



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:42 AM UTC

PDB ID : 1T1R / pdb_00001t1r
Title : Crystal Structure of the Reductoisomerase Complexed with a Bisphosphonate
Authors : Yajima, S.; Hara, K.; Sanders, J.M.; Yin, F.; Ohsawa, K.; Wiesner, J.; Jomaa, H.; Oldfield, E.
Deposited on : 2004-04-17
Resolution : 2.30 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

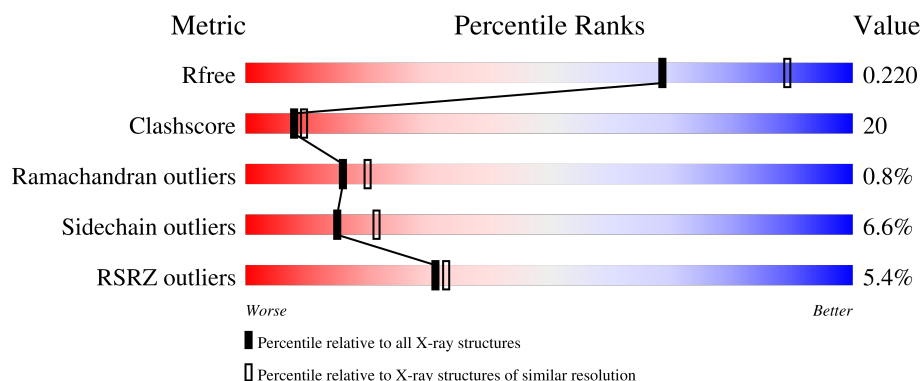
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	398	6% 63% 31% 6%
1	B	398	5% 63% 33% .

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6192 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 1-deoxy-D-xylulose 5-phosphate reductoisomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	398	Total	C	N	O	S	0	0	0
			3026	1889	534	577	26			
1	B	398	Total	C	N	O	S	0	0	0
			3026	1889	534	577	26			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	cloning artifact	UNP P45568
B	0	GLY	-	cloning artifact	UNP P45568

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



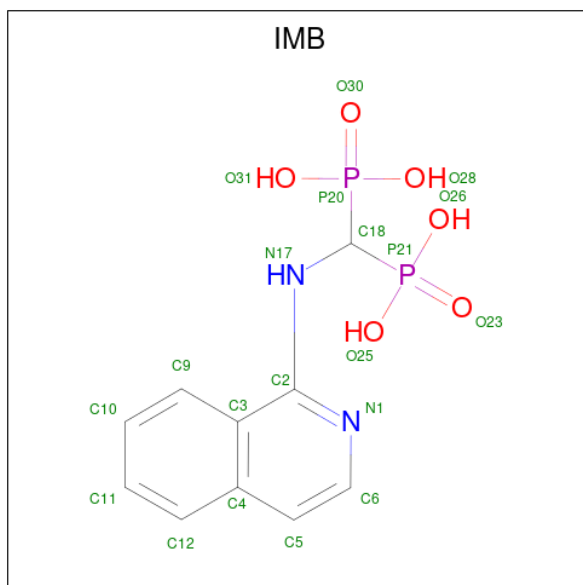
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	O S	0	0
			5	4 1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is [(ISOQUINOLIN-1-YLAMINO)-PHOSPHONO-METHYL]-PHOSPHONIC ACID (CCD ID: IMB) (formula: C₁₀H₁₂N₂O₆P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			20	10	2	6	2		
3	B	1	Total	C	N	O	P	0	0
			20	10	2	6	2		

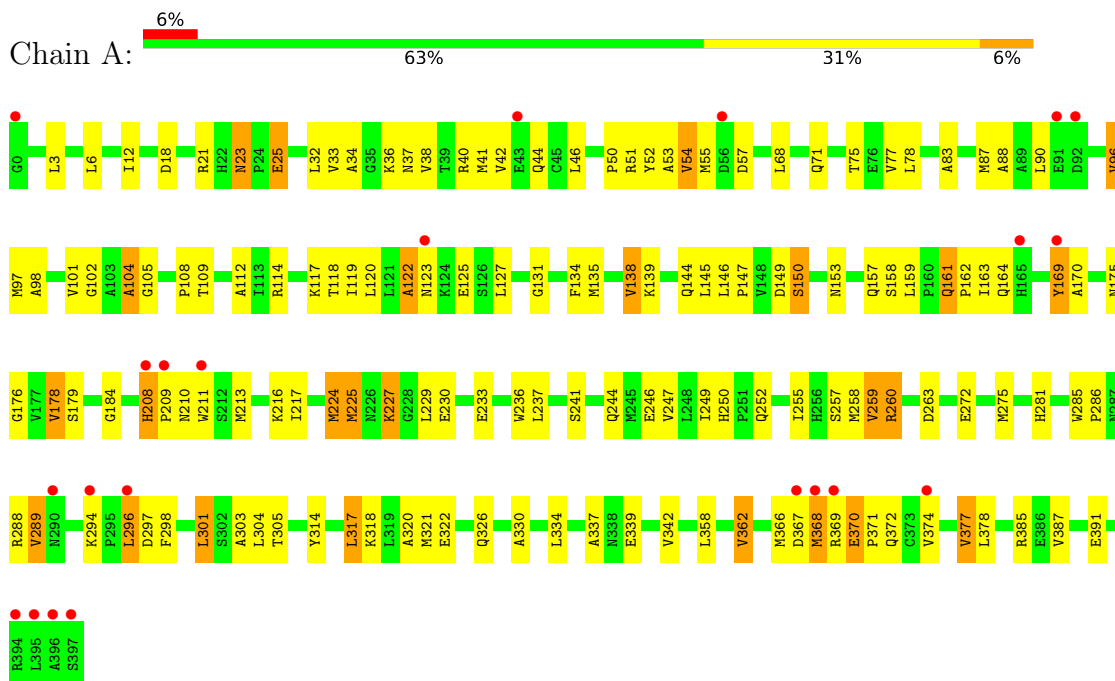
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	47	Total	O	0	0
			47	47		
4	B	43	Total	O	0	0
			43	43		

