



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:00 PM UTC

PDB ID : 9IHK / pdb_00009ihk
Title : Crystal structure of carrageenan sulfatase Bt3731_S1_30A from human gut bacterium Bacteroides thetaiotaomicron VPI-3731
Authors : Solanki, V.; Parnami, J.; Hehemann, J.H.
Deposited on : 2025-02-21
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

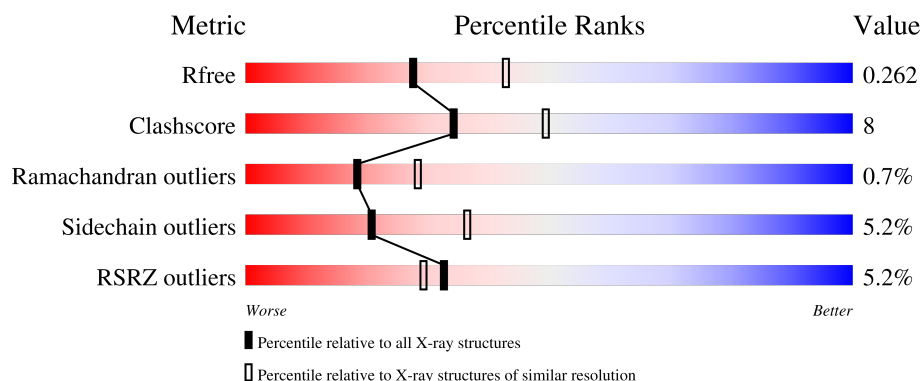
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

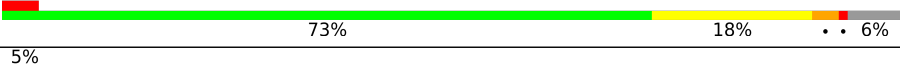
The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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

Mol	Chain	Length	Quality of chain
1	A	522	 6% 72% 20% • 6%
1	B	522	 4% 73% 18% • • 6%
1	C	522	 5% 75% 17% • 6%
1	D	522	 5% 70% 22% • 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16282 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 Sulfatase_S1_30A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	492	Total	C	N	O	S	0	0	0
			3997	2558	672	742	25			
1	C	492	Total	C	N	O	S	0	0	0
			3997	2558	672	742	25			
1	A	493	Total	C	N	O	S	0	0	0
			4005	2562	674	744	25			
1	B	493	Total	C	N	O	S	0	0	0
			4005	2562	674	744	25			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

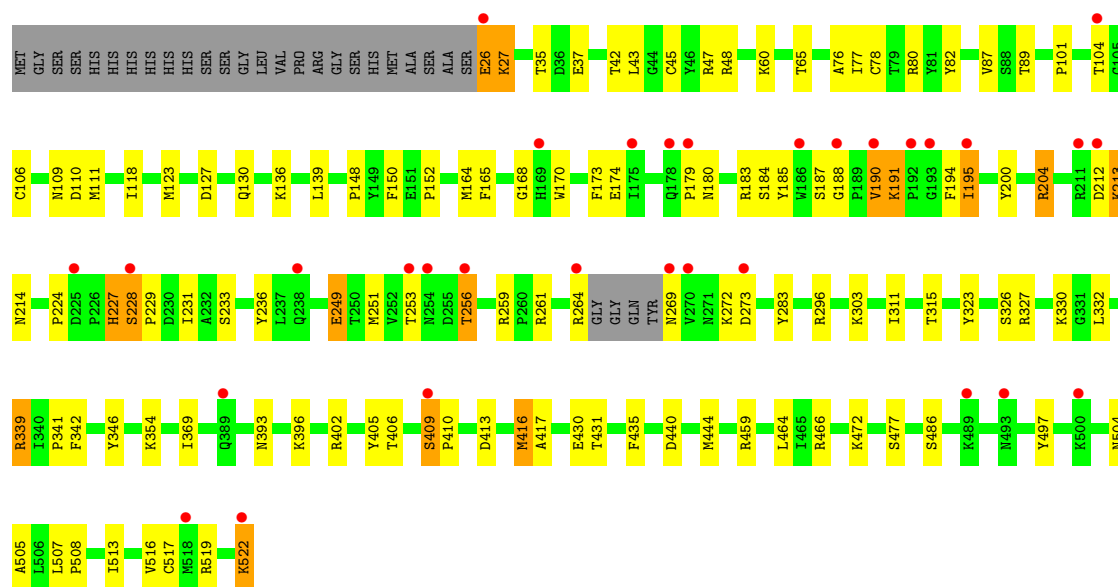
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	65	Total	O	0	0
			65	65		
3	C	61	Total	O	0	0
			61	61		
3	A	65	Total	O	0	0
			65	65		
3	B	83	Total	O	0	0
			83	83		

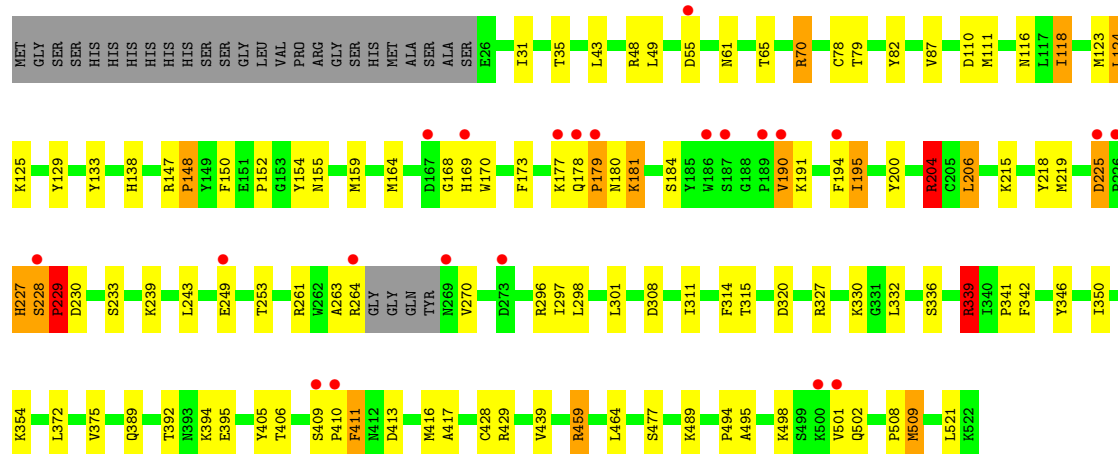
• Molecule 1: Sulfatase_S1_30A

Chain A: 



• Molecule 1: Sulfatase_S1_30A

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	52.97Å 115.93Å 177.21Å 90.00° 94.72° 90.00°	Depositor
Resolution (Å)	176.60 – 2.40 176.60 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (176.60-2.40) 99.1 (176.60-2.40)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.40Å)	Xtriage
Refinement program	REFMAC 5.8.0430	Depositor
R, R_{free}	0.192 , 0.249 0.219 , 0.262	Depositor DCC
R_{free} test set	4010 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	33.7	Xtriage
Anisotropy	0.148	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16282	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.94 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.1933e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: 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	0.88	0/4111	1.36	11/5582 (0.2%)
1	B	0.88	0/4111	1.36	15/5582 (0.3%)
1	C	0.89	0/4103	1.36	16/5571 (0.3%)
1	D	0.89	0/4103	1.36	11/5571 (0.2%)
All	All	0.88	0/16428	1.36	53/22306 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	12
1	B	0	10
1	C	0	9
1	D	0	12
All	All	0	43

There are no bond length outliers.

