



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 08:16 AM GMT

PDB ID : 1HT5
Title : THE 2.75 ANGSTROM RESOLUTION MODEL OF OVINE COX-1 COM-
PLEXED WITH METHYL ESTER FLURBIPROFEN
Authors : Selinsky, B.S.; Gupta, K.; Sharkey, C.T.; Loll, P.J.
Deposited on : 2000-12-28
Resolution : 2.75 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

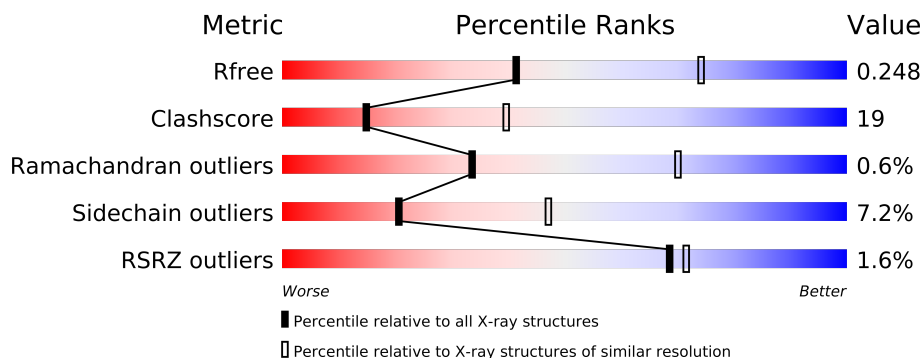
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.75 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	2406 (2.80-2.72)
Clashscore	79885	2995 (2.80-2.72)
Ramachandran outliers	78287	2941 (2.80-2.72)
Sidechain outliers	78261	2944 (2.80-2.72)
RSRZ outliers	66119	2409 (2.80-2.72)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	551	
1	B	551	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	BOG	A	1802	-	X
2	BOG	B	2801	-	X
2	BOG	B	2802	-	X
3	NAG	A	1681	-	X
3	NAG	A	2672	-	X
3	NAG	B	2661	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	NAG	B	2681	-	X
5	FL2	A	1701	-	X
5	FL2	B	2701	-	X

2 Entry composition i

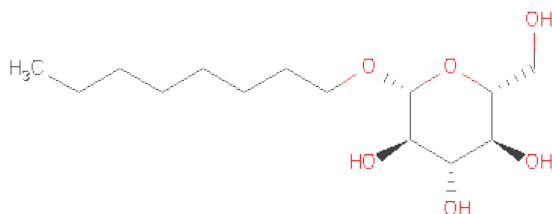
There are 6 unique types of molecules in this entry. The entry contains 9428 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PROSTAGLANDIN H2 SYNTHASE-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	551	Total	C	N	O	S	0	0	0
			4477	2903	758	788	28			
1	B	551	Total	C	N	O	S	0	0	0
			4477	2903	758	788	28			

- Molecule 2 is SUGAR (B-OCTYLGLUCOSIDE) (three-letter code: BOG) (formula: C₁₄H₂₈O₆).



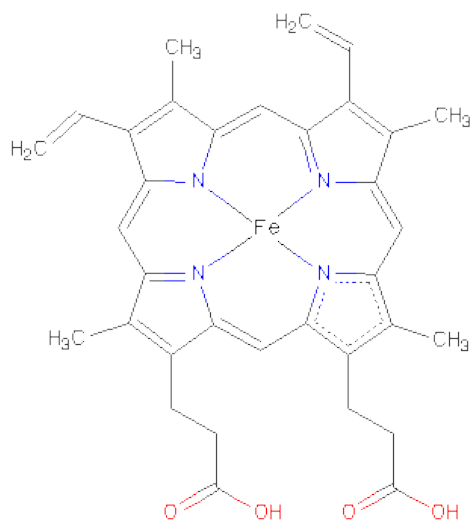
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			20	14	6		
2	B	1	Total	C	O	0	0
			20	14	6		
2	B	1	Total	C	O	0	0
			20	14	6		

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



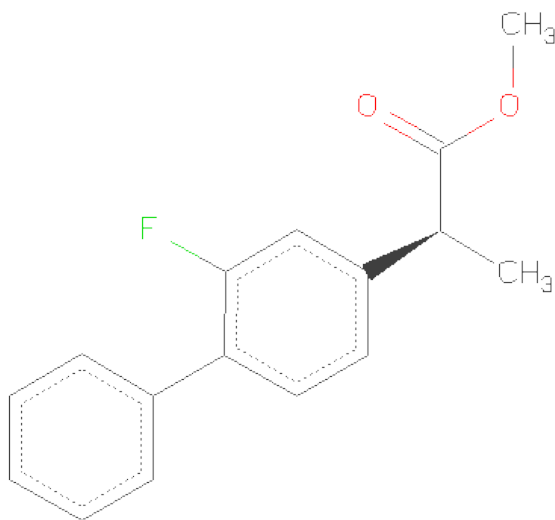
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1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

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

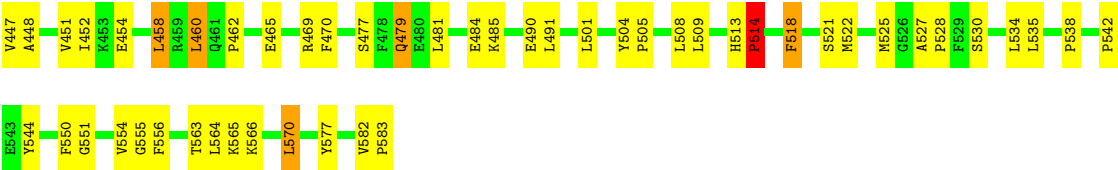
- Molecule 5 is FLURBIPROFEN METHYL ESTER (three-letter code: FL2) (formula: $C_{16}H_{15}FO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	F	O	0	0
			19	16	1	2		
5	B	1	Total	C	F	O	0	0
			19	16	1	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	79	Total 79	O 79	0	0
6	B	71	Total 71	O 71	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	98.89Å 209.45Å 223.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.89 – 2.75 50.89 – 2.70	Depositor EDS
% Data completeness (in resolution range)	88.2 (50.89-2.75) 88.3 (50.89-2.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.31 (at 2.69Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.223 , 0.252 0.215 , 0.248	Depositor DCC
R_{free} test set	5438 reflections (11.35%)	DCC
Wilson B-factor (Å ²)	42.7	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 26.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 57793 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9428	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, FL2, NAG, BOG

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	0.41	0/4615	0.63	0/6264
1	B	0.39	0/4615	0.64	0/6264
All	All	0.40	0/9230	0.64	0/12528

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4477	0	4386	186	0
1	B	4477	0	4386	170	0
2	A	20	0	28	8	0
2	B	40	0	56	6	0
3	A	70	0	65	11	0
3	B	70	0	65	8	0
4	A	43	0	30	5	0
4	B	43	0	30	6	0
5	A	19	0	15	4	0
5	B	19	0	15	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	79	0	0	0	0
6	B	71	0	0	0	0
All	All	9428	0	9076	350	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 19.