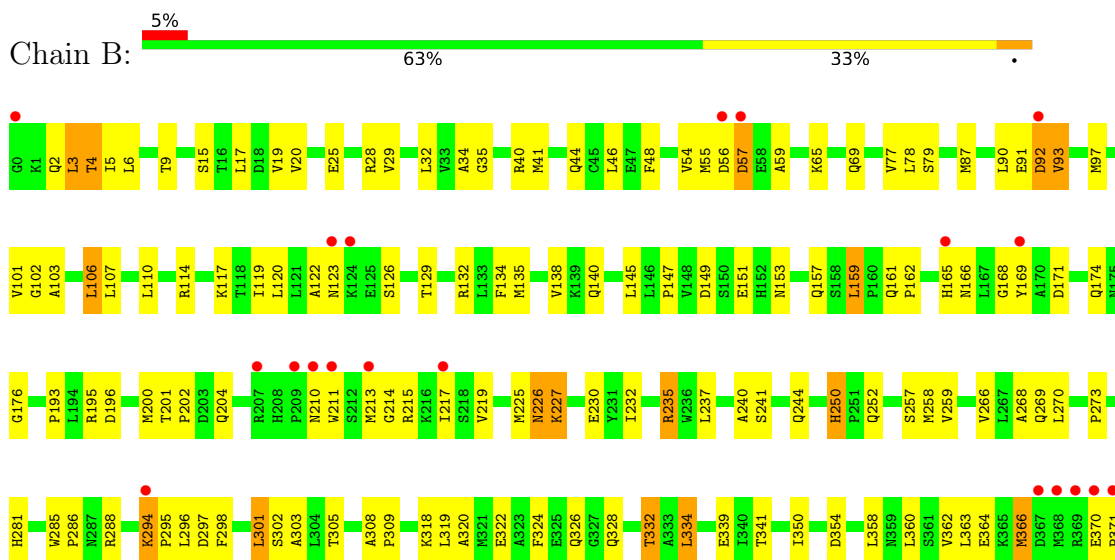
3 Residue-property plots

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: 1-deoxy-D-xylulose 5-phosphate reductoisomerase



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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	182.38Å 59.04Å 86.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.00 – 2.30 45.00 – 2.39	Depositor EDS
% Data completeness (in resolution range)	(Not available) (45.00-2.30) 97.4 (45.00-2.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 2.39Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.218 , 0.270 0.223 , 0.220	Depositor DCC
R_{free} test set	3671 reflections (9.91%)	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtriage
Anisotropy	0.375	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 38.7	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	6192	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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: SO4, IMB

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	0/3074	0.95	14/4166 (0.3%)
1	B	0.43	0/3074	0.92	8/4166 (0.2%)
All	All	0.45	0/6148	0.93	22/8332 (0.3%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	165	HIS	N-CA-C	-7.25	99.80	110.52
1	A	208	HIS	CA-C-N	6.94	128.52	119.84
1	A	208	HIS	C-N-CA	6.94	128.52	119.84
1	A	225	MET	N-CA-C	-6.44	104.31	111.71
1	B	35	GLY	N-CA-C	6.20	115.85	110.21
1	B	93	VAL	N-CA-C	5.93	117.23	109.58
1	B	122	ALA	N-CA-C	-5.63	106.55	113.41
1	B	92	ASP	N-CA-C	5.51	116.96	111.07
1	B	250	HIS	CA-C-N	5.47	126.68	119.84
1	B	250	HIS	C-N-CA	5.47	126.68	119.84
1	A	104	ALA	N-CA-C	-5.38	103.79	110.41
1	B	302	SER	N-CA-C	-5.34	101.83	110.32
1	A	255	ILE	N-CA-C	-5.33	101.86	108.89
1	A	77	VAL	N-CA-C	5.24	116.52	108.71
1	A	3	LEU	N-CA-C	5.23	117.14	109.24
1	A	23	ASN	CA-C-N	5.20	124.65	119.24
1	A	23	ASN	C-N-CA	5.20	124.65	119.24
1	A	179	SER	N-CA-C	5.17	116.38	108.42
1	A	150	SER	N-CA-C	5.12	117.25	111.11
1	A	250	HIS	CA-C-N	5.09	125.12	119.32
1	A	250	HIS	C-N-CA	5.09	125.12	119.32
1	A	122	ALA	N-CA-C	-5.02	104.45	110.88

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	3026	0	3049	115	0
1	B	3026	0	3049	131	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	20	0	8	1	0
3	B	20	0	8	5	0
4	A	47	0	0	0	0
4	B	43	0	0	1	0
All	All	6192	0	6114	239	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 20.