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	191	LYS	O-C-N	12.12	135.26	121.32
1	D	227	HIS	CB-CA-C	-10.35	93.33	109.89
1	C	228	SER	N-CA-C	7.44	126.25	109.81
1	C	88	SER	N-CA-C	7.14	118.75	110.97
1	B	110	ASP	CB-CA-C	7.13	116.89	109.83
1	D	110	ASP	CB-CA-C	7.04	116.80	109.83
1	C	412	ASN	CB-CA-C	6.57	119.97	111.50
1	D	274	LYS	N-CA-C	-6.45	104.99	112.92

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	191	LYS	CB-CA-C	6.34	118.73	109.48
1	C	190	VAL	O-C-N	-6.30	115.80	122.67
1	C	181	LYS	CB-CA-C	6.11	121.69	111.30
1	A	111	MET	N-CA-C	-6.10	102.39	110.07
1	B	181	LYS	CB-CA-C	6.05	121.28	111.05
1	D	323	TYR	CB-CA-C	5.99	118.68	110.06
1	B	173	PHE	CA-CB-CG	5.91	119.71	113.80
1	B	253	THR	N-CA-C	-5.86	100.84	109.81
1	C	323	TYR	CB-CA-C	5.80	118.41	110.06
1	A	224	PRO	CB-CA-C	-5.80	102.79	110.27
1	C	428	CYS	N-CA-C	-5.72	105.97	113.17
1	B	225	ASP	N-CA-C	5.68	120.48	112.75
1	A	173	PHE	CA-CB-CG	5.62	119.42	113.80
1	B	55	ASP	CA-CB-CG	5.59	118.19	112.60
1	B	411	PHE	N-CA-CB	-5.57	101.78	110.98
1	B	428	CYS	N-CA-C	-5.57	106.25	113.16
1	C	190	VAL	CA-C-N	5.57	135.39	121.80
1	C	190	VAL	C-N-CA	5.57	135.39	121.80
1	D	272	LYS	N-CA-C	-5.49	102.88	110.35
1	C	191	LYS	CA-C-N	-5.49	112.96	119.05
1	C	191	LYS	C-N-CA	-5.49	112.96	119.05
1	D	284	PHE	CA-CB-CG	5.47	119.27	113.80
1	C	191	LYS	CB-CA-C	5.47	120.94	110.17
1	B	227	HIS	N-CA-C	5.47	117.78	110.35
1	A	249	GLU	N-CA-CB	-5.45	100.86	110.39
1	A	435	PHE	CA-CB-CG	5.31	119.11	113.80
1	C	183	ARG	CB-CA-C	5.30	118.39	109.48
1	D	272	LYS	CA-C-O	-5.29	115.95	121.55
1	D	382	GLN	CB-CA-C	5.26	118.56	110.14
1	B	148	PRO	CB-CA-C	5.26	118.27	111.64
1	B	314	PHE	N-CA-CB	5.24	118.80	110.57
1	A	227	HIS	CA-CB-CG	5.24	119.04	113.80
1	B	218	TYR	N-CA-CB	5.19	118.73	110.84
1	C	410	PRO	N-CA-C	-5.18	106.46	113.40
1	A	249	GLU	CB-CG-CD	5.17	121.39	112.60
1	A	440	ASP	CA-CB-CG	5.17	117.77	112.60
1	D	54	ASN	N-CA-C	-5.14	106.86	112.72
1	D	181	LYS	CB-CA-C	5.13	120.02	111.30
1	A	190	VAL	N-CA-CB	5.12	119.67	111.23
1	D	194	PHE	CA-CB-CG	5.11	118.91	113.80
1	A	497	TYR	N-CA-CB	-5.09	103.12	110.56
1	C	227	HIS	N-CA-C	5.06	117.06	110.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	229	PRO	CB-CA-C	5.05	119.89	111.56
1	B	70	ARG	CB-CA-C	-5.04	102.42	110.79
1	B	439	VAL	N-CA-CB	-5.00	102.21	110.56

There are no chirality outliers.

All (43) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	183	ARG	Sidechain
1	A	204	ARG	Sidechain
1	A	261	ARG	Sidechain
1	A	296	ARG	Sidechain
1	A	327	ARG	Sidechain
1	A	339	ARG	Sidechain
1	A	402	ARG	Sidechain
1	A	459	ARG	Sidechain
1	A	466	ARG	Sidechain
1	A	47	ARG	Sidechain
1	A	519	ARG	Sidechain
1	A	80	ARG	Sidechain
1	B	147	ARG	Sidechain
1	B	204	ARG	Sidechain
1	B	261	ARG	Sidechain
1	B	264	ARG	Sidechain
1	B	296	ARG	Sidechain
1	B	339	ARG	Sidechain
1	B	429	ARG	Sidechain
1	B	459	ARG	Sidechain
1	B	48	ARG	Sidechain
1	B	70	ARG	Sidechain
1	C	204	ARG	Sidechain
1	C	211	ARG	Sidechain
1	C	259	ARG	Sidechain
1	C	264	ARG	Sidechain
1	C	296	ARG	Sidechain
1	C	429	ARG	Sidechain
1	C	47	ARG	Sidechain
1	C	48	ARG	Sidechain
1	C	80	ARG	Sidechain
1	D	183	ARG	Sidechain
1	D	204	ARG	Sidechain
1	D	211	ARG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	D	259	ARG	Sidechain
1	D	264	ARG	Sidechain
1	D	296	ARG	Sidechain
1	D	327	ARG	Sidechain
1	D	402	ARG	Sidechain
1	D	459	ARG	Sidechain
1	D	466	ARG	Sidechain
1	D	47	ARG	Sidechain
1	D	70	ARG	Sidechain

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	4005	0	3950	64	0
1	B	4005	0	3950	58	0
1	C	3997	0	3944	61	0
1	D	3997	0	3944	65	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	65	0	0	2	0
3	B	83	0	0	1	0
3	C	61	0	0	1	0
3	D	65	0	0	1	0
All	All	16282	0	15788	242	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 8.

