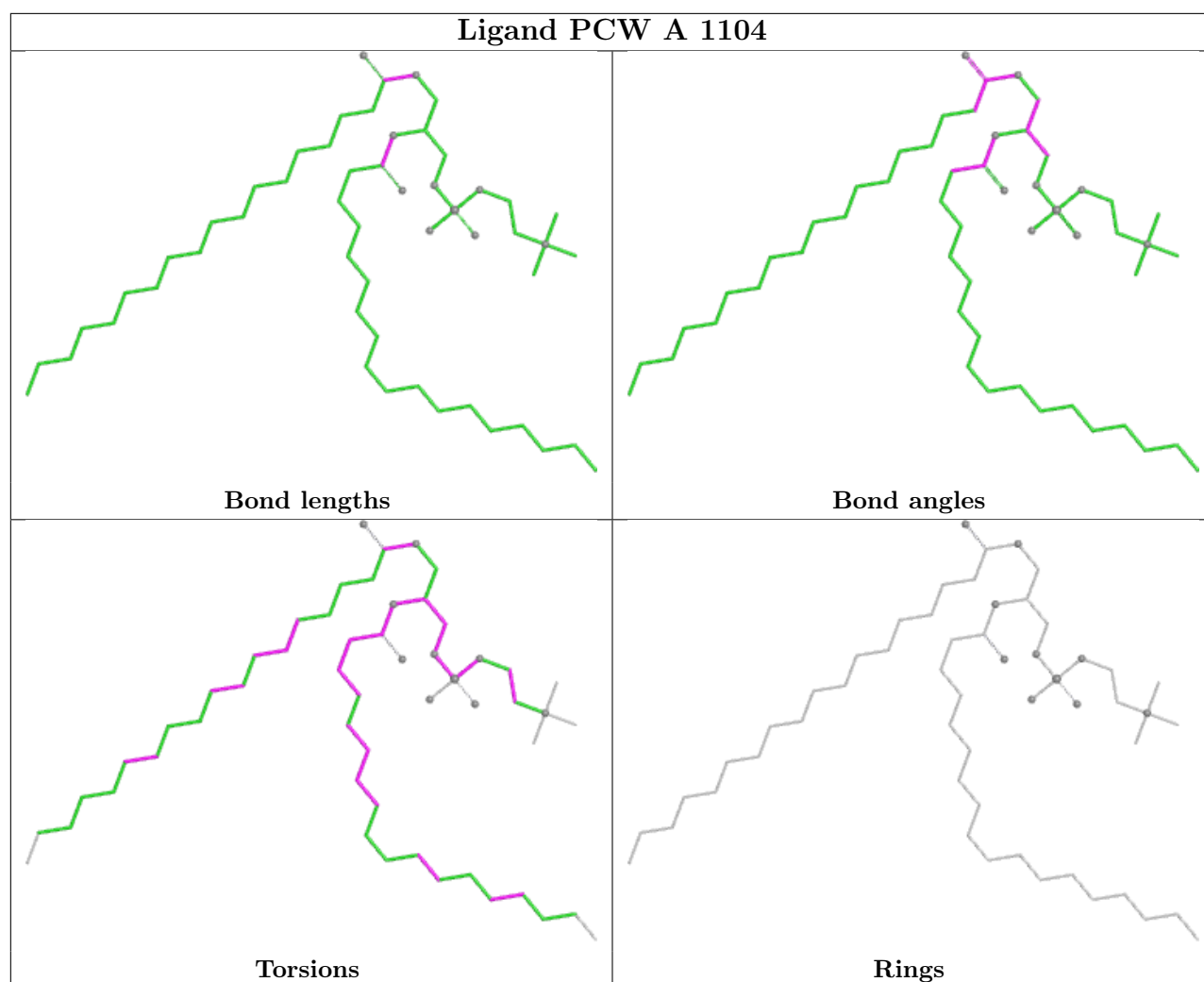
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	301	CLR	7	0
4	A	1105	PCW	3	0
9	B	303	NAG	2	0
9	B	302	NAG	2	0
5	A	1106	CE1	2	0
4	A	1103	PCW	2	0
6	A	1107	ALF	1	0
4	A	1104	PCW	1	0
9	B	306	NAG	1	0
4	A	1102	PCW	3	0