All (350) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:144:ASN:HD21	3:B:2671:NAG:C1	1.80	0.94
1:B:410:ASN:HD21	3:B:2681:NAG:C1	1.81	0.94
1:A:391:MET:HG3	4:A:601:HEM:HAB	1.47	0.92
1:B:185:ARG:HH21	1:B:438:ARG:NH1	1.70	0.90
1:A:410:ASN:HD21	3:A:1681:NAG:C1	1.85	0.90
1:B:291:VAL:HG13	1:B:294:LEU:HD12	1.54	0.88
1:A:144:ASN:HD21	3:A:1671:NAG:C1	1.87	0.87
1:A:400:GLN:HE21	1:A:401:ASP:N	1.74	0.85
1:B:180:ARG:HD3	1:B:490:GLU:OE2	1.77	0.83
1:B:294:LEU:HD22	1:B:409:PHE:CE2	2.12	0.83
1:A:120:ARG:HG2	5:A:1701:FL2:H161	1.59	0.83
1:B:49:ARG:HH11	1:B:49:ARG:HG3	1.46	0.81
1:B:185:ARG:HH21	1:B:438:ARG:HH11	1.30	0.80
1:B:563:THR:HG22	1:B:565:LYS:H	1.48	0.78
1:B:295:LEU:HD12	1:B:298:LEU:HD22	1.63	0.78
1:B:185:ARG:NH2	1:B:438:ARG:HH11	1.82	0.77
1:B:144:ASN:ND2	3:B:2671:NAG:C1	2.48	0.77
1:A:400:GLN:HE21	1:A:401:ASP:H	1.32	0.77
1:B:295:LEU:HD11	4:B:601:HEM:HBB2	1.65	0.76
1:B:454:GLU:HG2	1:B:458:LEU:HD22	1.68	0.75
1:A:144:ASN:ND2	3:A:1671:NAG:C1	2.49	0.75
1:A:400:GLN:NE2	1:A:401:ASP:H	1.85	0.74
1:B:208:GLN:NE2	1:B:230:LEU:H	1.84	0.74
1:B:150:ARG:HD3	1:B:152:LEU:O	1.87	0.73
1:A:140:GLU:CD	1:A:144:ASN:HD22	1.91	0.73
1:A:582:VAL:HG22	1:A:583:PRO:HD2	1.71	0.71
1:B:243:GLN:HG3	1:B:270:PRO:HD2	1.72	0.71
1:A:563:THR:HG22	1:A:565:LYS:H	1.55	0.71
1:A:89:ILE:HD12	2:A:1802:BOG:H62	1.73	0.71
1:A:563:THR:HG22	1:A:565:LYS:N	2.06	0.70
1:A:208:GLN:NE2	1:A:230:LEU:H	1.89	0.70
1:B:272:LEU:HD13	1:B:273:MET:N	2.07	0.69
1:B:389:PRO:HG3	1:B:440:ILE:HG12	1.74	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:165:THR:HG22	1:A:166:LYS:HD3	1.74	0.69
1:A:462:PRO:HG2	1:A:465:GLU:HG2	1.74	0.69
1:A:374:ARG:NH1	1:B:374:ARG:HB3	2.08	0.69
1:B:237:ASN:ND2	1:B:240:ARG:H	1.92	0.68
1:A:295:LEU:HD11	4:A:601:HEM:HBB2	1.74	0.68
1:B:120:ARG:HG2	5:B:2701:FL2:H161	1.74	0.68
1:B:295:LEU:CD1	4:B:601:HEM:HBB2	2.24	0.67
1:A:114:ARG:HD3	1:A:365:LEU:O	1.95	0.66
1:B:563:THR:HG22	1:B:565:LYS:N	2.10	0.66
1:B:116:VAL:HG13	5:B:2701:FL2:H162	1.77	0.66
1:A:91:PHE:O	1:A:95:HIS:HD2	1.78	0.66
1:A:447:VAL:O	1:A:451:VAL:HG23	1.96	0.66
1:B:185:ARG:HH11	1:B:185:ARG:HG2	1.61	0.65
1:A:276:PRO:HD2	1:A:279:ILE:HD12	1.78	0.65
1:A:280:PRO:HB2	1:A:282:GLN:OE1	1.96	0.65
1:A:344:VAL:O	1:A:348:TYR:HB3	1.97	0.65
1:B:120:ARG:NH1	2:B:2802:BOG:H1	2.12	0.64
1:A:504:TYR:HB3	1:A:505:PRO:HD3	1.79	0.64
1:A:237:ASN:ND2	1:A:239:GLU:HG2	2.13	0.64
1:A:320:HIS:HD2	1:B:49:ARG:O	1.81	0.64
1:A:482:THR:O	1:A:484:GLU:N	2.31	0.63
1:A:150:ARG:HD3	1:A:152:LEU:O	1.98	0.63
1:A:208:GLN:HE21	1:A:230:LEU:H	1.47	0.63
1:A:527:ALA:HB3	1:A:528:PRO:HD3	1.81	0.63
1:A:513:HIS:NE2	1:A:520:GLU:HB3	2.14	0.63
1:B:123:LEU:HD23	1:B:470:PHE:HD1	1.64	0.62
1:A:49:ARG:HG3	1:A:49:ARG:HH11	1.63	0.62
1:B:504:TYR:HB3	1:B:505:PRO:HD3	1.81	0.62
1:B:86:PRO:HG3	2:B:2802:BOG:H61	1.82	0.62
1:A:483:GLY:H	1:A:511:LYS:HB3	1.65	0.62
1:B:447:VAL:O	1:B:451:VAL:HG23	2.00	0.61
1:B:410:ASN:ND2	3:B:2681:NAG:C1	2.60	0.61
1:A:294:LEU:HD22	1:A:409:PHE:CE2	2.36	0.61
1:A:67:PRO:C	1:A:68:ASN:HD22	2.02	0.61
1:B:49:ARG:HH11	1:B:49:ARG:CG	2.12	0.61
1:B:116:VAL:O	1:B:120:ARG:HB2	2.00	0.61
1:B:554:VAL:HG13	1:B:555:GLY:N	2.16	0.61
1:A:582:VAL:CG2	1:A:583:PRO:HD2	2.31	0.61
1:B:213:SER:OG	1:B:215:LYS:HG2	2.01	0.61
1:B:387:TRP:HB2	4:B:601:HEM:HAC	1.83	0.61
1:A:410:ASN:ND2	3:A:1681:NAG:C1	2.61	0.60
1:A:172:PRO:HB2	1:A:177:LEU:HD22	1.82	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:180:ARG:O	1:A:438:ARG:NH1	2.33	0.60
1:B:120:ARG:HE	5:B:2701:FL2:C16	2.15	0.60
1:A:116:VAL:O	1:A:120:ARG:HB2	2.02	0.60
1:B:276:PRO:HD2	1:B:279:ILE:HD12	1.84	0.60
1:B:566:LYS:O	1:B:570:LEU:HB2	2.02	0.59
1:B:185:ARG:CZ	1:B:438:ARG:HD3	2.32	0.59
1:B:237:ASN:ND2	1:B:239:GLU:HG2	2.17	0.59
1:A:387:TRP:HB2	4:A:601:HEM:HAC	1.83	0.59
1:B:293:GLY:HA2	1:B:299:MET:HE2	1.83	0.59
1:B:294:LEU:HD22	1:B:409:PHE:HE2	1.65	0.58
1:A:230:LEU:HG	1:A:233:ILE:HD12	1.86	0.58
1:B:120:ARG:HE	5:B:2701:FL2:H161	1.69	0.58