All (242) 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:C:321:MET:HE1	1:C:334:TYR:HB2	1.33	1.11
1:A:409:SER:HB3	1:A:410:PRO:HD3	1.50	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:253:THR:H	1:D:256:THR:HG22	1.37	0.86
1:A:253:THR:H	1:A:256:THR:HG22	1.48	0.79
1:A:409:SER:CB	1:A:410:PRO:HD3	2.12	0.79
1:C:241:ILE:HD11	1:C:278:LYS:HG3	1.66	0.77
1:A:195:ILE:HG12	1:A:200:TYR:HB2	1.66	0.77
1:C:409:SER:HB3	1:C:410:PRO:HD3	1.69	0.74
1:C:191:LYS:HB2	1:C:192:PRO:HD3	1.69	0.74
1:D:140:GLY:H	1:D:166:ASN:HD21	1.37	0.71
1:A:406:THR:OG1	1:A:416:MET:HG3	1.92	0.70
1:C:191:LYS:HB2	1:C:192:PRO:CD	2.23	0.68
1:A:330:LYS:HG3	1:A:332:LEU:HG	1.76	0.68
1:A:409:SER:HB3	1:A:410:PRO:CD	2.24	0.67
1:C:87:VAL:HG21	1:C:409:SER:CB	2.24	0.67
1:A:87:VAL:HG21	1:A:409:SER:CB	2.24	0.66
1:A:339:ARG:NH1	3:A:701:HOH:O	2.28	0.66
1:B:169:HIS:HB3	1:B:229:PRO:HG3	1.78	0.66
1:A:259:ARG:O	1:A:264:ARG:HD2	1.96	0.66
1:A:228:SER:HB2	1:A:229:PRO:HD2	1.79	0.65
1:A:26:GLU:HG2	1:A:27:LYS:H	1.61	0.65
1:C:409:SER:CB	1:C:410:PRO:HD3	2.28	0.63
1:C:321:MET:CE	1:C:332:LEU:HB2	2.29	0.63
1:C:171:LYS:HE2	1:C:229:PRO:HB2	1.81	0.63
1:A:87:VAL:HG21	1:A:409:SER:HB2	1.79	0.63
1:C:321:MET:HE2	1:C:337:SER:CB	2.29	0.62
1:A:504:ASN:HB3	1:A:507:LEU:HG	1.80	0.62
1:B:339:ARG:NH1	3:B:702:HOH:O	2.32	0.62
1:A:431:THR:OG1	1:A:486:SER:HA	2.00	0.61
1:B:87:VAL:HG21	1:B:409:SER:HB3	1.83	0.61
1:A:409:SER:CB	1:A:410:PRO:CD	2.79	0.60
1:D:228:SER:OG	1:D:230:ASP:N	2.35	0.60
1:B:43:LEU:HD23	1:B:65:THR:HG21	1.83	0.60
1:D:87:VAL:HG21	1:D:409:SER:HB3	1.82	0.60
1:A:104:THR:HG23	1:A:106:CYS:H	1.67	0.59
1:D:272:LYS:O	1:D:273:ASP:HB2	2.03	0.59
1:C:314:PHE:HB3	1:C:343:VAL:CG2	2.32	0.59
1:D:251:MET:HB2	1:D:272:LYS:HE3	1.84	0.58
1:C:195:ILE:HG12	1:C:200:TYR:HB2	1.85	0.58
1:A:101:PRO:O	1:A:104:THR:HG22	2.03	0.58
1:B:195:ILE:HG12	1:B:200:TYR:HB2	1.84	0.58
1:B:82:TYR:CE2	1:B:339:ARG:HG3	2.39	0.57
1:C:321:MET:HE2	1:C:337:SER:HB2	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:GLU:HB2	1:A:185:TYR:HE2	1.70	0.57
1:D:262:TRP:CZ3	1:D:333:PRO:HD2	2.40	0.57
1:D:465:ILE:HA	1:D:468:MET:HE2	1.86	0.57
1:A:417:ALA:HB2	1:A:464:LEU:HD13	1.87	0.56
1:A:315:THR:HA	1:A:341:PRO:O	2.05	0.56
1:C:321:MET:HE3	1:C:332:LEU:HB2	1.88	0.55
1:A:87:VAL:HG21	1:A:409:SER:OG	2.06	0.55
1:D:116:ASN:HD21	1:B:155:ASN:H	1.53	0.55
1:C:314:PHE:HB3	1:C:343:VAL:HG23	1.88	0.55
1:C:315:THR:HA	1:C:341:PRO:O	2.06	0.55
1:A:82:TYR:CE2	1:A:339:ARG:HG3	2.41	0.55
1:D:187:SER:HB3	1:D:231:ILE:HG21	1.88	0.55
1:D:314:PHE:HB3	1:D:343:VAL:CG2	2.37	0.55
1:C:354:LYS:NZ	1:C:393:ASN:OD1	2.39	0.55
1:B:330:LYS:HG3	1:B:332:LEU:HG	1.89	0.55
1:C:87:VAL:HG21	1:C:409:SER:HB2	1.87	0.55
1:A:339:ARG:NH2	3:A:703:HOH:O	2.39	0.55
1:D:131:THR:OG1	1:D:159:MET:HG2	2.07	0.54
1:D:228:SER:C	1:D:230:ASP:H	2.14	0.54
1:C:54:ASN:O	1:C:60:LYS:HA	2.07	0.54
1:A:118:ILE:HG21	1:A:123:MET:HE3	1.89	0.54
1:D:315:THR:HA	1:D:341:PRO:O	2.07	0.54
1:A:249:GLU:CD	1:A:249:GLU:H	2.15	0.54
1:B:191:LYS:HB2	1:B:194:PHE:CE1	2.41	0.54
1:C:225:ASP:C	1:C:227:HIS:N	2.66	0.54
1:D:228:SER:HG	1:D:286:MET:HE1	1.73	0.54
1:D:155:ASN:H	1:B:116:ASN:HD21	1.55	0.53
1:B:228:SER:O	1:B:230:ASP:N	2.41	0.53
1:B:417:ALA:HB2	1:B:464:LEU:HD13	1.91	0.53
1:B:177:LYS:HB2	1:B:181:LYS:HD2	1.89	0.53
1:B:125:LYS:HG3	1:B:159:MET:HE2	1.91	0.53
1:B:168:GLY:HA3	1:B:170:TRP:CZ3	2.44	0.53
1:A:78:CYS:HB2	1:A:342:PHE:HB3	1.90	0.53
1:D:188:GLY:C	1:D:190:VAL:H	2.16	0.52
1:B:354:LYS:HE3	1:B:395:GLU:O	2.09	0.52
1:A:187:SER:OG	1:A:188:GLY:N	2.40	0.52
1:A:229:PRO:HB2	1:A:231:ILE:HD12	1.91	0.52
1:B:170:TRP:CG	1:B:184:SER:HB2	2.45	0.52
1:D:171:LYS:NZ	1:D:228:SER:HB2	2.25	0.52