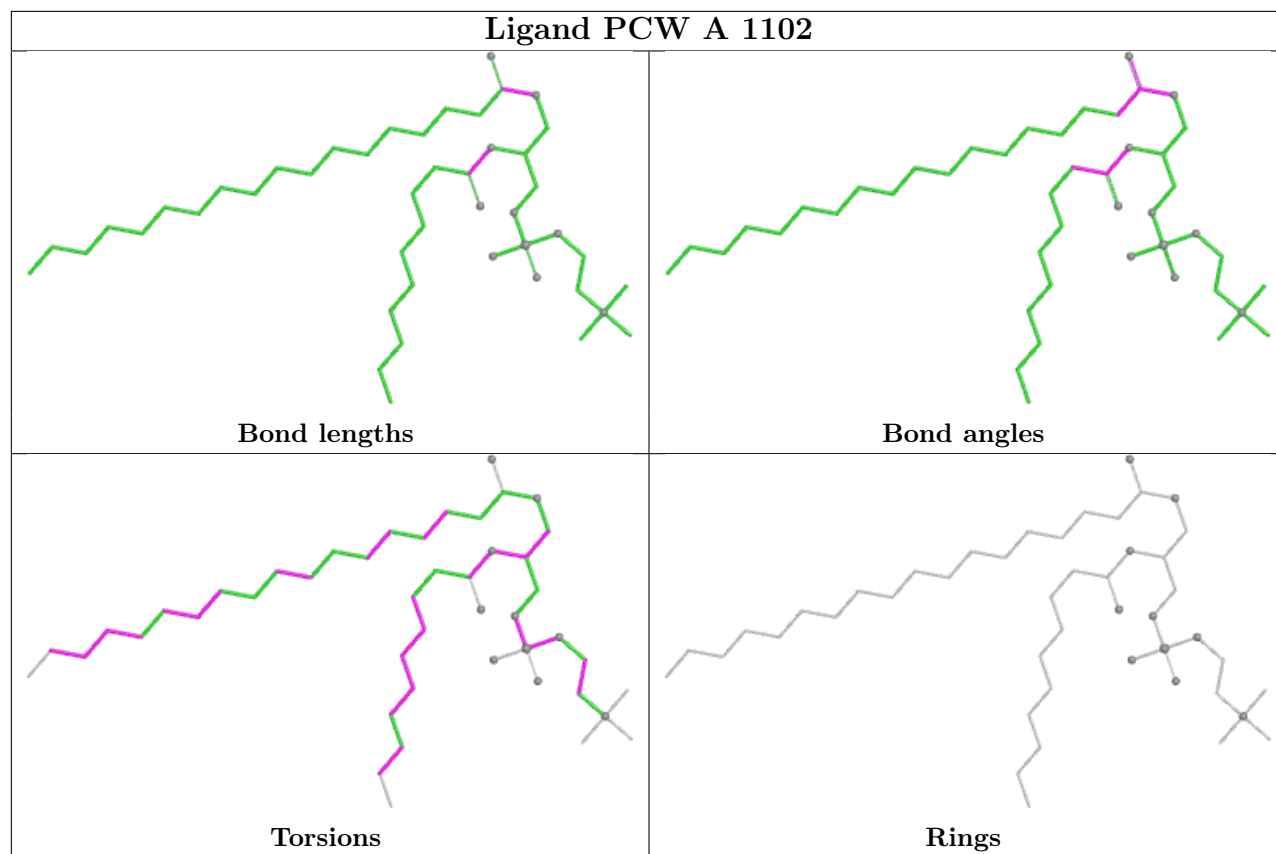
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	987/987 (100%)	0.35	67 (6%)	23 20	26, 49, 97, 168	0
2	B	262/289 (90%)	0.49	17 (6%)	25 22	35, 59, 101, 179	0
All	All	1249/1276 (97%)	0.38	84 (6%)	24 21	26, 52, 99, 179	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	174	VAL	7.5
1	A	102	ALA	4.5
1	A	572	LYS	4.3
1	A	1032	TYR	4.0
1	A	276	ILE	3.7
2	B	213	LEU	3.6
1	A	94	GLY	3.5
1	A	673	VAL	3.4
1	A	101	PHE	3.4
1	A	105	LEU	3.4
2	B	246	ALA	3.4
1	A	419	THR	3.4
1	A	158	TYR	3.3
1	A	254	PHE	3.3
1	A	175	PRO	3.3
1	A	300	PHE	3.2
1	A	311	PHE	3.1
1	A	89	LEU	3.1
1	A	932	PHE	3.1
1	A	98	TYR	3.1
2	B	91	GLU	3.1
1	A	598	VAL	3.0
1	A	177	GLN	3.0
1	A	87	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
2	B	92	LYS	3.0
1	A	933	ILE	3.0
1	A	155	PHE	3.0
1	A	192	ASP	3.0
1	A	384	SER	2.9
1	A	275	ILE	2.9
1	A	226	SER	2.9
1	A	959	PHE	2.8
1	A	489	ILE	2.8
2	B	216	GLU	2.8
1	A	287	GLU	2.7
1	A	232	GLU	2.7
1	A	955	GLN	2.7
1	A	540	ASP	2.6
1	A	420	PHE	2.6
1	A	1031	LEU	2.6
1	A	255	SER	2.6
1	A	633	ALA	2.6
2	B	130	ASN	2.6
1	A	965	VAL	2.6
1	A	154	CYS	2.5
1	A	685	SER	2.5
2	B	90	GLY	2.5
1	A	434	LEU	2.5
1	A	277	GLY	2.5
1	A	165	ASN	2.5
2	B	88	VAL	2.5
1	A	543	TRP	2.4
1	A	631	ILE	2.4
1	A	164	THR	2.4
2	B	218	PHE	2.4
1	A	173	LEU	2.3
1	A	48	MET	2.3
1	A	159	GLN	2.3
1	A	958	PHE	2.3
2	B	38	VAL	2.3
1	A	560	ARG	2.3
1	A	647	SER	2.3
1	A	1026	TRP	2.3
2	B	252	VAL	2.2
1	A	284	SER	2.2
2	B	35	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	49	GLU	2.2
1	A	304	ILE	2.2
1	A	538	PRO	2.2
1	A	956	GLN	2.1
2	B	159	LEU	2.1
1	A	137	ASP	2.1
1	A	451	VAL	2.1
1	A	479	TYR	2.1
2	B	87	ASP	2.1
2	B	39	TRP	2.1
1	A	262	THR	2.1
1	A	325	THR	2.1
1	A	568	TYR	2.1
1	A	163	SER	2.1
1	A	327	LEU	2.0
2	B	174	GLU	2.0
2	B	253	PRO	2.0
1	A	653	ILE	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	NAG	B	305	14/15	0.62	0.17	138,151,159,161	0
9	NAG	B	303	14/15	0.78	0.18	93,126,141,145	0
4	PCW	A	1104	54/54	0.84	0.20	69,110,166,174	0
4	PCW	A	1103	47/54	0.85	0.16	38,76,155,169	0
4	PCW	A	1102	46/54	0.85	0.23	57,110,138,146	0