1:A:382:ASN:OD1	1:A:386:HIS:HE1	1.87	0.58
1:B:156:PRO:HB2	1:B:159:CYS:SG	2.43	0.58
1:B:518:PHE:CD1	1:B:522:MET:HG2	2.37	0.58
1:B:294:LEU:O	1:B:295:LEU:HG	2.04	0.58
1:A:86:PRO:HG3	2:A:1802:BOG:H61	1.84	0.57
1:A:504:TYR:CZ	1:A:508:LEU:HD11	2.39	0.57
1:A:294:LEU:O	1:A:295:LEU:HG	2.04	0.57
1:B:582:VAL:CG2	1:B:583:PRO:HD2	2.34	0.57
1:B:185:ARG:NE	1:B:438:ARG:HD3	2.19	0.57
1:B:116:VAL:CG1	5:B:2701:FL2:H162	2.34	0.57
1:A:518:PHE:CD1	1:A:522:MET:HG2	2.40	0.57
1:B:89:ILE:HD12	2:B:2802:BOG:H62	1.87	0.57
1:B:389:PRO:HG3	1:B:440:ILE:CG1	2.35	0.56
1:A:102:PHE:O	1:A:106:THR:HG23	2.05	0.56
1:A:389:PRO:HG3	1:A:440:ILE:HG12	1.86	0.56
1:A:323:TRP:CE3	1:A:327:GLN:HG2	2.41	0.56
1:A:49:ARG:O	1:B:320:HIS:HD2	1.89	0.56
1:A:295:LEU:HD11	4:A:601:HEM:CBB	2.35	0.56
1:A:379:MET:SD	1:A:458:LEU:HG	2.46	0.55
1:A:183:LEU:HD13	1:A:184:ARG:O	2.07	0.55
1:B:366:LEU:HD12	1:B:535:LEU:HD12	1.86	0.55
1:A:275:TYR:CE2	1:A:284:GLN:HB3	2.41	0.55
1:A:120:ARG:NH1	2:A:1802:BOG:H1	2.21	0.55
1:B:132:ILE:HD13	1:B:458:LEU:HD12	1.89	0.55
1:B:462:PRO:HG2	1:B:465:GLU:HG2	1.89	0.55
1:A:306:LEU:HD23	1:A:306:LEU:C	2.26	0.55
1:B:77:TRP:CZ2	2:B:2801:BOG:H7'2	2.41	0.55
1:B:391:MET:HE3	1:B:395:PHE:HE2	1.71	0.54
1:A:88:PHE:CZ	1:A:92:LEU:HD11	2.43	0.54
1:A:524:GLU:OE1	2:A:1802:BOG:H5	2.08	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:208:GLN:NE2	1:A:228:VAL:HA	2.23	0.54
1:A:504:TYR:OH	1:A:508:LEU:HD11	2.08	0.54
1:B:527:ALA:HB3	1:B:528:PRO:HD3	1.90	0.54
1:A:388:HIS:N	1:A:389:PRO:CD	2.71	0.54
1:A:240:ARG:NH1	1:A:271:VAL:HG13	2.22	0.53
1:A:563:THR:HB	1:A:566:LYS:HG3	1.89	0.53
1:B:577:TYR:CE2	1:B:583:PRO:HD3	2.44	0.53
1:A:374:ARG:HH12	1:B:374:ARG:HB3	1.71	0.53
1:A:554:VAL:HG13	1:A:555:GLY:N	2.23	0.53
1:A:179:ARG:HG2	1:A:179:ARG:HH11	1.74	0.52
1:A:352:LEU:HD11	1:A:387:TRP:HH2	1.74	0.52
1:A:306:LEU:HD23	1:A:306:LEU:O	2.09	0.52
1:A:391:MET:HE1	1:A:395:PHE:HE2	1.75	0.52
1:B:550:PHE:O	1:B:555:GLY:HA3	2.08	0.52
1:B:340:THR:O	1:B:344:VAL:HG23	2.08	0.52
1:A:140:GLU:OE2	1:A:144:ASN:ND2	2.42	0.52
1:B:208:GLN:NE2	1:B:228:VAL:HA	2.25	0.52
1:B:123:LEU:HD23	1:B:470:PHE:CD1	2.43	0.52
1:A:34:ASN:HB3	1:A:37:CYS:SG	2.49	0.52
1:A:294:LEU:HD22	1:A:409:PHE:CD2	2.45	0.52
1:B:63:GLY:O	1:B:73:GLU:HG3	2.10	0.52
1:A:144:ASN:OD1	3:A:1671:NAG:C1	2.58	0.52
3:A:1671:NAG:H61	3:B:1672:NAG:HN2	1.75	0.52
1:B:293:GLY:HA2	1:B:299:MET:CE	2.40	0.52
1:B:185:ARG:NH2	1:B:438:ARG:NH1	2.43	0.51
1:B:208:GLN:HE21	1:B:230:LEU:H	1.56	0.51
1:B:477:SER:OG	1:B:479:GLN:HG2	2.10	0.51
1:A:180:ARG:HD3	1:A:490:GLU:OE2	2.10	0.51
1:A:213:SER:OG	1:A:215:LYS:HG2	2.11	0.51
1:B:114:ARG:HD3	1:B:365:LEU:O	2.09	0.51
1:B:49:ARG:NH1	1:B:49:ARG:CG	2.71	0.51
1:A:203:GLN:HA	4:A:601:HEM:HBC2	1.93	0.50
1:B:344:VAL:O	1:B:348:TYR:HB3	2.11	0.50
1:B:491:LEU:HD11	1:B:509:LEU:HD13	1.92	0.50
1:A:269:ALA:O	1:A:271:VAL:N	2.45	0.50
1:B:140:GLU:OE2	1:B:144:ASN:ND2	2.40	0.50
1:B:479:GLN:H	1:B:479:GLN:CD	2.13	0.50
1:B:300:LEU:HD21	1:B:419:VAL:HG13	1.94	0.50
1:A:123:LEU:O	1:A:469:ARG:NH2	2.45	0.50
1:B:513:HIS:HB3	1:B:514:PRO:HD2	1.93	0.50
1:B:140:GLU:CD	1:B:144:ASN:HD22	2.15	0.49
1:A:403:SER:OG	1:A:405:GLU:HG2	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:35:PRO:HB2	1:B:55:TYR:CD2	2.47	0.49
1:B:582:VAL:HG23	1:B:583:PRO:HD2	1.94	0.49
1:A:400:GLN:HE21	1:A:400:GLN:CA	2.25	0.49
1:A:384:LEU:HD23	1:A:384:LEU:C	2.32	0.49
1:B:49:ARG:HG3	1:B:49:ARG:NH1	2.23	0.49
1:A:291:VAL:O	1:A:291:VAL:HG12	2.12	0.49
1:A:352:LEU:HD11	1:A:387:TRP:CH2	2.48	0.49
1:B:295:LEU:HD12	1:B:298:LEU:CD2	2.36	0.49
1:A:77:TRP:CZ2	1:A:81:THR:HG21	2.48	0.49
1:B:391:MET:HG3	4:B:601:HEM:HAB	1.95	0.48
1:A:179:ARG:HG2	1:A:179:ARG:NH1	2.28	0.48
1:A:117:LEU:HD12	1:A:531:LEU:HD13	1.95	0.48
1:B:291:VAL:O	1:B:291:VAL:HG12	2.13	0.48
1:B:150:ARG:NH1	1:B:154:SER:HA	2.27	0.48
1:B:243:GLN:OE1	1:B:243:GLN:HA	2.13	0.48
1:A:151:ILE:CG2	1:A:469:ARG:NH1	2.76	0.48