All (239) 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:B:201:THR:HG22	1:B:204:GLN:HG3	1.45	0.98
1:B:129:THR:HA	1:B:332:THR:HG22	1.53	0.90
1:B:241:SER:H	1:B:244:GLN:HE21	1.16	0.89
1:B:328:GLN:O	1:B:332:THR:HG23	1.73	0.89
1:A:105:GLY:O	1:A:109:THR:HG23	1.71	0.88
1:A:33:VAL:HG13	1:A:54:VAL:HG22	1.54	0.87
1:A:241:SER:H	1:A:244:GLN:HE21	1.21	0.85
1:A:252:GLN:HE22	1:A:305:THR:H	1.21	0.84
1:A:317:LEU:HD22	1:A:321:MET:HE3	1.60	0.83
1:A:296:LEU:HD11	1:B:266:VAL:HG21	1.62	0.81
1:A:23:ASN:ND2	1:A:289:VAL:HG22	1.97	0.80
1:B:201:THR:HG22	1:B:204:GLN:CG	2.13	0.79
1:B:366:MET:HE1	1:B:387:VAL:HG21	1.66	0.77
1:A:184:GLY:HA3	1:A:227:LYS:HD3	1.65	0.77
1:B:241:SER:H	1:B:244:GLN:NE2	1.80	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:MET:HE1	1:A:145:LEU:HD11	1.65	0.77
1:B:123:ASN:ND2	1:B:126:SER:HB3	2.02	0.75
1:B:159:LEU:HD13	1:B:259:VAL:HG21	1.69	0.75
1:A:96:VAL:HG11	1:A:112:ALA:HB1	1.68	0.75
1:A:144:GLN:HG3	1:A:146:LEU:CD2	2.17	0.74
1:B:201:THR:CG2	1:B:204:GLN:HG3	2.17	0.74
1:A:134:PHE:O	1:A:138:VAL:HG13	1.88	0.74
1:B:3:LEU:HD12	1:B:5:ILE:HD11	1.68	0.73
1:B:4:THR:HG22	1:B:93:VAL:HG11	1.70	0.73
1:A:97:MET:HA	1:A:120:LEU:HB2	1.71	0.72
1:A:275:MET:HE2	1:A:275:MET:HA	1.72	0.71
1:B:87:MET:HA	1:B:90:LEU:HD13	1.70	0.71
1:B:9:THR:HG22	1:B:40:ARG:HG2	1.73	0.71
1:A:252:GLN:NE2	1:A:305:THR:H	1.90	0.70
1:B:54:VAL:HG22	1:B:78:LEU:HB2	1.74	0.69
1:A:18:ASP:HA	1:A:21:ARG:NH1	2.07	0.69
1:A:225:MET:HE1	1:A:320:ALA:HB2	1.75	0.68
1:B:153:ASN:HD21	1:B:157:GLN:HE21	1.42	0.67
1:B:226:ASN:ND2	1:B:227:LYS:H	1.93	0.67
1:A:105:GLY:C	1:A:108:PRO:HD2	2.20	0.67
1:A:288:ARG:HB2	1:B:176:GLY:HA3	1.76	0.66
1:B:103:ALA:HA	1:B:106:LEU:HD22	1.77	0.66
1:B:4:THR:HG21	1:B:87:MET:O	1.95	0.66
1:A:225:MET:HE3	1:A:225:MET:HA	1.77	0.65
1:A:303:ALA:HB1	1:B:303:ALA:HB1	1.79	0.65
1:A:150:SER:HB2	1:A:275:MET:HE1	1.79	0.65
1:B:87:MET:HE2	1:B:90:LEU:HD11	1.79	0.64
1:A:96:VAL:HG11	1:A:112:ALA:CB	2.28	0.64
1:B:193:PRO:HB3	1:B:195:ARG:HH21	1.62	0.64
1:A:164:GLN:NE2	1:A:285:TRP:HE1	1.96	0.64
1:A:144:GLN:HG3	1:A:146:LEU:HD21	1.79	0.63
1:B:273:PRO:HA	3:B:2001:IMB:H5	1.78	0.63
1:A:90:LEU:O	1:A:117:LYS:HE3	1.99	0.63
1:A:211:TRP:HE1	1:A:213:MET:HE2	1.64	0.63
1:A:51:ARG:HG2	1:A:52:TYR:CD1	2.34	0.63
1:A:36:LYS:HE2	1:A:57:ASP:OD2	1.99	0.62
1:B:40:ARG:O	1:B:44:GLN:HG3	2.00	0.62
1:A:50:PRO:O	1:A:75:THR:HG22	2.00	0.61
1:B:226:ASN:HD22	1:B:227:LYS:H	1.45	0.61
1:A:131:GLY:HA3	1:A:236:TRP:CD1	2.35	0.61
1:B:225:MET:HE1	1:B:320:ALA:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:ASN:HD21	1:B:126:SER:HB3	1.65	0.61
1:A:362:VAL:O	1:A:366:MET:HG2	2.01	0.60
1:A:337:ALA:HB2	1:A:362:VAL:HG21	1.82	0.60
1:A:358:LEU:O	1:A:362:VAL:HG13	2.01	0.60
1:B:97:MET:HE2	1:B:120:LEU:HD23	1.84	0.59
1:A:260:ARG:NH2	1:B:296:LEU:O	2.35	0.59
1:A:246:GLU:OE2	1:A:260:ARG:HD2	2.01	0.59
1:A:101:VAL:HG22	1:A:102:GLY:N	2.16	0.58
1:A:51:ARG:HG2	1:A:52:TYR:CE1	2.38	0.58
1:A:135:MET:HE1	1:A:145:LEU:CD1	2.33	0.58
1:B:294:LYS:HE3	1:B:295:PRO:HD2	1.85	0.58
1:B:211:TRP:HE1	1:B:213:MET:HE3	1.69	0.57
1:B:132:ARG:HB3	1:B:328:GLN:NE2	2.20	0.57
1:B:211:TRP:NE1	1:B:213:MET:HE3	2.20	0.57
1:B:17:LEU:O	1:B:20:VAL:HG22	2.04	0.57
1:A:40:ARG:O	1:A:44:GLN:HG3	2.05	0.57
1:B:211:TRP:HE1	1:B:213:MET:CE	2.18	0.57
1:B:135:MET:CE	1:B:168:GLY:HA3	2.35	0.56
1:A:139:LYS:HE2	1:A:169:TYR:HD2	1.70	0.56
1:B:195:ARG:HD3	1:B:195:ARG:N	2.20	0.56
1:B:226:ASN:ND2	1:B:227:LYS:N	2.54	0.56
1:A:241:SER:H	1:A:244:GLN:NE2	1.98	0.56
1:A:263:ASP:OD2	1:B:288:ARG:HD2	2.05	0.56
1:B:235:ARG:HD2	1:B:240:ALA:O	2.06	0.56
1:B:3:LEU:HD12	1:B:5:ILE:CD1	2.35	0.56
1:B:34:ALA:HB3	1:B:41:MET:HE2	1.88	0.56
1:B:210:ASN:HB2	1:B:211:TRP:CE3	2.41	0.56
1:B:166:ASN:HA	1:B:169:TYR:CZ	2.40	0.55
1:A:318:LYS:O	1:A:322:GLU:HG3	2.06	0.55
1:A:387:VAL:O	1:A:391:GLU:HG2	2.07	0.55
1:B:2:GLN:HE21	1:B:28:ARG:HB3	1.71	0.55
1:B:385:ARG:O	1:B:389:ARG:HG3	2.07	0.55
1:A:297:ASP:O	1:A:301:LEU:HD13	2.07	0.55
1:B:29:VAL:HG11	1:B:32:LEU:HD21	1.88	0.55
1:B:252:GLN:HE22	1:B:305:THR:H	1.55	0.54
1:B:87:MET:HA	1:B:87:MET:HE2	1.89	0.54
1:B:360:LEU:O	1:B:364:GLU:HG3	2.08	0.54
1:B:252:GLN:NE2	1:B:305:THR:H	2.05	0.54
1:B:288:ARG:HG2	1:B:288:ARG:HH11	1.71	0.54
1:B:87:MET:HA	1:B:90:LEU:CD1	2.38	0.54
1:B:4:THR:CG2	1:B:93:VAL:HG11	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:269:GLN:C	1:B:270:LEU:HD12	2.34	0.53
1:A:298:PHE:HA	1:A:301:LEU:HD22	1.90	0.53
1:B:319:LEU:HD11	1:B:363:LEU:HD12	1.90	0.53
1:A:176:GLY:HA3	1:B:288:ARG:HB2	1.91	0.53
1:B:298:PHE:HA	1:B:301:LEU:HD22	1.90	0.53
1:A:123:ASN:HD21	1:A:125:GLU:HB3	1.74	0.52
1:A:97:MET:HE3	1:A:98:ALA:N	2.23	0.52
1:B:226:ASN:HD22	1:B:226:ASN:N	2.07	0.52
1:A:326:GLN:HB2	1:A:330:ALA:CB	2.39	0.52
1:A:158:SER:HB2	1:A:259:VAL:HG13	1.92	0.52
1:B:153:ASN:ND2	1:B:157:GLN:HE21	2.07	0.52
1:A:367:ASP:O	1:A:368:MET:C	2.53	0.52
1:B:161:GLN:HB3	1:B:162:PRO:HD3	1.92	0.51
1:A:98:ALA:HB1	1:A:109:THR:HG22	1.92	0.51
1:A:117:LYS:O	1:A:119:ILE:HD12	2.11	0.51
1:B:297:ASP:O	1:B:301:LEU:HD13	2.10	0.51
1:A:38:VAL:HG12	1:A:55:MET:HE2	1.93	0.51
1:A:213:MET:SD	1:A:217:ILE:HG22	2.50	0.51
1:A:224:MET:HB2	1:A:314:TYR:CD2	2.45	0.51
1:A:272:GLU:OE1	1:A:296:LEU:HA	2.11	0.51
1:A:252:GLN:NE2	1:A:304:LEU:HA	2.26	0.50
1:B:285:TRP:CD1	1:B:286:PRO:HA	2.45	0.50
1:B:132:ARG:HB3	1:B:328:GLN:CD	2.37	0.50
