



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:54 AM UTC

PDB ID : 2FB3 / pdb_00002fb3
Title : Structure of MoaA in complex with 5'-GTP
Authors : Haenzelmann, P.; Schindelin, H.
Deposited on : 2005-12-08
Resolution : 2.35 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

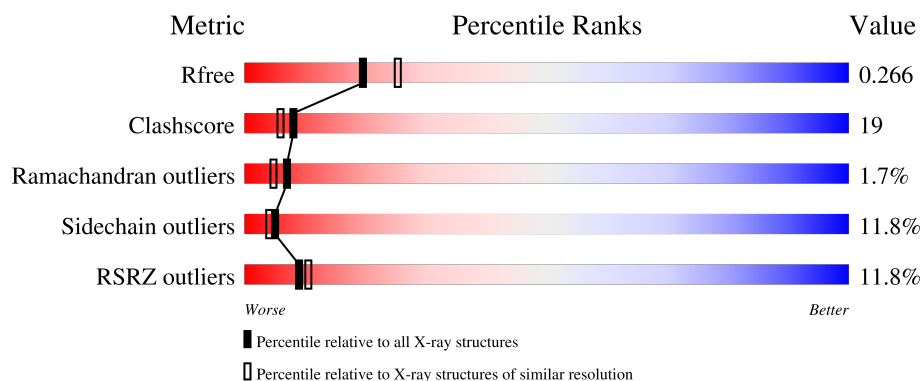
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	340	8% 65% 23% 7% • •
1	B	340	15% 54% 32% 9% • •

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5518 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 Molybdenum cofactor biosynthesis protein A.

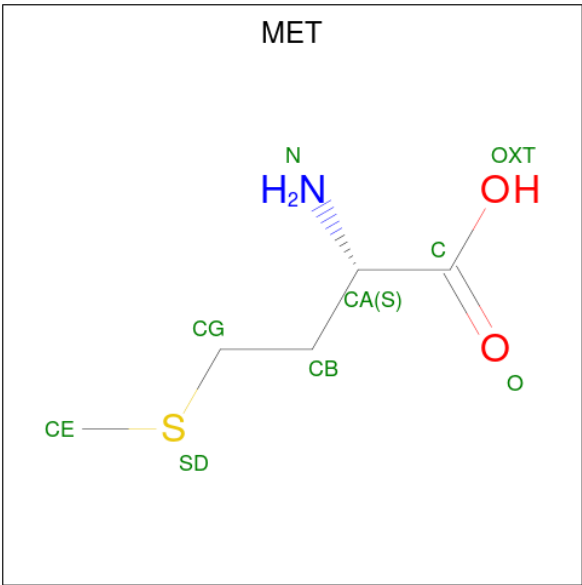
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	0	0
			2641	1673	455	500	13			
1	B	326	Total	C	N	O	S	0	0	0
			2632	1668	454	497	13			

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



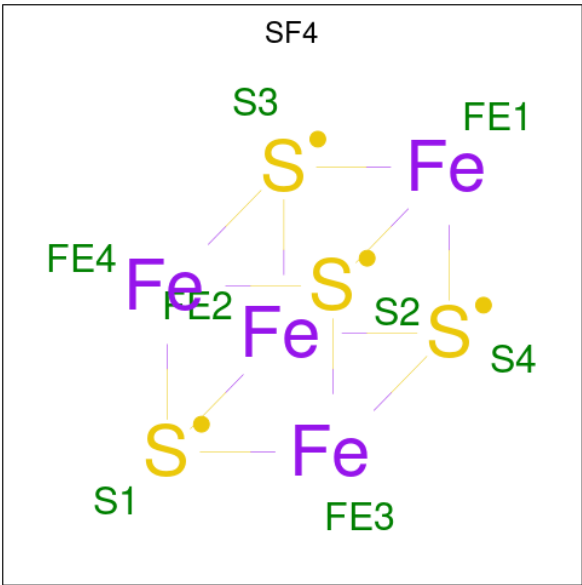
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is METHIONINE (CCD ID: MET) (formula: C₅H₁₁NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			9	5	1	2	1		
3	B	1	Total	C	N	O	S	0	0
			9	5	1	2	1		