1:D:251:MET:HB3	1:D:272:LYS:HG2	1.92	0.52
1:C:177:LYS:HB3	1:C:181:LYS:HB2	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:PHE:HA	1:B:164:MET:O	2.09	0.51
1:C:321:MET:HE2	1:C:337:SER:HB3	1.90	0.51
1:D:354:LYS:NZ	1:D:393:ASN:OD1	2.43	0.51
1:D:410:PRO:HG3	3:D:765:HOH:O	2.11	0.51
1:A:43:LEU:HD23	1:A:65:THR:HG21	1.93	0.51
1:C:29:ASN:HD22	1:C:217:PHE:H	1.60	0.50
1:B:495:ALA:HA	1:B:498:LYS:HD2	1.94	0.50
1:C:409:SER:HB3	1:C:410:PRO:CD	2.38	0.50
1:D:187:SER:CB	1:D:231:ILE:HG21	2.42	0.50
1:C:168:GLY:HA3	1:C:170:TRP:CZ3	2.47	0.50
1:C:114:ASN:HD22	1:C:117:LEU:HG	1.77	0.50
1:C:225:ASP:O	1:C:226:PRO:C	2.53	0.50
1:C:170:TRP:CG	1:C:184:SER:HB2	2.46	0.50
1:D:245:TYR:HB2	1:D:277:LYS:HG2	1.94	0.49
1:C:80:ARG:HD2	1:C:420:GLY:HA2	1.93	0.49
1:B:311:ILE:HD13	1:B:372:LEU:HD23	1.95	0.49
1:B:320:ASP:O	1:B:336:SER:OG	2.29	0.49
1:A:45:CYS:O	1:A:48:ARG:HG2	2.12	0.49
1:B:118:ILE:CG2	1:B:123:MET:HE3	2.43	0.49
1:B:118:ILE:HG21	1:B:123:MET:HE3	1.93	0.49
1:B:177:LYS:HB2	1:B:181:LYS:HB2	1.95	0.49
1:A:430:GLU:OE1	1:A:431:THR:HG22	2.12	0.49
1:C:225:ASP:C	1:C:227:HIS:H	2.21	0.49
1:D:168:GLY:HA3	1:D:170:TRP:CZ3	2.48	0.48
1:B:206:LEU:HD13	1:B:297:ILE:HD13	1.95	0.48
1:D:330:LYS:HZ3	1:D:332:LEU:HD21	1.77	0.48
1:D:481:PRO:HG2	1:D:492:TYR:HB2	1.95	0.48
1:C:225:ASP:O	1:C:227:HIS:N	2.46	0.48
1:B:410:PRO:HB2	1:B:411:PHE:CD2	2.48	0.48
1:A:42:THR:HG21	1:A:283:TYR:HE1	1.78	0.48
1:D:417:ALA:HB2	1:D:464:LEU:HD13	1.95	0.48
1:D:369:ILE:HD12	1:D:369:ILE:HA	1.81	0.47
1:D:133:TYR:CD1	1:D:164:MET:HG3	2.49	0.47
1:C:191:LYS:CB	1:C:192:PRO:CD	2.89	0.47
1:B:129:TYR:O	1:B:159:MET:HE1	2.14	0.47
1:D:409:SER:HB3	1:D:410:PRO:HD3	1.96	0.47
1:D:505:ALA:O	1:D:508:PRO:HD2	2.15	0.47
1:B:204:ARG:HA	1:B:204:ARG:HD3	1.66	0.47
1:D:92:ARG:NH1	1:D:136:LYS:O	2.48	0.47
1:A:168:GLY:HA3	1:A:170:TRP:CZ3	2.50	0.47
1:C:99:LEU:HD23	1:C:383:GLU:HG3	1.96	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:409:SER:CB	1:C:410:PRO:CD	2.93	0.46
1:D:116:ASN:HD21	1:B:155:ASN:N	2.13	0.46
1:C:239:LYS:HE2	1:C:239:LYS:HB2	1.71	0.46
1:A:505:ALA:O	1:A:508:PRO:HD2	2.15	0.46
1:B:190:VAL:HG23	1:B:194:PHE:HB2	1.97	0.46
1:D:37:GLU:HB3	1:D:227:HIS:HA	1.96	0.46
1:D:186:TRP:O	1:D:187:SER:HB3	2.15	0.46
1:D:178:GLN:O	1:D:179:PRO:C	2.57	0.46
1:A:522:LYS:HB3	1:A:522:LYS:HE2	1.82	0.46
1:C:130:GLN:HG2	1:C:212:ASP:CG	2.41	0.46
1:B:169:HIS:HB3	1:B:229:PRO:CG	2.46	0.46
1:C:152:PRO:HD2	1:C:164:MET:SD	2.55	0.46
1:C:253:THR:H	1:C:256:THR:HB	1.80	0.45
1:C:409:SER:N	3:C:705:HOH:O	2.48	0.45
1:A:89:THR:HG23	1:A:139:LEU:HD23	1.97	0.45
1:D:171:LYS:HZ1	1:D:228:SER:CB	2.30	0.45
1:C:58:TRP:HB3	1:C:280:LEU:HD21	1.98	0.45
1:B:49:LEU:HD13	1:B:79:THR:HG22	1.98	0.45
1:B:263:ALA:O	1:B:327:ARG:HD3	2.15	0.45
1:D:253:THR:N	1:D:256:THR:HG22	2.17	0.45
1:D:359:VAL:HG23	1:D:404:VAL:HG13	1.98	0.45
1:A:148:PRO:HD3	1:A:184:SER:HB3	1.98	0.45
1:B:394:LYS:HE3	1:B:394:LYS:HB3	1.88	0.45
1:D:462:LYS:HB2	1:D:462:LYS:HE2	1.63	0.45
1:C:410:PRO:HD2	1:C:411:PHE:H	1.82	0.45
1:B:315:THR:HA	1:B:341:PRO:O	2.16	0.45
1:A:109:ASN:O	1:A:110:ASP:HB2	2.17	0.45
1:D:180:ASN:OD1	1:D:180:ASN:N	2.49	0.45
1:B:78:CYS:HB2	1:B:342:PHE:HB3	1.98	0.45
1:D:231:ILE:O	1:D:286:MET:HE3	2.16	0.45
1:C:505:ALA:O	1:C:508:PRO:HD2	2.17	0.45
1:B:148:PRO:HD3	1:B:184:SER:HB3	1.99	0.45
1:C:37:GLU:OE2	1:C:329:ASN:ND2	2.50	0.45
1:C:276:ASP:HB3	1:C:323:TYR:OH	2.16	0.45
1:B:508:PRO:HB2	1:B:509:MET:HE3	1.98	0.45
1:B:152:PRO:HD2	1:B:164:MET:SD	2.57	0.44
1:D:171:LYS:HZ1	1:D:228:SER:HB2	1.82	0.44
1:C:109:ASN:O	1:C:110:ASP:HB2	2.16	0.44
1:C:270:VAL:HG11	1:C:323:TYR:CD1	2.52	0.44
1:A:150:PHE:CD2	1:A:180:ASN:HB2	2.53	0.44