1:B:386:HIS:CE1	4:B:601:HEM:HAD2	2.47	0.48
1:A:49:ARG:CG	1:A:49:ARG:HH11	2.25	0.48
1:A:261:VAL:O	1:A:307:ARG:NH1	2.41	0.48
1:A:482:THR:C	1:A:484:GLU:H	2.17	0.48
1:B:388:HIS:CE1	1:B:447:VAL:HG11	2.49	0.48
1:A:68:ASN:N	1:A:68:ASN:HD22	2.11	0.48
1:A:35:PRO:CG	1:A:55:TYR:HB3	2.44	0.48
1:B:388:HIS:N	1:B:389:PRO:CD	2.76	0.48
1:A:88:PHE:O	1:A:91:PHE:HB3	2.13	0.48
1:A:491:LEU:HD11	1:A:509:LEU:HD13	1.95	0.48
1:A:497:ASP:OD2	1:A:498:ILE:N	2.47	0.48
1:A:84:PRO:HG2	1:A:89:ILE:HD11	1.95	0.48
1:B:70:THR:O	1:B:72:PRO:HD3	2.14	0.48
1:A:374:ARG:HB3	1:B:374:ARG:NH1	2.29	0.48
1:A:160:PRO:HD2	1:A:164:GLY:O	2.13	0.48
1:B:116:VAL:HG13	5:B:2701:FL2:C16	2.43	0.48
1:A:134:HIS:HD2	1:A:138:SER:OG	1.96	0.47
1:A:86:PRO:HA	2:A:1802:BOG:H61	1.96	0.47
1:A:214:GLY:H	1:A:215:LYS:HZ1	1.61	0.47
1:B:99:LEU:O	1:B:103:VAL:HG23	2.14	0.47
1:B:352:LEU:HD11	1:B:387:TRP:CH2	2.48	0.47
1:A:400:GLN:NE2	1:A:401:ASP:N	2.48	0.47
1:B:291:VAL:CG1	1:B:291:VAL:O	2.61	0.47
1:A:120:ARG:HE	5:A:1701:FL2:C16	2.27	0.47
1:A:120:ARG:HG2	5:A:1701:FL2:C16	2.37	0.47
1:B:240:ARG:NH1	1:B:271:VAL:HG13	2.30	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:513:HIS:HB3	1:A:514:PRO:HD2	1.96	0.47
1:A:77:TRP:CE2	1:A:81:THR:HG21	2.49	0.47
1:B:223:ALA:C	1:B:224:LEU:O	2.46	0.47
1:A:142:PHE:CE2	1:B:538:PRO:HG3	2.49	0.47
1:A:566:LYS:O	1:A:570:LEU:HB2	2.15	0.47
1:A:340:THR:O	1:A:344:VAL:HG23	2.15	0.47
1:A:145:VAL:HG13	1:A:145:VAL:O	2.15	0.47
1:A:180:ARG:HH21	1:A:490:GLU:CD	2.18	0.46
1:B:93:LEU:HD13	1:B:355:TYR:CE1	2.50	0.46
1:A:180:ARG:NH2	1:A:490:GLU:OE1	2.48	0.46
1:A:420:GLU:HG3	1:A:572:THR:HB	1.97	0.46
1:B:513:HIS:O	1:B:514:PRO:C	2.53	0.46
1:A:530:SER:O	1:A:534:LEU:HD22	2.15	0.46
1:B:109:ARG:NH2	1:B:360:LYS:HB2	2.31	0.46
1:B:144:ASN:HD21	3:B:2671:NAG:C2	2.29	0.46
1:A:294:LEU:HD22	1:A:409:PHE:HE2	1.81	0.46
1:A:320:HIS:CE1	1:A:551:GLY:O	2.69	0.46
1:B:74:ILE:HG23	1:B:75:TRP:N	2.31	0.46
1:A:234:TYR:CE2	1:A:333:ARG:HG3	2.51	0.46
1:A:452:ILE:O	1:A:455:SER:HB3	2.16	0.46
1:A:144:ASN:HD21	3:A:1671:NAG:C2	2.27	0.46
1:B:142:PHE:C	1:B:376:ARG:HH22	2.19	0.46
1:B:530:SER:O	1:B:534:LEU:HD22	2.16	0.46
1:A:151:ILE:HG22	1:A:469:ARG:NH1	2.30	0.46
1:B:126:SER:HA	1:B:127:PRO:C	2.35	0.46
1:A:230:LEU:HD21	1:A:336:LEU:HB3	1.98	0.46
1:A:156:PRO:HD2	1:A:159:CYS:SG	2.56	0.45
1:B:382:ASN:OD1	1:B:386:HIS:HE1	1.98	0.45
1:A:144:ASN:CG	3:A:1671:NAG:C1	2.83	0.45
1:B:538:PRO:HB2	1:B:544:TYR:CE1	2.51	0.45
1:A:163:MET:CE	1:A:171:LEU:HD21	2.46	0.45
1:B:206:THR:HB	1:B:210:PHE:CD2	2.51	0.45
1:B:183:LEU:HD22	1:B:184:ARG:N	2.30	0.45
1:A:513:HIS:HB2	1:A:516:SER:OG	2.16	0.45
1:A:342:LYS:HG2	1:A:562:ALA:HB3	1.99	0.45
1:A:520:GLU:HG3	1:A:521:SER:N	2.31	0.45
1:B:43:HIS:O	1:B:44:GLN:HB2	2.16	0.45
1:A:479:GLN:HG3	1:A:485:LYS:HZ2	1.81	0.45
1:B:256:MET:O	1:B:257:LEU:HD23	2.17	0.45
1:A:367:PHE:CE2	1:A:542:PRO:HG3	2.52	0.45
1:B:102:PHE:O	1:B:106:THR:HG23	2.17	0.45
1:A:353:SER:HB2	1:A:355:TYR:CE2	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:88:PHE:O	1:A:92:LEU:HD13	2.17	0.44
1:A:367:PHE:CD2	1:A:542:PRO:HG3	2.52	0.44
1:B:234:TYR:CE2	1:B:333:ARG:HG3	2.51	0.44
1:A:400:GLN:C	1:A:400:GLN:HE21	2.19	0.44
1:B:39:TYR:N	1:B:40:PRO:CD	2.79	0.44
1:B:504:TYR:CZ	1:B:508:LEU:HD11	2.53	0.44
1:B:323:TRP:CE3	1:B:327:GLN:HG2	2.52	0.44
1:B:521:SER:O	1:B:525:MET:HB2	2.17	0.44
1:B:210:PHE:CE1	1:B:382:ASN:HA	2.52	0.44
1:A:116:VAL:CG1	5:A:1701:FL2:H162	2.47	0.44
1:A:482:THR:C	1:A:484:GLU:N	2.71	0.44
1:A:554:VAL:HG13	1:A:555:GLY:H	1.82	0.44
1:B:266:VAL:O	1:B:266:VAL:HG12	2.17	0.44
1:A:237:ASN:HD22	1:A:239:GLU:HG2	1.83	0.44
1:B:408:LEU:HB3	1:B:409:PHE:CD1	2.53	0.44
1:B:185:ARG:NH1	1:B:185:ARG:HG2	2.32	0.44
1:B:77:TRP:CZ2	2:B:2801:BOG:H5'2	2.53	0.44
1:A:375:ASN:HD22	1:A:532:LYS:HG3	1.83	0.44
1:B:384:LEU:HG	1:B:522:MET:SD	2.58	0.43
1:A:98:TRP:CG	1:A:99:LEU:N	2.86	0.43
1:A:323:TRP:CD2	1:A:327:GLN:HG2	2.54	0.43
1:B:180:ARG:O	1:B:438:ARG:NH1	2.51	0.43