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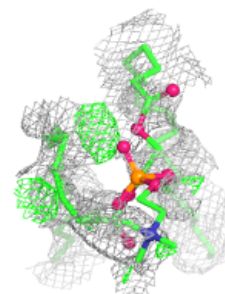
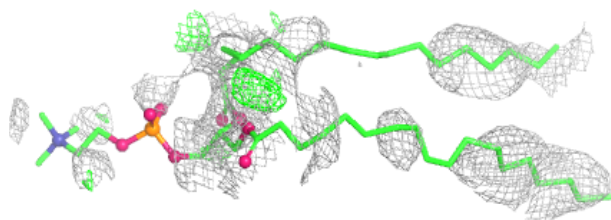
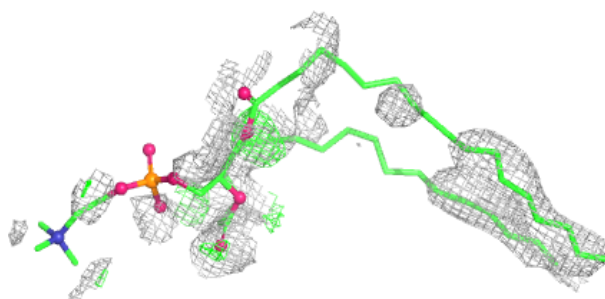
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	NAG	B	306	14/15	0.85	0.13	98,132,137,139	0
7	RB	A	1114	1/1	0.86	0.15	151,151,151,151	0
8	CLR	B	301	28/28	0.87	0.19	110,129,135,141	0
9	NAG	B	304	14/15	0.88	0.11	60,78,88,90	0
5	CE1	A	1106	37/37	0.89	0.19	52,79,118,119	0
9	NAG	B	307	14/15	0.89	0.18	121,136,141,141	0
9	NAG	B	302	14/15	0.90	0.12	84,92,106,108	0
4	PCW	A	1105	54/54	0.93	0.15	45,78,113,126	0
6	ALF	A	1107	5/5	0.94	0.07	34,35,41,42	0
7	RB	A	1111	1/1	0.94	0.08	138,138,138,138	0
7	RB	B	308	1/1	0.96	0.06	93,93,93,93	0
7	RB	A	1113	1/1	0.97	0.06	50,50,50,50	0
7	RB	A	1108	1/1	0.97	0.06	82,82,82,82	0
3	MG	A	1101	1/1	0.99	0.03	33,33,33,33	0
7	RB	A	1112	1/1	0.99	0.03	41,41,41,41	0
7	RB	A	1110	1/1	0.99	0.03	71,71,71,71	0
7	RB	A	1109	1/1	1.00	0.04	45,45,45,45	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.