1:B:133:TYR:CD1	1:B:164:MET:HG3	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:HIS:CB	1:B:229:PRO:HG3	2.47	0.44
1:A:354:LYS:NZ	1:A:393:ASN:O	2.48	0.44
1:C:177:LYS:HB3	1:C:181:LYS:HD2	2.00	0.44
1:B:178:GLN:O	1:B:179:PRO:C	2.59	0.44
1:D:116:ASN:HD21	1:B:154:TYR:HA	1.83	0.43
1:A:369:ILE:HD12	1:A:369:ILE:HA	1.83	0.43
1:B:311:ILE:HG12	1:B:346:TYR:CG	2.53	0.43
1:A:118:ILE:CG2	1:A:123:MET:HE3	2.48	0.43
1:A:444:MET:HE3	1:A:444:MET:HB3	1.83	0.43
1:D:426:LEU:HD11	1:D:461:GLN:HG3	2.01	0.43
1:C:58:TRP:HA	1:C:246:GLU:O	2.18	0.43
1:C:150:PHE:HA	1:C:164:MET:O	2.18	0.43
1:A:37:GLU:HB2	1:A:227:HIS:HD2	1.84	0.43
1:A:228:SER:CB	1:A:229:PRO:HD2	2.47	0.43
1:D:228:SER:OG	1:D:286:MET:HE1	2.17	0.43
1:C:519:ARG:HD3	1:C:519:ARG:HA	1.87	0.43
1:C:78:CYS:HB2	1:C:342:PHE:HB3	1.99	0.43
1:A:251:MET:HG2	1:A:323:TYR:O	2.19	0.43
1:A:311:ILE:HG12	1:A:346:TYR:CG	2.53	0.43
1:C:417:ALA:HB2	1:C:464:LEU:HD13	2.01	0.42
1:D:58:TRP:HA	1:D:246:GLU:O	2.19	0.42
1:D:155:ASN:N	1:B:116:ASN:HD21	2.16	0.42
1:A:259:ARG:HH12	1:A:269:ASN:HD21	1.67	0.42
1:D:314:PHE:HB3	1:D:343:VAL:HG22	2.01	0.42
1:C:45:CYS:O	1:C:49:LEU:HG	2.19	0.42
1:A:152:PRO:HD2	1:A:164:MET:SD	2.59	0.42
1:D:204:ARG:HA	1:D:204:ARG:HD3	1.83	0.42
1:C:213:LYS:HG3	1:C:214:ASN:N	2.34	0.42
1:C:83:ALA:HA	1:C:362:CYS:SG	2.59	0.42
1:A:227:HIS:ND1	1:A:228:SER:HB3	2.35	0.42
1:D:228:SER:C	1:D:230:ASP:N	2.77	0.42
1:D:395:GLU:HB2	1:D:398:VAL:HG22	2.01	0.42
1:B:124:LEU:CD1	1:B:375:VAL:HG21	2.49	0.42
1:B:389:GLN:HA	1:B:392:THR:OG1	2.18	0.42
1:C:227:HIS:CG	1:C:228:SER:H	2.38	0.42
1:B:61:ASN:HB3	1:B:243:LEU:HD13	2.02	0.42
1:C:87:VAL:HG21	1:C:409:SER:OG	2.19	0.42
1:C:359:VAL:HG23	1:C:404:VAL:HG13	2.02	0.42
1:B:406:THR:OG1	1:B:416:MET:HB3	2.20	0.42
1:D:367:PRO:HA	1:D:377:GLN:HE22	1.82	0.42
1:C:204:ARG:HA	1:C:204:ARG:HD3	1.83	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:LYS:HB2	1:A:194:PHE:CE1	2.55	0.42
1:D:514:GLU:HA	1:D:518:MET:HB2	2.01	0.42
1:B:180:ASN:OD1	1:B:180:ASN:N	2.52	0.41
1:D:177:LYS:HE2	1:D:177:LYS:HB3	1.73	0.41
1:D:29:ASN:HD22	1:D:217:PHE:H	1.68	0.41
1:A:150:PHE:HA	1:A:164:MET:O	2.20	0.41
1:D:136:LYS:HA	1:D:165:PHE:O	2.20	0.41
1:D:205:CYS:SG	1:D:219:MET:HG2	2.60	0.41
1:B:494:PRO:HB2	1:B:498:LYS:HE3	2.02	0.41
1:D:215:LYS:HE2	1:D:215:LYS:HB3	1.78	0.41
1:A:213:LYS:HG3	1:A:214:ASN:HD22	1.85	0.41
1:A:430:GLU:HG3	1:A:431:THR:N	2.36	0.41
1:B:346:TYR:HB3	1:B:350:ILE:HG13	2.02	0.41
1:B:521:LEU:HD23	1:B:521:LEU:HA	1.87	0.41
1:D:109:ASN:O	1:D:110:ASP:HB2	2.20	0.41
1:C:270:VAL:HG11	1:C:323:TYR:HD1	1.85	0.41
1:A:303:LYS:HB3	1:A:303:LYS:HE2	1.72	0.41
1:A:516:VAL:HG23	1:A:517:CYS:SG	2.61	0.41
1:B:31:ILE:HA	1:B:219:MET:O	2.21	0.41
1:B:413:ASP:OD1	1:B:413:ASP:N	2.46	0.41
1:A:37:GLU:HB2	1:A:227:HIS:CD2	2.56	0.41
1:A:101:PRO:HA	1:A:104:THR:HG22	2.02	0.41
1:D:311:ILE:HD12	1:D:373:MET:HG2	2.03	0.41
1:D:322:LEU:HD12	1:D:322:LEU:HA	1.90	0.41
1:D:188:GLY:C	1:D:190:VAL:N	2.78	0.40
1:A:130:GLN:HG2	1:A:212:ASP:CG	2.46	0.40
1:A:409:SER:OG	1:A:410:PRO:HD3	2.21	0.40
1:B:225:ASP:C	1:B:227:HIS:N	2.78	0.40
1:D:510:ILE:HG23	1:B:111:MET:HE3	2.03	0.40
1:D:137:TRP:NE1	1:D:139:LEU:HB2	2.36	0.40
1:A:76:ALA:HA	1:A:354:LYS:O	2.22	0.40
1:B:225:ASP:O	1:B:227:HIS:N	2.53	0.40
1:C:29:ASN:HB2	1:C:310:THR:HG23	2.04	0.40
1:A:233:SER:OG	1:A:236:TYR:HD2	2.04	0.40
1:A:136:LYS:HA	1:A:165:PHE:O	2.20	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	489/522 (94%)	472 (96%)	13 (3%)	4 (1%)	16	25
1	B	489/522 (94%)	468 (96%)	18 (4%)	3 (1%)	21	32
1	C	488/522 (94%)	471 (96%)	15 (3%)	2 (0%)	30	43
1	D	488/522 (94%)	466 (96%)	18 (4%)	4 (1%)	16	25
All	All	1954/2088 (94%)	1877 (96%)	64 (3%)	13 (1%)	18	28