1:B:185:ARG:NH2	1:B:438:ARG:HD3	2.33	0.43
1:B:237:ASN:HD21	1:B:240:ARG:H	1.66	0.43
1:A:569:CYS:HA	1:A:572:THR:OG1	2.18	0.43
1:B:280:PRO:HA	1:B:281:PRO:HD3	1.91	0.43
1:B:130:TYR:HB3	1:B:134:HIS:O	2.18	0.43
1:A:159:CYS:HB3	1:A:164:GLY:O	2.18	0.43
1:B:74:ILE:HG23	1:B:75:TRP:CD1	2.53	0.43
1:B:91:PHE:O	1:B:95:HIS:HD2	2.01	0.43
1:A:322:THR:OG1	1:B:49:ARG:HG2	2.18	0.43
1:A:367:PHE:HE1	1:B:61:ARG:HH21	1.65	0.43
1:A:74:ILE:HG23	1:A:75:TRP:N	2.34	0.43
1:B:441:ASP:OD2	1:B:443:HIS:CD2	2.72	0.43
1:B:384:LEU:C	1:B:384:LEU:HD23	2.39	0.43
1:B:230:LEU:CD2	1:B:336:LEU:HB3	2.48	0.43
1:A:275:TYR:CD2	1:A:284:GLN:HG2	2.53	0.43
1:A:245:ARG:NH1	1:A:326:GLU:OE2	2.48	0.43
1:A:202:ALA:O	1:A:206:THR:HG23	2.18	0.43
1:A:246:LEU:O	1:A:246:LEU:HD23	2.19	0.43
1:A:544:TYR:O	1:A:546:LYS:N	2.50	0.43
1:B:448:ALA:O	1:B:452:ILE:HG13	2.19	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:230:LEU:HA	1:B:232:HIS:CE1	2.54	0.43
1:A:68:ASN:OD1	3:A:1661:NAG:C1	2.67	0.43
1:A:454:GLU:HG2	1:A:458:LEU:HD22	2.01	0.43
1:B:352:LEU:HD22	1:B:518:PHE:CZ	2.53	0.42
1:A:183:LEU:C	1:A:183:LEU:HD13	2.39	0.42
1:A:479:GLN:HG3	1:A:485:LYS:NZ	2.34	0.42
1:A:391:MET:HB3	1:A:404:TYR:OH	2.18	0.42
1:B:554:VAL:CG1	1:B:555:GLY:N	2.80	0.42
1:A:458:LEU:HB3	1:A:460:LEU:HD13	2.01	0.42
1:A:293:GLY:HA2	1:A:299:MET:HE2	2.01	0.42
1:A:86:PRO:CA	2:A:1802:BOG:H61	2.49	0.42
1:B:206:THR:HB	1:B:210:PHE:HD2	1.84	0.42
1:A:54:ARG:HH11	1:A:54:ARG:HG3	1.84	0.42
1:A:96:GLY:O	1:A:97:ARG:C	2.57	0.42
1:A:287:VAL:HG11	1:A:302:ALA:HB1	2.00	0.42
1:A:43:HIS:O	1:A:44:GLN:HB2	2.20	0.42
1:A:49:ARG:CG	1:A:49:ARG:NH1	2.83	0.42
1:B:367:PHE:CZ	1:B:542:PRO:HA	2.55	0.42
1:A:394:SER:HB2	1:A:402:TYR:O	2.20	0.42
1:B:250:GLY:HA2	1:B:325:ASP:OD1	2.19	0.42
1:A:582:VAL:HG22	1:A:583:PRO:CD	2.46	0.42
1:A:206:THR:HB	1:A:210:PHE:CD2	2.55	0.42
1:B:272:LEU:HD13	1:B:272:LEU:C	2.39	0.42
1:A:295:LEU:HB2	1:A:298:LEU:HD22	2.01	0.42
3:A:1671:NAG:O4	3:B:1672:NAG:C1	2.68	0.42
1:B:504:TYR:OH	1:B:508:LEU:HD11	2.19	0.42
1:B:485:LYS:HD3	1:B:485:LYS:HA	1.90	0.41
1:A:39:TYR:N	1:A:40:PRO:CD	2.83	0.41
1:B:172:PRO:HB2	1:B:177:LEU:HD22	2.02	0.41
1:B:144:ASN:OD1	3:B:2671:NAG:C1	2.68	0.41
1:B:79:ARG:HG2	1:B:79:ARG:HH11	1.85	0.41
1:A:64:TYR:CE1	1:A:76:THR:HG21	2.54	0.41
1:A:196:LEU:HD21	1:A:392:PRO:HD3	2.02	0.41
1:B:210:PHE:HB3	4:B:601:HEM:HBD1	2.02	0.41
1:B:481:LEU:HD22	1:B:501:LEU:CD2	2.50	0.41
1:A:251:LYS:HB3	1:A:310:ASN:OD1	2.21	0.41
1:B:320:HIS:HE1	1:B:551:GLY:O	2.04	0.41
1:B:145:VAL:HG13	1:B:145:VAL:O	2.19	0.41
1:B:173:ASP:OD2	1:B:175:GLU:HB3	2.21	0.41
1:B:176:PHE:CZ	1:B:180:ARG:HG3	2.56	0.41
1:B:269:ALA:O	1:B:271:VAL:N	2.52	0.41
1:A:344:VAL:O	1:A:349:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:238:LEU:HD23	1:B:238:LEU:HA	1.88	0.41
1:B:292:PHE:CD1	1:B:298:LEU:HG	2.56	0.41
1:B:240:ARG:NH1	1:B:290:GLU:HG3	2.36	0.41
1:B:527:ALA:HB1	5:B:2701:FL2:H163	2.02	0.41
1:A:364:GLU:HG2	1:A:367:PHE:CE1	2.56	0.41
1:B:68:ASN:N	1:B:68:ASN:HD22	2.18	0.41
1:A:115:LEU:HD23	2:A:1802:BOG:H5'1	2.03	0.40
1:A:213:SER:HB3	1:A:216:MET:HB2	2.02	0.40
1:A:238:LEU:HD23	1:A:238:LEU:HA	1.80	0.40
1:B:290:GLU:CD	1:B:290:GLU:H	2.25	0.40
1:A:91:PHE:O	1:A:95:HIS:CD2	2.65	0.40
1:A:306:LEU:CD2	1:A:306:LEU:C	2.90	0.40
1:B:383:GLN:HG3	1:B:460:LEU:HD21	2.04	0.40
1:A:406:GLN:HA	3:A:1681:NAG:C8	2.52	0.40
1:A:320:HIS:HE1	1:A:551:GLY:O	2.04	0.40
1:B:116:VAL:HG22	2:B:2802:BOG:H2'1	2.02	0.40
1:A:223:ALA:O	1:A:224:LEU:C	2.59	0.40
1:B:445:LEU:HG	1:B:445:LEU:O	2.22	0.40
1:B:245:ARG:HD2	1:B:329:PHE:CZ	2.57	0.40
1:A:86:PRO:CG	2:A:1802:BOG:H61	2.50	0.40
1:A:206:THR:C	1:A:208:GLN:H	2.25	0.40
1:B:77:TRP:CE3	1:B:78:LEU:HD23	2.56	0.40
1:A:513:HIS:O	1:A:514:PRO:C	2.60	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	549/551 (100%)	509 (93%)	36 (7%)	4 (1%)	30	67
1	B	549/551 (100%)	504 (92%)	42 (8%)	3 (0%)	38	74
All	All	1098/1102 (100%)	1013 (92%)	78 (7%)	7 (1%)	33	70