1:B:157:GLN:HG2	1:B:281:HIS:CE1	2.47	0.50
1:B:195:ARG:CD	1:B:195:ARG:H	2.25	0.50
1:A:163:ILE:HD13	1:A:170:ALA:HB1	1.93	0.50
1:A:367:ASP:O	1:A:368:MET:O	2.29	0.50
1:B:65:LYS:O	1:B:69:GLN:HG3	2.11	0.50
1:B:119:ILE:N	1:B:119:ILE:HD12	2.27	0.49
1:B:56:ASP:O	1:B:57:ASP:HB2	2.13	0.49
1:B:101:VAL:HG22	1:B:102:GLY:N	2.27	0.49
1:B:273:PRO:CA	3:B:2001:IMB:H5	2.43	0.49
1:A:12:ILE:HD12	1:A:12:ILE:N	2.28	0.48
1:B:166:ASN:HA	1:B:169:TYR:OH	2.14	0.48
1:A:105:GLY:CA	1:A:108:PRO:HD2	2.44	0.48
1:A:213:MET:HE1	3:A:3001:IMB:O30	2.13	0.48
1:B:147:PRO:HB3	1:B:237:LEU:HD21	1.95	0.48
1:A:68:LEU:HD13	1:A:75:THR:OG1	2.13	0.48
1:A:153:ASN:HD21	1:A:281:HIS:CD2	2.32	0.47
1:B:252:GLN:NE2	1:B:252:GLN:H	2.12	0.47
1:A:37:ASN:OD1	1:A:40:ARG:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:MET:HE3	1:A:120:LEU:O	2.14	0.47
1:B:387:VAL:O	1:B:391:GLU:HG3	2.14	0.47
1:A:54:VAL:HA	1:A:78:LEU:O	2.15	0.47
1:A:296:LEU:H	1:A:296:LEU:HD12	1.80	0.47
1:B:34:ALA:CB	1:B:41:MET:HE2	2.44	0.47
1:A:211:TRP:NE1	1:A:213:MET:HE2	2.30	0.47
1:A:46:LEU:HD11	1:A:71:GLN:HG2	1.97	0.47
1:B:87:MET:CE	1:B:90:LEU:HD11	2.44	0.46
1:B:341:THR:O	1:B:350:ILE:HD11	2.15	0.46
1:A:145:LEU:C	1:A:146:LEU:HD22	2.39	0.46
1:B:201:THR:HG23	1:B:204:GLN:H	1.81	0.46
1:B:366:MET:HA	1:B:366:MET:HE2	1.97	0.46
1:A:33:VAL:HG13	1:A:54:VAL:CG2	2.34	0.46
1:B:213:MET:HB2	1:B:217:ILE:HD11	1.97	0.46
1:B:294:LYS:HE3	1:B:294:LYS:HA	1.97	0.46
1:B:20:VAL:HG23	1:B:48:PHE:CE2	2.51	0.46
1:B:91:GLU:CD	1:B:91:GLU:H	2.23	0.46
1:A:101:VAL:CG2	1:A:102:GLY:N	2.79	0.45
1:A:144:GLN:CG	1:A:146:LEU:HD21	2.46	0.45
1:A:162:PRO:HB2	1:A:175:ASN:ND2	2.31	0.45
1:A:169:TYR:CD1	1:A:169:TYR:C	2.94	0.45
1:A:216:LYS:HG2	1:A:342:VAL:HG11	1.99	0.45
1:A:247:VAL:HG23	1:A:247:VAL:O	2.17	0.45
1:B:129:THR:CA	1:B:332:THR:HG22	2.34	0.45
1:B:258:MET:HG2	1:B:268:ALA:HB2	1.99	0.45
1:B:15:SER:O	1:B:19:VAL:HG23	2.17	0.45
1:B:97:MET:HA	1:B:120:LEU:HB2	1.98	0.45
1:A:38:VAL:O	1:A:42:VAL:HG23	2.16	0.45
1:B:25:GLU:HB2	4:B:2003:HOH:O	2.16	0.45
1:B:55:MET:O	1:B:79:SER:HA	2.16	0.45
1:B:114:ARG:HG2	1:B:114:ARG:HH11	1.81	0.45
1:B:395:LEU:O	1:B:395:LEU:HD13	2.16	0.45
1:A:71:GLN:O	1:A:71:GLN:HG3	2.16	0.44
1:B:134:PHE:O	1:B:138:VAL:HG23	2.16	0.44
1:B:334:LEU:HG	1:B:363:LEU:HD11	1.99	0.44
1:A:161:GLN:NE2	1:A:161:GLN:C	2.76	0.44
1:A:285:TRP:CD1	1:A:286:PRO:HA	2.52	0.44
1:B:195:ARG:N	1:B:195:ARG:CD	2.80	0.44
1:A:32:LEU:O	1:A:53:ALA:HA	2.18	0.44
1:B:252:GLN:H	1:B:252:GLN:CD	2.25	0.44
1:B:214:GLY:H	1:B:217:ILE:HD11	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:MET:CE	1:B:320:ALA:HB2	2.47	0.44
1:B:250:HIS:CE1	1:B:252:GLN:HE21	2.36	0.44
1:A:161:GLN:HB3	1:A:162:PRO:HD3	2.00	0.43
1:A:208:HIS:HB3	1:A:211:TRP:O	2.18	0.43
1:A:258:MET:HE1	1:B:298:PHE:CE2	2.53	0.43
1:B:117:LYS:O	1:B:119:ILE:HD12	2.18	0.43
1:B:370:GLU:HA	1:B:371:PRO:HD3	1.89	0.43
1:A:296:LEU:HD12	1:A:296:LEU:N	2.33	0.43
1:A:139:LYS:HE2	1:A:169:TYR:CD2	2.53	0.43
1:B:2:GLN:HG2	1:B:92:ASP:OD1	2.18	0.43
1:B:140:GLN:HG3	1:B:140:GLN:O	2.18	0.43
1:B:195:ARG:HD3	1:B:195:ARG:H	1.82	0.43
1:B:213:MET:HE1	3:B:2001:IMB:O30	2.19	0.43
1:A:147:PRO:HB3	1:A:237:LEU:HD21	2.01	0.43
1:A:88:ALA:HB1	1:A:112:ALA:HB2	2.01	0.42
1:A:210:ASN:HB2	1:A:211:TRP:CE3	2.54	0.42
1:B:354:ASP:O	1:B:358:LEU:HB2	2.19	0.42
1:A:272:GLU:HG3	1:A:294:LYS:O	2.19	0.42
1:B:2:GLN:HE21	1:B:28:ARG:HE	1.67	0.42
1:A:34:ALA:HB3	1:A:41:MET:HE2	2.00	0.42
1:B:386:GLU:O	1:B:390:LYS:HG3	2.19	0.42
1:A:368:MET:O	1:A:369:ARG:HD3	2.19	0.42
1:B:196:ASP:O	1:B:200:MET:HE3	2.19	0.42
1:A:227:LYS:HE2	1:A:230:GLU:OE1	2.19	0.42
1:B:288:ARG:HH11	1:B:288:ARG:CG	2.33	0.42
1:B:362:VAL:O	1:B:366:MET:HG2	2.19	0.42
1:A:224:MET:HG2	1:A:317:LEU:HG	2.02	0.42
1:B:151:GLU:OE2	3:B:2001:IMB:O25	2.38	0.42
1:A:102:GLY:O	1:A:104:ALA:O	2.38	0.42
1:B:57:ASP:OD2	1:B:59:ALA:HB3	2.20	0.42
1:A:178:VAL:CG2	1:A:260:ARG:HD3	2.50	0.41
1:A:224:MET:HE1	1:A:249:ILE:HG12	2.02	0.41
1:B:20:VAL:HG23	1:B:48:PHE:HE2	1.85	0.41
1:B:215:ARG:O	1:B:219:VAL:HG23	2.19	0.41
1:B:171:ASP:HB3	1:B:174:GLN:HB3	2.03	0.41
1:A:157:GLN:HG2	1:A:281:HIS:CE1	2.55	0.41
1:B:149:ASP:OD1	3:B:2001:IMB:O25	2.37	0.41
1:A:371:PRO:HG3	1:A:377:VAL:HG12	2.03	0.41
1:B:138:VAL:HG21	1:B:145:LEU:HD11	2.03	0.41
1:B:201:THR:OG1	1:B:202:PRO:HD2	2.21	0.41
1:A:37:ASN:ND2	1:A:40:ARG:HG3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:GLN:HE22	1:A:285:TRP:HE1	1.68	0.41
1:B:2:GLN:NE2	1:B:28:ARG:HE	2.19	0.41
1:A:83:ALA:O	1:A:87:MET:HG2	2.21	0.41
1:A:374:VAL:O	1:A:377:VAL:HG22	2.21	0.41
1:B:258:MET:HG2	1:B:268:ALA:CB	2.51	0.41
1:A:229:LEU:O	1:A:233:GLU:HG3	2.21	0.41
1:A:296:LEU:O	1:A:296:LEU:HD13	2.21	0.41
1:B:87:MET:CA	1:B:90:LEU:HD13	2.45	0.41
1:B:226:ASN:O	1:B:230:GLU:HG3	2.20	0.41
1:B:232:ILE:HG23	1:B:324:PHE:HD1	1.86	0.41
1:B:308:ALA:HA	1:B:309:PRO:HD3	1.94	0.41
1:B:318:LYS:O	1:B:322:GLU:HG3	2.21	0.41
1:A:118:THR:HG23	1:A:146:LEU:HD23	2.02	0.40
1:A:25:GLU:CD	1:A:25:GLU:H	2.29	0.40
1:A:97:MET:HE1	1:A:122:ALA:HB2	2.04	0.40
1:A:208:HIS:HA	1:A:209:PRO:HD3	1.87	0.40
1:A:339:GLU:OE2	1:A:385:ARG:NH2	2.51	0.40
1:B:77:VAL:O	1:B:78:LEU:HD23	2.20	0.40
1:B:252:GLN:CD	1:B:252:GLN:N	2.79	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	396/398 (100%)	382 (96%)	11 (3%)	3 (1%)	16	20
1	B	396/398 (100%)	386 (98%)	7 (2%)	3 (1%)	16	20
All	All	792/796 (100%)	768 (97%)	18 (2%)	6 (1%)	16	20