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	187	SER
1	C	409	SER
1	A	179	PRO
1	A	228	SER
1	A	409	SER
1	B	228	SER
1	D	179	PRO
1	C	179	PRO
1	A	190	VAL
1	B	179	PRO
1	D	190	VAL
1	D	273	ASP
1	B	229	PRO

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	445/467 (95%)	424 (95%)	21 (5%)	23	41
1	B	445/467 (95%)	421 (95%)	24 (5%)	20	35
1	C	444/467 (95%)	425 (96%)	19 (4%)	26	44
1	D	444/467 (95%)	416 (94%)	28 (6%)	16	29
All	All	1778/1868 (95%)	1686 (95%)	92 (5%)	21	36

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	35	THR
1	D	50	VAL
1	D	60	LYS
1	D	63	VAL
1	D	71	LEU
1	D	182	ILE
1	D	213	LYS
1	D	244	ASP
1	D	256	THR
1	D	270	VAL
1	D	272	LYS
1	D	274	LYS
1	D	288	GLU
1	D	308	ASP
1	D	326	SER
1	D	330	LYS
1	D	348	GLU
1	D	351	ILE
1	D	389	GLN
1	D	396	LYS
1	D	405	TYR
1	D	452	LYS
1	D	462	LYS
1	D	486	SER
1	D	500	LYS
1	D	502	GLN
1	D	507	LEU
1	D	516	VAL
1	C	35	THR
1	C	60	LYS
1	C	71	LEU
1	C	80	ARG
1	C	84	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	187	SER
1	C	190	VAL
1	C	195	ILE
1	C	204	ARG
1	C	233	SER
1	C	238	GLN
1	C	239	LYS
1	C	273	ASP
1	C	298	LEU
1	C	326	SER
1	C	396	LYS
1	C	405	TYR
1	C	466	ARG
1	C	507	LEU
1	A	26	GLU
1	A	27	LYS
1	A	35	THR
1	A	60	LYS
1	A	77	ILE
1	A	127	ASP
1	A	195	ILE
1	A	204	ARG
1	A	213	LYS
1	A	256	THR
1	A	272	LYS
1	A	273	ASP
1	A	326	SER
1	A	396	LYS
1	A	405	TYR
1	A	413	ASP
1	A	416	MET
1	A	472	LYS
1	A	477	SER
1	A	513	ILE
1	A	522	LYS
1	B	35	THR
1	B	118	ILE
1	B	124	LEU
1	B	138	HIS
1	B	190	VAL
1	B	195	ILE
1	B	204	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	206	LEU
1	B	215	LYS
1	B	233	SER
1	B	239	LYS
1	B	249	GLU
1	B	270	VAL
1	B	298	LEU
1	B	301	LEU
1	B	308	ASP
1	B	339	ARG
1	B	405	TYR
1	B	459	ARG
1	B	477	SER
1	B	489	LYS
1	B	501	VAL
1	B	502	GLN
1	B	509	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	29	ASN
1	D	34	GLN
1	D	67	ASN
1	D	116	ASN
1	D	166	ASN
1	D	178	GLN
1	D	196	HIS
1	D	214	ASN
1	D	238	GLN
1	D	271	ASN
1	D	329	ASN
1	D	377	GLN
1	D	382	GLN
1	D	461	GLN
1	D	467	GLN
1	D	511	HIS
1	C	29	ASN
1	C	34	GLN
1	C	38	HIS
1	C	67	ASN
1	C	114	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	130	GLN
1	C	238	GLN
1	C	377	GLN
1	C	382	GLN
1	C	467	GLN
1	C	511	HIS
1	A	38	HIS
1	A	54	ASN
1	A	61	ASN
1	A	67	ASN
1	A	214	ASN
1	A	269	ASN
1	A	329	ASN
1	A	382	GLN
1	A	397	ASN
1	A	412	ASN
1	A	449	ASN
1	B	29	ASN
1	B	38	HIS
1	B	61	ASN
1	B	116	ASN
1	B	138	HIS
1	B	254	ASN
1	B	329	ASN
1	B	382	GLN
1	B	397	ASN
1	B	412	ASN
1	B	467	GLN
1	B	504	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 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	493/522 (94%)	0.46	31 (6%) 26 22	20, 35, 69, 105	0
1	B	493/522 (94%)	0.33	22 (4%) 38 34	17, 31, 62, 102	0
1	C	492/522 (94%)	0.47	25 (5%) 33 30	20, 37, 69, 108	0
1	D	492/522 (94%)	0.45	24 (4%) 35 31	18, 37, 67, 104	0
All	All	1970/2088 (94%)	0.43	102 (5%) 33 29	17, 36, 68, 108	0

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	409	SER	6.7
1	C	178	GLN	5.6
1	D	273	ASP	5.3
1	D	409	SER	4.9
1	B	186	TRP	4.8
1	B	228	SER	4.7
1	D	225	ASP	4.3
1	D	270	VAL	4.1
1	D	187	SER	4.0
1	B	169	HIS	3.9
1	B	409	SER	3.9
1	A	228	SER	3.8
1	D	189	PRO	3.7
1	D	186	TRP	3.7
1	D	188	GLY	3.7
1	C	409	SER	3.7
1	B	225	ASP	3.6
1	C	229	PRO	3.5
1	A	186	TRP	3.5
1	D	229	PRO	3.5
1	A	188	GLY	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	330	LYS	3.4
1	A	264	ARG	3.4
1	D	228	SER	3.4
1	D	522	LYS	3.3
1	B	187	SER	3.2
1	A	225	ASP	3.2
1	D	499	SER	3.1
1	A	179	PRO	3.1
1	A	192	PRO	3.1
1	A	253	THR	2.9
1	D	328	VAL	2.9
1	D	272	LYS	2.9
1	A	190	VAL	2.8
1	C	26	GLU	2.8
1	D	169	HIS	2.8
1	D	501	VAL	2.8
1	A	178	GLN	2.8
1	C	225	ASP	2.7
1	A	26	GLU	2.7
1	A	256	THR	2.7
1	C	278	LYS	2.7
1	A	269	ASN	2.7
1	C	270	VAL	2.7
1	A	238	GLN	2.7
1	B	55	ASP	2.6
1	B	273	ASP	2.6
1	B	226	PRO	2.6
1	B	194	PHE	2.6
1	C	501	VAL	2.6
1	B	501	VAL	2.6
1	C	228	SER	2.6
1	D	26	GLU	2.6
1	D	178	GLN	2.6
1	A	175	ILE	2.5
1	A	254	ASN	2.5
1	A	389	GLN	2.5
1	C	329	ASN	2.5
1	B	179	PRO	2.5
1	C	275	PHE	2.4
1	B	189	PRO	2.4
1	C	215	LYS	2.4
1	A	193	GLY	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	273	ASP	2.4
1	C	489	LYS	2.4
1	B	500	LYS	2.4
1	D	500	LYS	2.4
1	C	420	GLY	2.4
1	A	195	ILE	2.3
1	B	264	ARG	2.3
1	D	256	THR	2.3
1	A	522	LYS	2.3
1	B	178	GLN	2.3
1	B	177	LYS	2.2
1	D	179	PRO	2.2
1	A	169	HIS	2.2
1	C	272	LYS	2.2
1	A	489	LYS	2.2
1	C	84	SER	2.2
1	C	179	PRO	2.2
1	C	169	HIS	2.2
1	C	274	LYS	2.2
1	A	500	LYS	2.2
1	A	104	THR	2.2
1	C	459	ARG	2.2
1	D	503	PRO	2.2
1	A	493	ASN	2.1
1	B	269	ASN	2.1
1	A	212	ASP	2.1
1	C	226	PRO	2.1
1	B	249	GLU	2.1
1	C	328	VAL	2.1
1	C	238	GLN	2.1
1	A	211	ARG	2.1
1	B	167	ASP	2.1
1	D	410	PRO	2.1
1	D	192	PRO	2.0
1	B	410	PRO	2.0
1	A	270	VAL	2.0
1	B	190	VAL	2.0
1	A	518	MET	2.0
1	C	233	SER	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](#)