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	514	PRO
1	B	514	PRO
1	A	483	GLY
1	A	270	PRO
1	B	290	GLU
1	A	157	ARG
1	B	270	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	486/486 (100%)	452 (93%)	34 (7%)	21	49	
1	B	486/486 (100%)	450 (93%)	36 (7%)	20	45	
All	All	972/972 (100%)	902 (93%)	70 (7%)	21	47	

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ARG
1	A	55	TYR
1	A	97	ARG
1	A	102	PHE
1	A	117	LEU
1	A	120	ARG
1	A	145	VAL
1	A	165	THR
1	A	171	LEU
1	A	215	LYS
1	A	232	HIS
1	A	238	LEU
1	A	244	LEU
1	A	246	LEU
1	A	252	LEU
1	A	271	VAL
1	A	277	ARG
1	A	298	LEU
1	A	300	LEU

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Mol	Chain	Res	Type
1	A	376	ARG
1	A	385	TYR
1	A	400	GLN
1	A	405	GLU
1	A	438	ARG
1	A	458	LEU
1	A	460	LEU
1	A	469	ARG
1	A	479	GLN
1	A	484	GLU
1	A	514	PRO
1	A	518	PHE
1	A	534	LEU
1	A	556	PHE
1	A	564	LEU
1	B	33	VAL
1	B	49	ARG
1	B	61	ARG
1	B	70	THR
1	B	97	ARG
1	B	117	LEU
1	B	120	ARG
1	B	143	SER
1	B	145	VAL
1	B	146	SER
1	B	171	LEU
1	B	180	ARG
1	B	183	LEU
1	B	190	ASP
1	B	238	LEU
1	B	244	LEU
1	B	246	LEU
1	B	252	LEU
1	B	271	VAL
1	B	289	GLN
1	B	298	LEU
1	B	300	LEU
1	B	316	LEU
1	B	376	ARG
1	B	385	TYR
1	B	405	GLU
1	B	458	LEU