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	368	MET
1	A	257	SER
1	B	57	ASP
1	B	257	SER
1	B	366	MET
1	A	370	GLU

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	327/327 (100%)	301 (92%)	26 (8%)	11	15
1	B	327/327 (100%)	310 (95%)	17 (5%)	21	31
All	All	654/654 (100%)	611 (93%)	43 (7%)	15	21

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	25	GLU
1	A	54	VAL
1	A	96	VAL
1	A	114	ARG
1	A	127	LEU
1	A	138	VAL
1	A	149	ASP
1	A	159	LEU
1	A	161	GLN
1	A	169	TYR
1	A	178	VAL
1	A	224	MET
1	A	227	LYS
1	A	259	VAL
1	A	260	ARG
1	A	289	VAL
1	A	296	LEU

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Mol	Chain	Res	Type
1	A	301	LEU
1	A	317	LEU
1	A	334	LEU
1	A	362	VAL
1	A	370	GLU
1	A	372	GLN
1	A	377	VAL
1	A	378	LEU
1	B	3	LEU
1	B	4	THR
1	B	6	LEU
1	B	46	LEU
1	B	106	LEU
1	B	107	LEU
1	B	110	LEU
1	B	159	LEU
1	B	226	ASN
1	B	227	LYS
1	B	235	ARG
1	B	294	LYS
1	B	301	LEU
1	B	326	GLN
1	B	332	THR
1	B	334	LEU
1	B	339	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	HIS
1	A	23	ASN
1	A	70	GLN
1	A	82	GLN
1	A	95	GLN
1	A	123	ASN
1	A	144	GLN
1	A	161	GLN
1	A	164	GLN
1	A	165	HIS
1	A	175	ASN
1	A	226	ASN
1	A	244	GLN

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Mol	Chain	Res	Type
1	A	252	GLN
1	A	256	HIS
1	A	281	HIS
1	A	290	ASN
1	A	328	GLN
1	A	349	GLN
1	A	383	ASN
1	B	2	GLN
1	B	69	GLN
1	B	82	GLN
1	B	123	ASN
1	B	144	GLN
1	B	157	GLN
1	B	175	ASN
1	B	226	ASN
1	B	244	GLN
1	B	252	GLN
1	B	269	GLN
1	B	281	HIS
1	B	349	GLN
1	B	383	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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
2	SO4	A	1001	-	4,4,4	0.28	0	6,6,6	0.08	0
3	IMB	A	3001	-	20,21,21	2.50	10 (50%)	27,32,32	2.19	10 (37%)
2	SO4	B	1002	-	4,4,4	0.28	0	6,6,6	0.08	0
3	IMB	B	2001	-	20,21,21	2.62	10 (50%)	27,32,32	2.19	11 (40%)

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	IMB	A	3001	-	-	2/16/16/16	0/2/2/2
3	IMB	B	2001	-	-	2/16/16/16	0/2/2/2