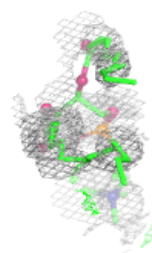
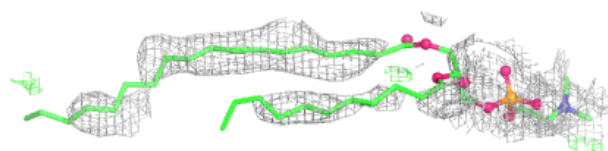
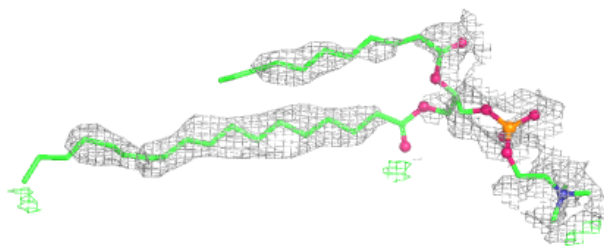
Electron density around PCW A 1104:

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

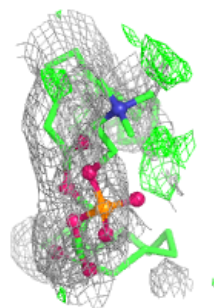
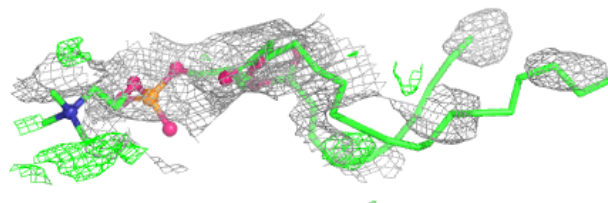
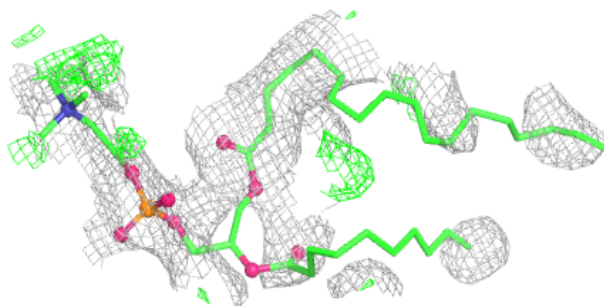


Electron density around PCW A 1103:

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

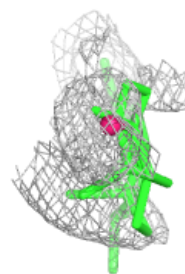
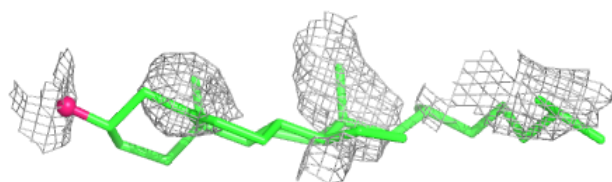
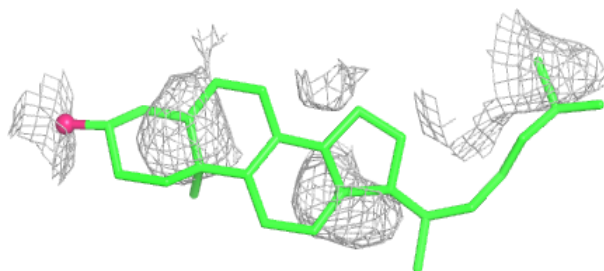
**Electron density around PCW A 1102:**