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Mol	Chain	Res	Type
1	B	460	LEU
1	B	469	ARG
1	B	479	GLN
1	B	484	GLU
1	B	514	PRO
1	B	518	PHE
1	B	556	PHE
1	B	564	LEU
1	B	570	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	ASN
1	A	95	HIS
1	A	134	HIS
1	A	144	ASN
1	A	208	GLN
1	A	237	ASN
1	A	241	GLN
1	A	320	HIS
1	A	370	GLN
1	A	375	ASN
1	A	386	HIS
1	A	400	GLN
1	A	443	HIS
1	B	68	ASN
1	B	95	HIS
1	B	134	HIS
1	B	208	GLN
1	B	237	ASN
1	B	241	GLN
1	B	320	HIS
1	B	375	ASN
1	B	386	HIS
1	B	400	GLN
1	B	410	ASN
1	B	442	HIS
1	B	443	HIS
1	B	479	GLN
1	B	557	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

17 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	A	1661	-	12,14,15	1.28	2 (16%)	15,19,21	0.87	0
3	NAG	A	1662	-	12,14,15	1.56	3 (25%)	15,19,21	0.90	1 (6%)
3	NAG	A	1671	-	12,14,15	1.12	1 (8%)	15,19,21	0.75	0
3	NAG	A	1681	-	12,14,15	1.55	3 (25%)	15,19,21	0.81	0
5	FL2	A	1701	-	20,20,20	3.02	11 (55%)	27,27,27	2.57	4 (14%)
2	BOG	A	1802	-	20,20,20	1.48	4 (20%)	25,25,25	0.93	2 (8%)
3	NAG	A	2672	-	12,14,15	1.75	4 (33%)	15,19,21	1.04	1 (6%)
4	HEM	A	601	1	49,50,50	2.50	16 (32%)	46,82,82	1.26	5 (10%)
3	NAG	B	1672	-	12,14,15	1.48	4 (33%)	15,19,21	1.00	1 (6%)
3	NAG	B	2661	-	12,14,15	1.29	2 (16%)	15,19,21	0.93	0
3	NAG	B	2662	-	12,14,15	1.50	2 (16%)	15,19,21	0.91	1 (6%)
3	NAG	B	2671	-	12,14,15	1.16	1 (8%)	15,19,21	0.83	0
3	NAG	B	2681	-	12,14,15	1.45	2 (16%)	15,19,21	0.95	0
5	FL2	B	2701	-	20,20,20	3.06	14 (70%)	27,27,27	2.57	4 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BOG	B	2801	-	20,20,20	1.63	6 (30%)	25,25,25	1.04	1 (4%)
2	BOG	B	2802	-	20,20,20	1.44	4 (20%)	25,25,25	0.94	2 (8%)
4	HEM	B	601	1	49,50,50	2.25	17 (34%)	46,82,82	1.29	4 (8%)

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
3	NAG	A	1661	-	-	0/6/23/26	0/1/1/1
3	NAG	A	1662	-	-	0/6/23/26	0/1/1/1
3	NAG	A	1671	-	-	0/6/23/26	0/1/1/1
3	NAG	A	1681	-	-	0/6/23/26	0/1/1/1
5	FL2	A	1701	-	-	1/14/14/14	0/2/2/2
2	BOG	A	1802	-	-	0/11/31/31	0/1/1/1
3	NAG	A	2672	-	-	0/6/23/26	0/1/1/1
4	HEM	A	601	1	-	0/14/114/114	0/0/8/8
3	NAG	B	1672	-	-	0/6/23/26	0/1/1/1
3	NAG	B	2661	-	-	0/6/23/26	0/1/1/1
3	NAG	B	2662	-	-	0/6/23/26	0/1/1/1
3	NAG	B	2671	-	-	0/6/23/26	0/1/1/1
3	NAG	B	2681	-	-	0/6/23/26	0/1/1/1
5	FL2	B	2701	-	-	1/14/14/14	0/2/2/2
2	BOG	B	2801	-	-	0/11/31/31	0/1/1/1
2	BOG	B	2802	-	-	0/11/31/31	0/1/1/1
4	HEM	B	601	1	-	0/14/114/114	0/0/8/8

All (96) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	HEM	C2D-C1D	9.85	1.47	1.44
5	B	2701	FL2	C6-C11	6.42	1.47	1.39
5	A	1701	FL2	C6-C11	5.95	1.46	1.39
5	A	1701	FL2	C7-C6	5.35	1.48	1.40
5	B	2701	FL2	C7-C6	5.26	1.48	1.40
5	A	1701	FL2	C8-C9	4.95	1.47	1.39
4	B	601	HEM	C3C-C2C	-4.93	1.35	1.43
4	A	601	HEM	C3C-C2C	-4.82	1.35	1.43
5	B	2701	FL2	C8-C9	4.74	1.47	1.39
4	A	601	HEM	C3B-CAB	4.52	1.54	1.40
4	B	601	HEM	C3C-CAC	4.48	1.54	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1701	FL2	C1-C2	4.44	1.48	1.39
4	A	601	HEM	C3C-CAC	4.34	1.54	1.40
4	A	601	HEM	C4A-C3A	4.29	1.45	1.40
4	B	601	HEM	C4A-C3A	4.24	1.45	1.40
4	B	601	HEM	C3D-C4D	4.20	1.45	1.44
4	B	601	HEM	C3B-CAB	4.16	1.53	1.40
5	B	2701	FL2	C1-C2	4.13	1.48	1.39
4	B	601	HEM	CBC-CAC	4.07	1.52	1.28
4	A	601	HEM	CBB-CAB	4.06	1.52	1.28
4	B	601	HEM	C2D-C1D	3.96	1.45	1.44
4	A	601	HEM	CBC-CAC	3.94	1.51	1.28
4	B	601	HEM	CBB-CAB	3.93	1.51	1.28
4	B	601	HEM	C3D-C2D	-3.90	1.36	1.43
5	A	1701	FL2	C8-C7	3.70	1.45	1.38
2	B	2801	BOG	O5-C1	3.68	1.51	1.41
3	A	2672	NAG	C2-N2	3.55	1.50	1.46
4	A	601	HEM	C3D-C2D	-3.54	1.37	1.43
5	B	2701	FL2	C8-C7	3.50	1.45	1.38
3	B	2662	NAG	C3-C2	3.45	1.59	1.52
4	B	601	HEM	CHA-C4D	3.35	1.40	1.35
4	B	601	HEM	C3B-C2B	-3.29	1.38	1.43
3	A	1662	NAG	C3-C2	3.28	1.59	1.52
2	A	1802	BOG	O5-C1	3.25	1.50	1.41
4	A	601	HEM	CHA-C4D	3.20	1.40	1.35
4	B	601	HEM	C3B-C4B	3.18	1.48	1.44
2	B	2802	BOG	O5-C1	3.17	1.50	1.41
3	A	1661	NAG	C3-C2	2.98	1.58	1.52
3	B	2661	NAG	C3-C2	2.98	1.58	1.52
5	B	2701	FL2	C3-C2	2.97	1.45	1.39
4	A	601	HEM	CMB-C2B	2.93	1.56	1.47
5	A	1701	FL2	C4-C3	2.93	1.45	1.39
3	A	1681	NAG	C3-C2	2.93	1.58	1.52
5	A	1701	FL2	C3-C2	2.91	1.45	1.39
5	B	2701	FL2	C-C1	2.88	1.45	1.39
5	B	2701	FL2	C4-C3	2.88	1.45	1.39
2	B	2801	BOG	O5-C5	2.87	1.51	1.44
5	A	1701	FL2	O-C14	2.86	1.28	1.21
4	B	601	HEM	CMB-C2B	2.84	1.56	1.47
2	B	2802	BOG	O5-C5	2.80	1.51	1.44
3	B	2681	NAG	C4-C5	2.76	1.59	1.53
4	A	601	HEM	C3B-C4B	2.75	1.47	1.44
3	B	1672	NAG	C3-C2	2.71	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1802	BOG	C4-C5	-2.70	1.47	1.53
3	A	2672	NAG	C3-C2	2.69	1.58	1.52
5	B	2701	FL2	O-C14	2.68	1.27	1.21
4	B	601	HEM	C1A-C2A	2.66	1.48	1.43
3	A	1681	NAG	C4-C5	2.65	1.58	1.53
3	A	1671	NAG	C4-C5	2.63	1.58	1.53
5	A	1701	FL2	C-C1	2.60	1.45	1.39
5	B	2701	FL2	C9-C12	2.53	1.57	1.52
3	B	2681	NAG	C3-C2	2.52	1.57	1.52
3	B	2671	NAG	C3-C2	2.50	1.57	1.52
2	B	2802	BOG	C4-C5	-2.50	1.47	1.53
2	A	1802	BOG	O5-C5	2.48	1.50	1.44
5	B	2701	FL2	C12-C14	2.47	1.55	1.52
3	A	1681	NAG	O5-C5	2.44	1.49	1.45
2	B	2801	BOG	C4-C5	-2.34	1.47	1.53
4	A	601	HEM	C1A-C2A	2.33	1.47	1.43
4	A	601	HEM	CMC-C2C	2.33	1.54	1.47
5	A	1701	FL2	C5-C4	2.31	1.44	1.37
4	A	601	HEM	C3B-C2B	-2.30	1.39	1.43
5	A	1701	FL2	C12-C14	2.30	1.55	1.52
3	A	1662	NAG	C4-C5	2.30	1.58	1.53
3	A	2672	NAG	C4-C3	2.28	1.58	1.52
5	B	2701	FL2	C5-C4	2.27	1.44	1.37
4	B	601	HEM	CMC-C2C	2.26	1.54	1.47
3	A	1661	NAG	C4-C5	2.24	1.58	1.53
2	B	2801	BOG	C4-C3	2.23	1.58	1.52
2	B	2801	BOG	C3'-C2'	-2.22	1.37	1.51
3	B	2661	NAG	C4-C5	2.22	1.57	1.53
3	A	2672	NAG	C4-C5	2.22	1.57	1.53
3	B	1672	NAG	C4-C5	2.20	1.57	1.53
3	A	1662	NAG	C2-N2	2.20	1.48	1.46
4	B	601	HEM	CMD-C2D	2.19	1.54	1.47
3	B	1672	NAG	C2-N2	2.17	1.48	1.46
2	B	2801	BOG	C3-C2	2.13	1.58	1.52
4	B	601	HEM	CHC-C1C	2.13	1.40	1.36
2	B	2802	BOG	C3'-C2'	-2.12	1.38	1.51
5	B	2701	FL2	C10-C9	2.09	1.42	1.38
3	B	1672	NAG	C4-C3	2.09	1.57	1.52
2	A	1802	BOG	C3'-C2'	-2.08	1.38	1.51
3	B	2662	NAG	C4-C5	2.06	1.57	1.53
4	A	601	HEM	C3D-C4D	-2.06	1.44	1.44
5	B	2701	FL2	C10-C11	2.04	1.41	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	HEM	CMD-C2D	2.02	1.53	1.47