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2001	IMB	P21-O25	-6.75	1.44	1.54
3	A	3001	IMB	P21-O25	-6.12	1.45	1.54
3	A	3001	IMB	C2-N1	5.68	1.41	1.34
3	B	2001	IMB	C2-N1	5.41	1.41	1.34
3	B	2001	IMB	P21-O23	3.15	1.55	1.49
3	A	3001	IMB	P21-O23	3.08	1.54	1.49
3	A	3001	IMB	C10-C9	2.89	1.42	1.36
3	B	2001	IMB	C10-C9	2.87	1.42	1.36
3	A	3001	IMB	C11-C12	2.84	1.42	1.36
3	B	2001	IMB	C6-N1	2.84	1.40	1.34
3	A	3001	IMB	C6-N1	2.83	1.40	1.34
3	B	2001	IMB	P21-C18	-2.82	1.80	1.83
3	B	2001	IMB	C11-C12	2.75	1.42	1.36
3	B	2001	IMB	P20-O30	-2.61	1.45	1.49
3	A	3001	IMB	C5-C6	2.28	1.39	1.36
3	A	3001	IMB	P20-O30	-2.26	1.46	1.49
3	B	2001	IMB	C5-C6	2.07	1.39	1.36
3	B	2001	IMB	C11-C10	2.05	1.42	1.38
3	A	3001	IMB	C11-C10	2.03	1.42	1.38
3	A	3001	IMB	P21-C18	-2.00	1.81	1.83

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	3001	IMB	C3-C2-N1	-5.66	117.16	121.35
3	B	2001	IMB	C3-C2-N1	-5.53	117.26	121.35
3	A	3001	IMB	O31-P20-O30	-3.97	103.49	113.45
3	A	3001	IMB	C5-C6-N1	-3.84	120.06	123.83
3	B	2001	IMB	O31-P20-O30	-3.82	103.88	113.45
3	B	2001	IMB	C5-C6-N1	-3.79	120.12	123.83
3	B	2001	IMB	P21-C18-P20	-3.46	110.26	116.24
3	A	3001	IMB	P21-C18-P20	-3.18	110.74	116.24
3	A	3001	IMB	C6-N1-C2	3.00	122.69	116.76
3	B	2001	IMB	C6-N1-C2	2.92	122.52	116.76
3	A	3001	IMB	O31-P20-C18	2.65	111.34	104.77
3	B	2001	IMB	C12-C4-C5	-2.56	117.17	123.01
3	B	2001	IMB	O26-P21-C18	2.51	111.00	104.77
3	A	3001	IMB	C12-C4-C5	-2.51	117.29	123.01
3	A	3001	IMB	O26-P21-C18	2.43	110.79	104.77
3	B	2001	IMB	O31-P20-C18	2.41	110.75	104.77
3	A	3001	IMB	O25-P21-C18	2.25	110.35	104.77
3	B	2001	IMB	O25-P21-C18	2.24	110.31	104.77
3	B	2001	IMB	O28-P20-C18	2.22	110.27	104.77
3	B	2001	IMB	N17-C2-N1	-2.21	114.94	118.12
3	A	3001	IMB	N17-C2-N1	-2.01	115.24	118.12

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	3001	IMB	C3-C2-N17-C18
3	B	2001	IMB	C3-C2-N17-C18
3	A	3001	IMB	N1-C2-N17-C18
3	B	2001	IMB	N1-C2-N17-C18

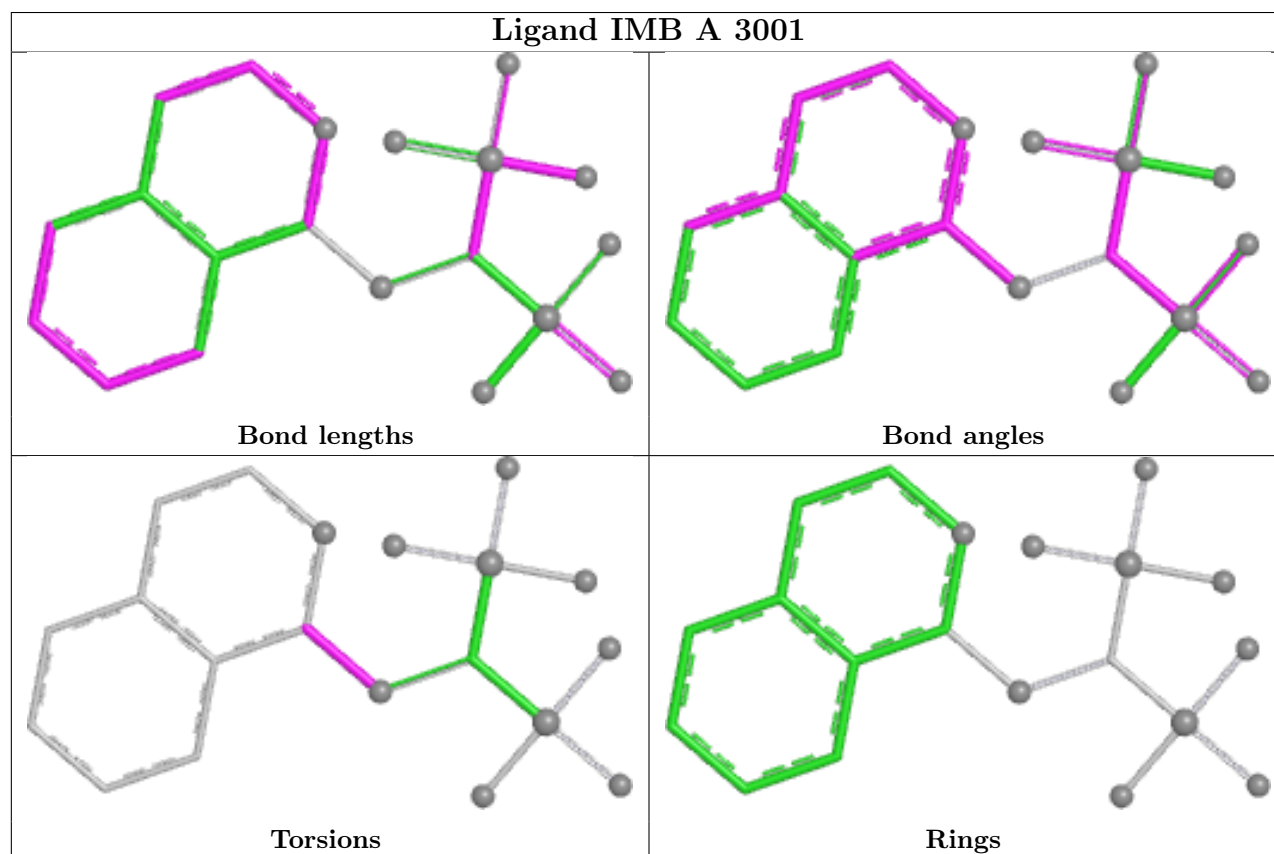
There are no ring outliers.