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

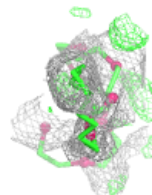
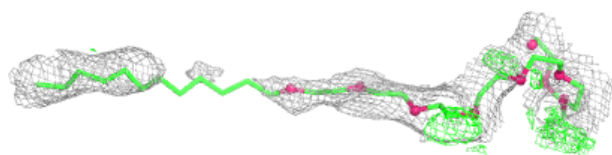
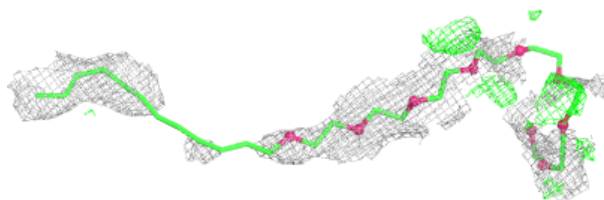


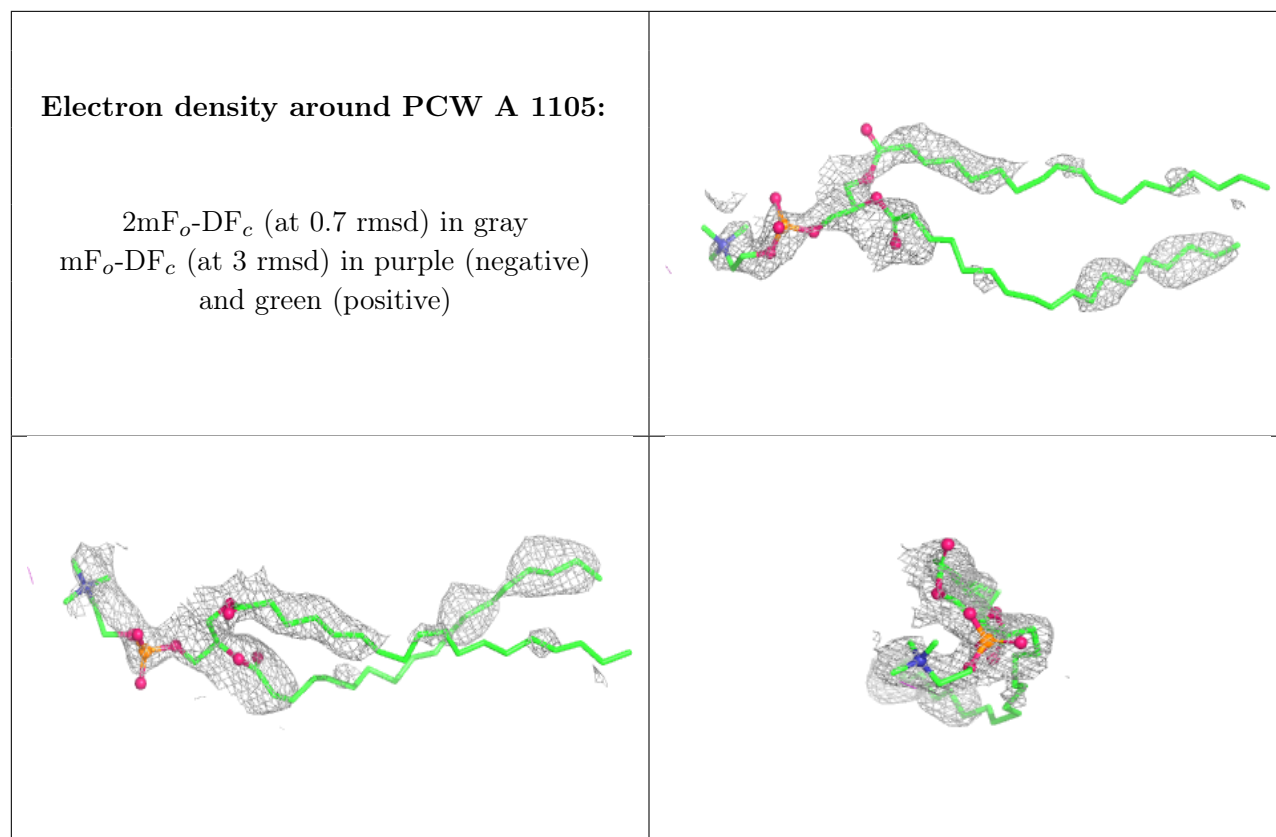
Electron density around CLR B 301:

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

**Electron density around CE1 A 1106:**

$2mF_o-DF_c$ (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.