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	2701	FL2	O1-C14-C12	10.52	129.04	111.33
5	A	1701	FL2	O1-C14-C12	10.40	128.83	111.33
5	A	1701	FL2	O-C14-C12	-5.00	109.95	124.20
5	B	2701	FL2	O-C14-C12	-4.97	110.03	124.20
5	A	1701	FL2	C13-C12-C14	4.55	119.27	111.22
5	B	2701	FL2	C13-C12-C14	4.34	118.90	111.22
4	B	601	HEM	C3B-C4B-NB	-4.23	110.97	114.00
2	B	2801	BOG	C1'-O1-C1	4.06	121.26	113.96
4	A	601	HEM	C3B-C4B-NB	-3.78	111.30	114.00
2	B	2802	BOG	C1'-O1-C1	3.44	120.15	113.96
4	B	601	HEM	CBA-CAA-C2A	-3.40	106.70	112.69
4	A	601	HEM	C3A-C4A-NA	3.36	111.95	109.41
2	A	1802	BOG	O1-C1-C2	3.36	112.46	108.18
4	B	601	HEM	C3A-C4A-NA	3.01	111.68	109.41
5	B	2701	FL2	C16-O1-C14	2.62	122.25	116.02
5	A	1701	FL2	C16-O1-C14	2.61	122.23	116.02
3	A	2672	NAG	O7-C7-C8	-2.45	117.27	122.04
3	B	1672	NAG	O7-C7-C8	-2.31	117.54	122.04
4	A	601	HEM	C4A-NA-C1A	-2.24	103.82	106.76
4	A	601	HEM	CBA-CAA-C2A	-2.19	108.83	112.69
3	B	2662	NAG	O7-C7-C8	-2.16	117.82	122.04
2	B	2802	BOG	O1-C1-C2	2.08	110.82	108.18
2	A	1802	BOG	C1'-O1-C1	2.07	117.68	113.96
3	A	1662	NAG	O7-C7-C8	-2.06	118.02	122.04
4	A	601	HEM	C1B-NB-C4B	-2.06	103.05	105.16
4	B	601	HEM	C4A-NA-C1A	-2.05	104.06	106.76

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1701	FL2	C16-O1-C14-C12
5	B	2701	FL2	C16-O1-C14-C12

There are no ring outliers.

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	551/551 (100%)	0.01	8 (1%) 70 73	22, 37, 53, 64	0
1	B	551/551 (100%)	-0.04	7 (1%) 74 77	23, 37, 53, 64	0
All	All	1102/1102 (100%)	-0.02	15 (1%) 68 75	22, 37, 53, 64	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	33	VAL	3.9
1	A	52	LEU	3.9
1	A	98	TRP	3.4
1	B	54	ARG	3.0
1	A	33	VAL	2.9
1	A	102	PHE	2.8
1	B	82	LEU	2.5
1	A	107	PHE	2.5
1	A	167	GLY	2.3
1	B	294	LEU	2.1
1	A	176	PHE	2.1
1	B	75	TRP	2.1
1	A	409	PHE	2.1
1	B	169	LYS	2.0
1	B	38	TYR	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	BOG	B	2801	20/20	1.07	10.50	37,63,68,68	0
5	FL2	A	1701	19/19	0.25	5.38	50,51,56,59	0
5	FL2	B	2701	19/19	0.26	4.82	50,52,56,59	0
2	BOG	A	1802	20/20	0.32	4.09	37,54,64,67	0
2	BOG	B	2802	20/20	0.33	3.52	37,54,64,67	0
3	NAG	B	2681	14/15	0.26	2.57	31,36,42,42	0
3	NAG	B	2661	14/15	0.33	2.29	50,60,64,78	0
3	NAG	A	2672	14/15	0.24	2.13	32,39,65,76	0
3	NAG	A	1681	14/15	0.27	2.08	31,36,42,42	0
3	NAG	A	1661	14/15	0.27	1.84	50,60,64,78	0
3	NAG	B	1672	14/15	0.25	0.90	32,39,65,76	0
4	HEM	A	601	43/43	0.19	0.81	36,41,53,61	0
4	HEM	B	601	43/43	0.18	0.66	36,40,55,65	0
3	NAG	A	1671	14/15	0.14	-0.76	6,16,23,25	0
3	NAG	B	2671	14/15	0.12	-1.72	6,16,23,25	0
3	NAG	A	1662	14/15	0.61	-	63,84,96,96	0
3	NAG	B	2662	14/15	0.83	-	63,84,96,96	0

6.5 Other polymers ⓘ

There are no such residues in this entry.