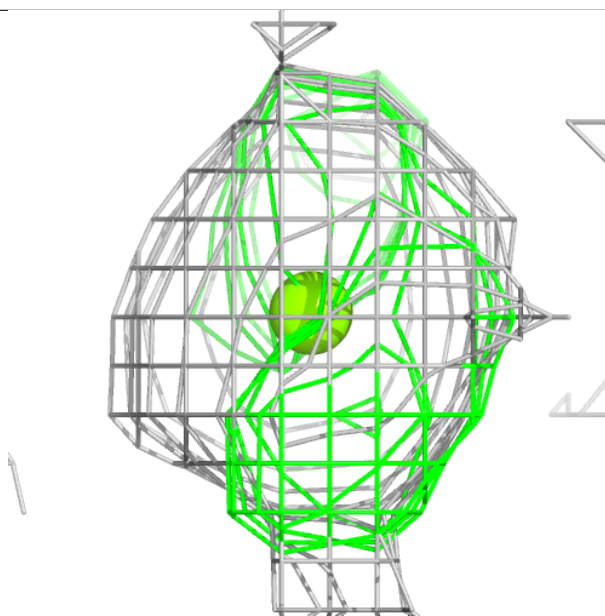
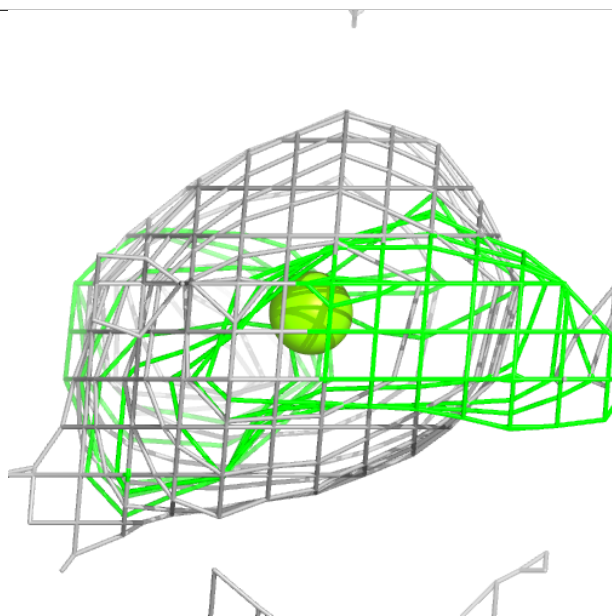
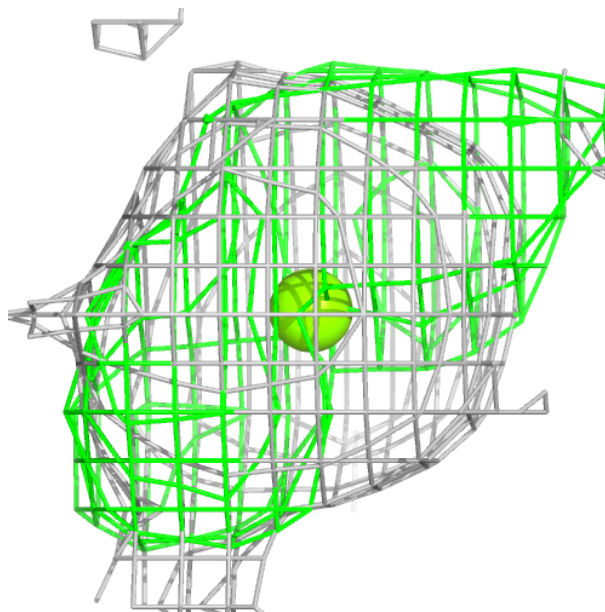
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	MG	D	601	1/1	0.95	0.21	28,28,28,28	0
2	MG	C	601	1/1	0.95	0.20	27,27,27,27	0
2	MG	B	601	1/1	0.95	0.17	33,33,33,33	0
2	MG	A	601	1/1	0.97	0.20	28,28,28,28	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.

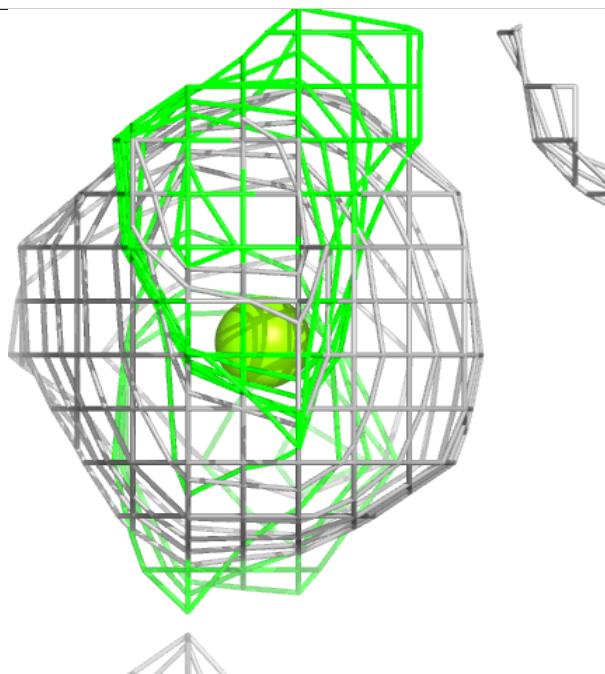
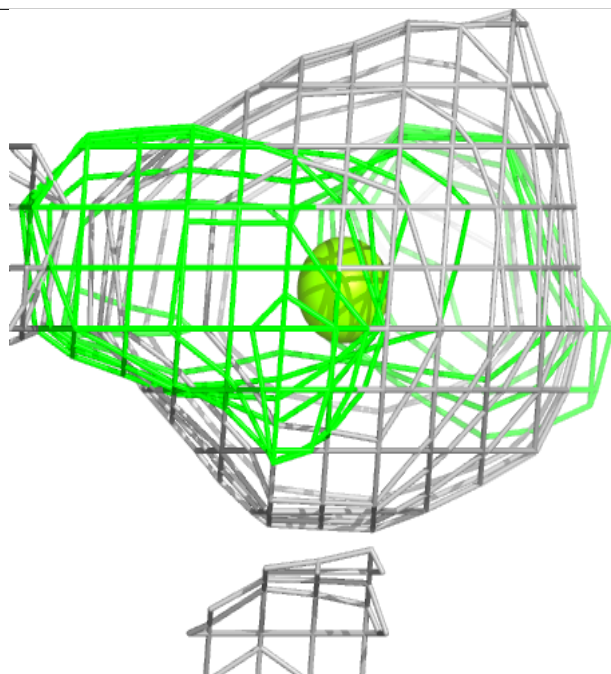
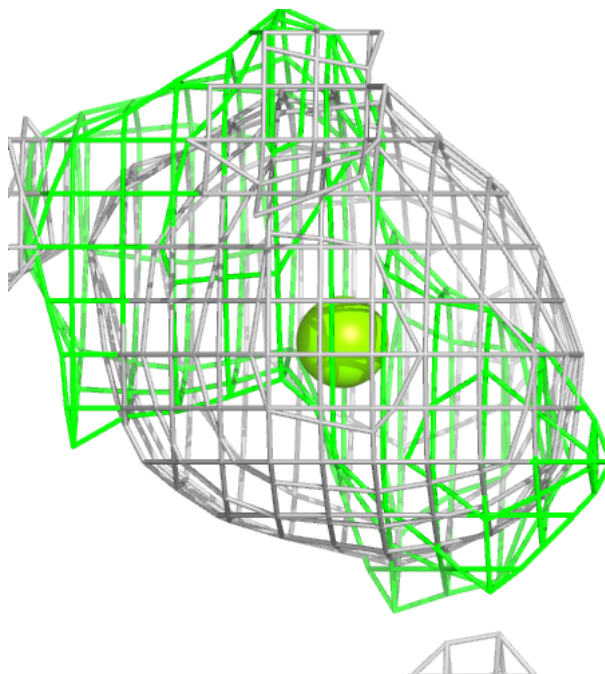
Electron density around MG D 601:

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



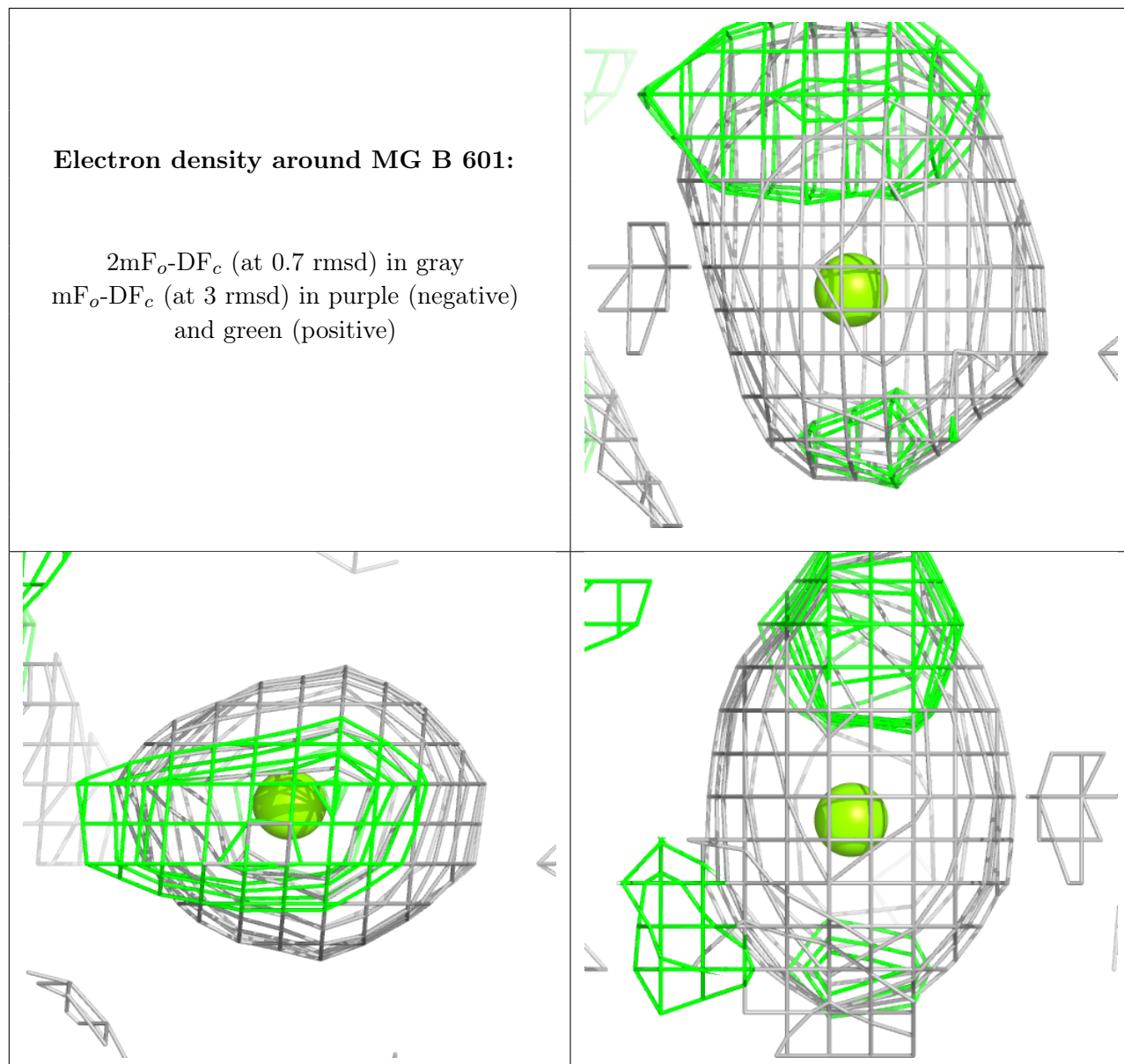
Electron density around MG C 601:

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



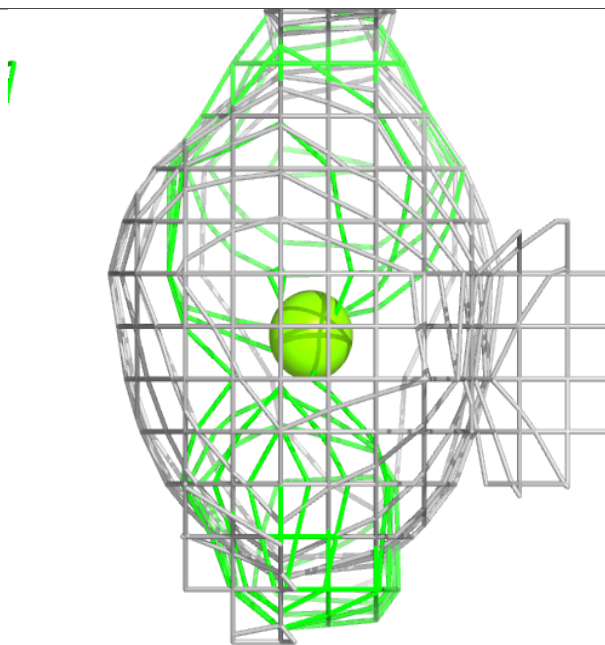
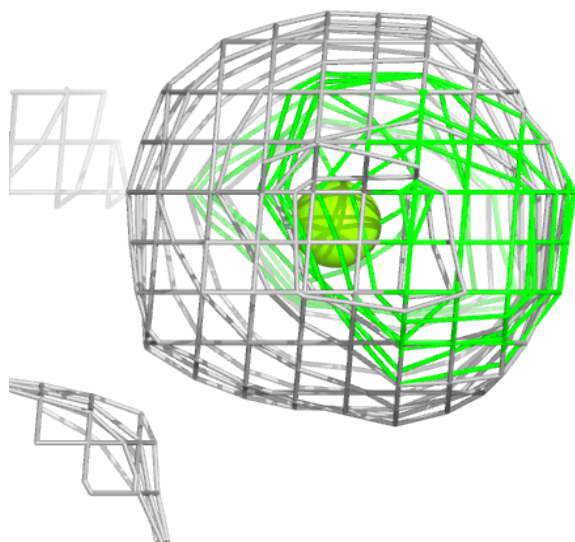
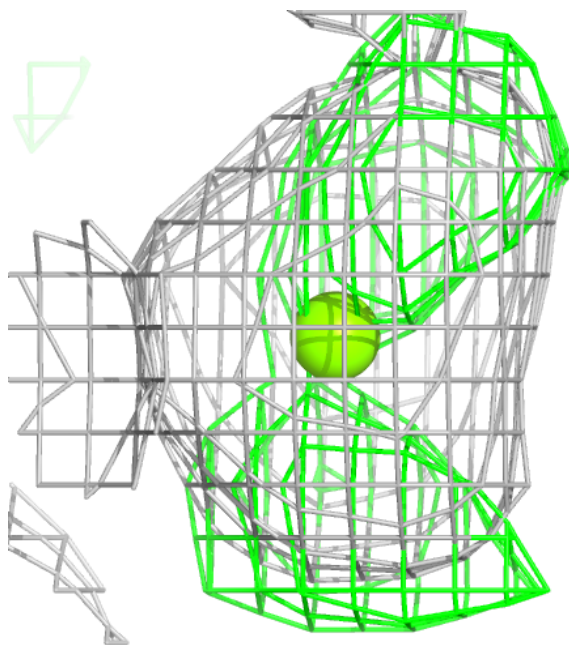
Electron density around MG B 601:

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



Electron density around MG A 601:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.