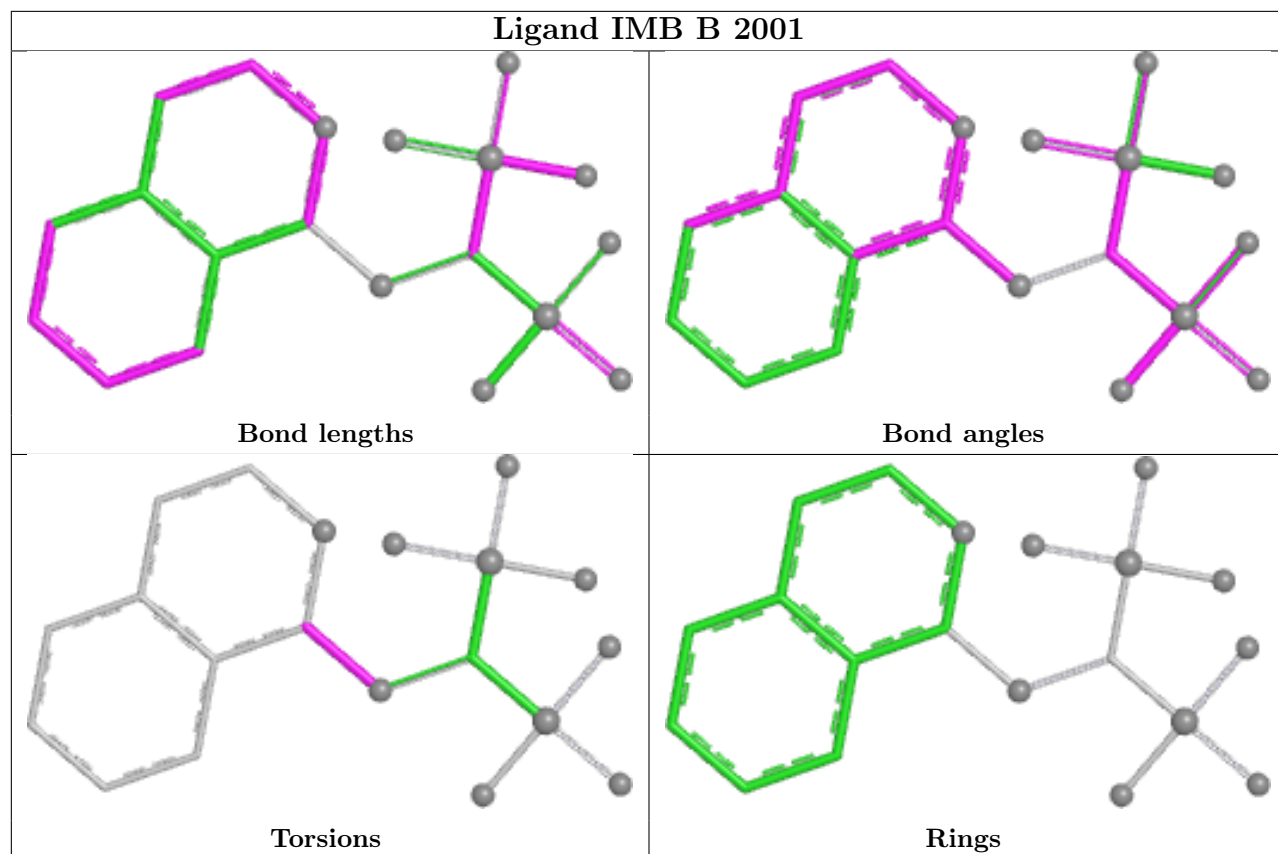
2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	3001	IMB	1	0
3	B	2001	IMB	5	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	398/398 (100%)	0.37	22 (5%) 30 32	26, 41, 69, 83	0
1	B	398/398 (100%)	0.42	21 (5%) 32 34	29, 44, 70, 90	0
All	All	796/796 (100%)	0.39	43 (5%) 31 33	26, 43, 70, 90	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	368	MET	5.0
1	A	0	GLY	4.8
1	B	217	ILE	4.3
1	A	211	TRP	4.1
1	A	209	PRO	3.8
1	B	368	MET	3.8
1	A	169	TYR	3.7
1	A	369	ARG	3.4
1	B	209	PRO	3.3
1	B	56	ASP	3.1
1	B	0	GLY	3.0
1	A	296	LEU	2.9
1	A	396	ALA	2.8
1	B	371	PRO	2.7
1	B	213	MET	2.7
1	B	211	TRP	2.6
1	B	92	ASP	2.6
1	B	165	HIS	2.6
1	B	369	ARG	2.6
1	B	169	TYR	2.5
1	A	92	ASP	2.3
1	A	208	HIS	2.3
1	B	123	ASN	2.3
1	A	165	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	394	ARG	2.3
1	B	396	ALA	2.3
1	A	374	VAL	2.3
1	A	56	ASP	2.2
1	A	43	GLU	2.2
1	B	367	ASP	2.2
1	B	207	ARG	2.2
1	B	294	LYS	2.2
1	A	123	ASN	2.1
1	B	124	LYS	2.1
1	A	91	GLU	2.1
1	A	395	LEU	2.1
1	A	290	ASN	2.1
1	A	294	LYS	2.1
1	B	57	ASP	2.1
1	B	210	ASN	2.1
1	B	370	GLU	2.0
1	A	367	ASP	2.0
1	A	397	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](#)

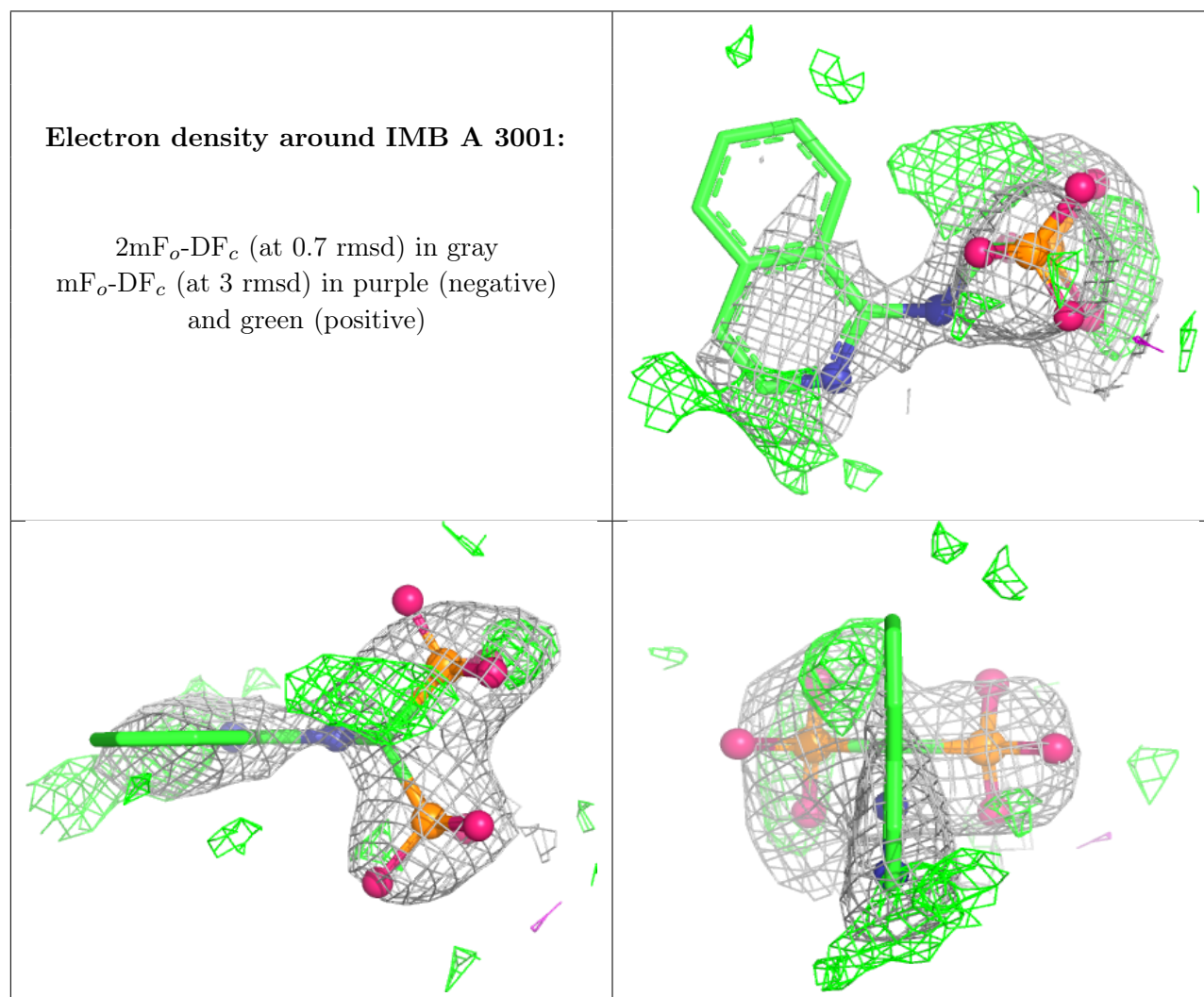
There are no oligosaccharides in this entry.

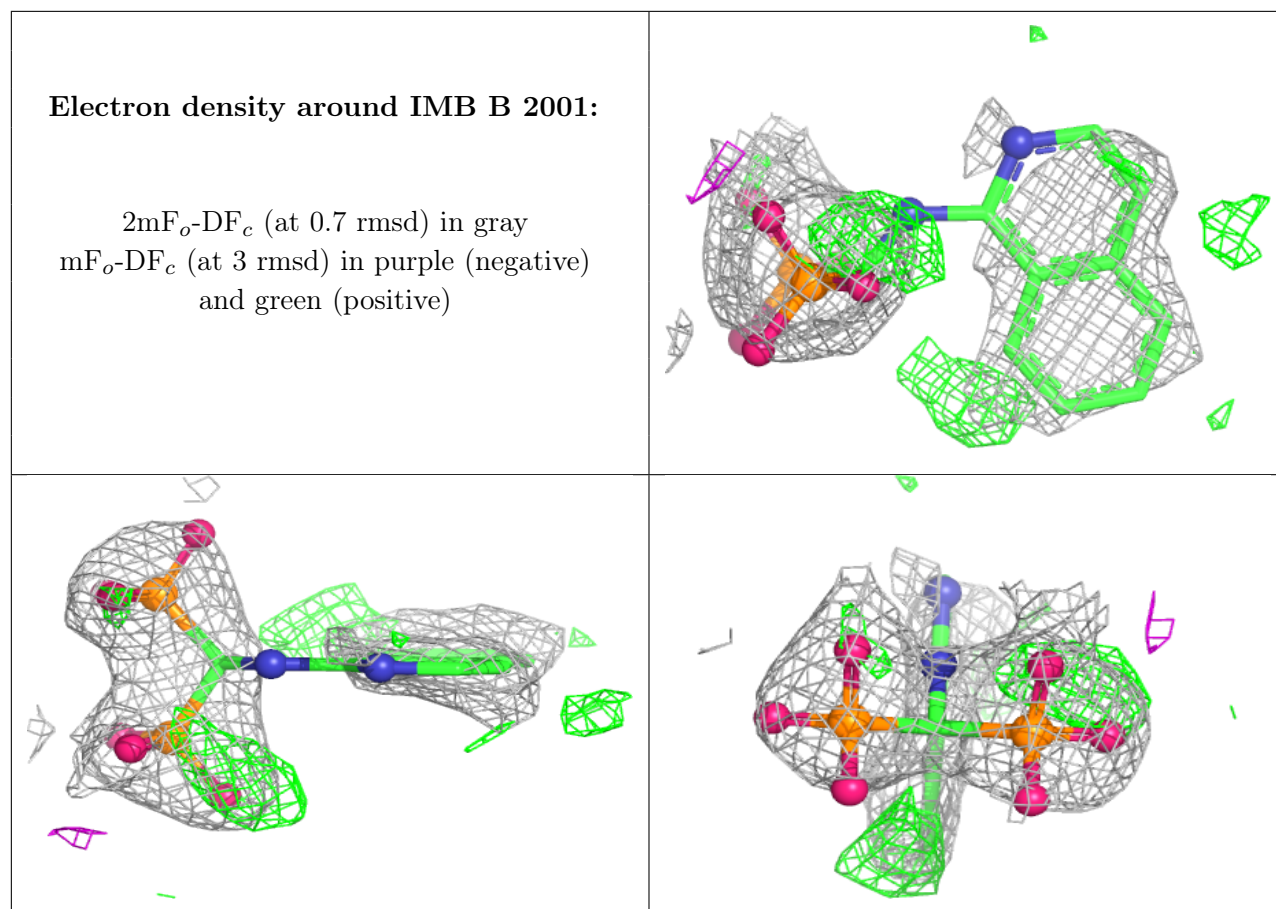
6.4 Ligands [i](#)

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(Å ²)	Q<0.9
3	IMB	A	3001	20/20	0.82	0.31	55,57,60,61	20
3	IMB	B	2001	20/20	0.86	0.22	46,49,51,51	20
2	SO4	B	1002	5/5	0.96	0.09	47,47,49,50	0
2	SO4	A	1001	5/5	0.98	0.05	42,43,44,44	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.





6.5 Other polymers ⓘ

There are no such residues in this entry.