- Molecule 4 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



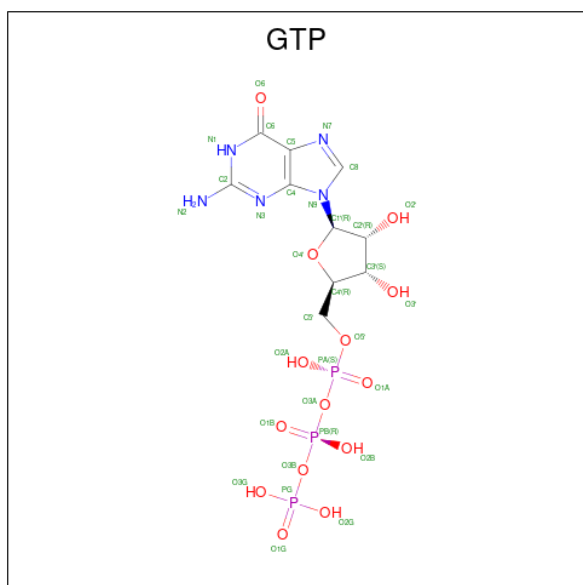
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	A	1	Total	Fe	S	0	0
			8	4	4		

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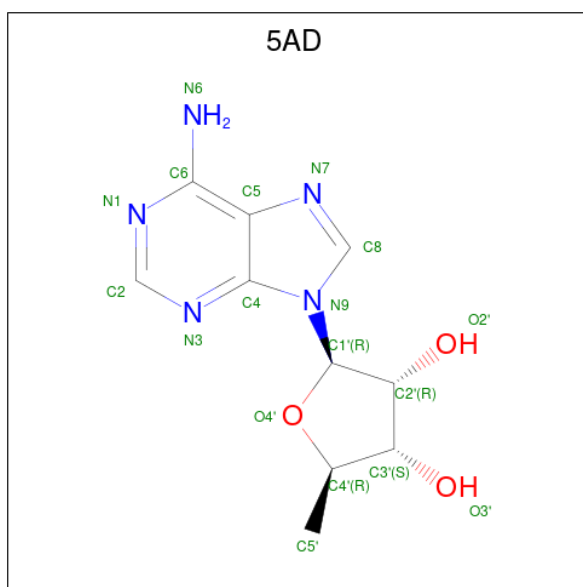
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



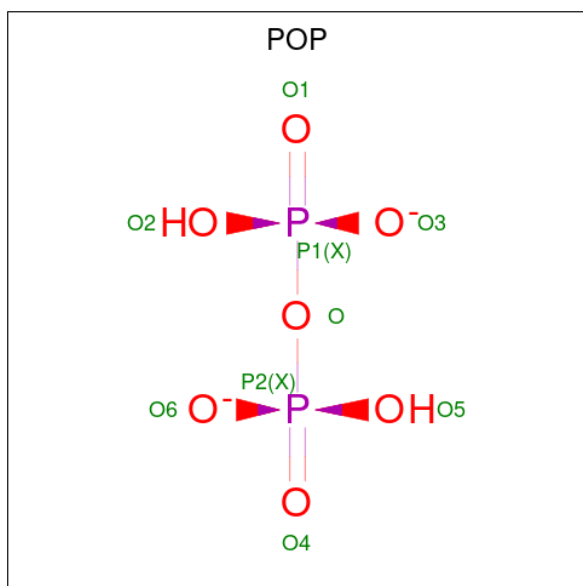
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 6 is 5'-DEOXYADENOSINE (CCD ID: 5AD) (formula: $C_{10}H_{13}N_5O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 7 is PYROPHOSPHATE 2- (CCD ID: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	O	P	0	0
			9	7	2		

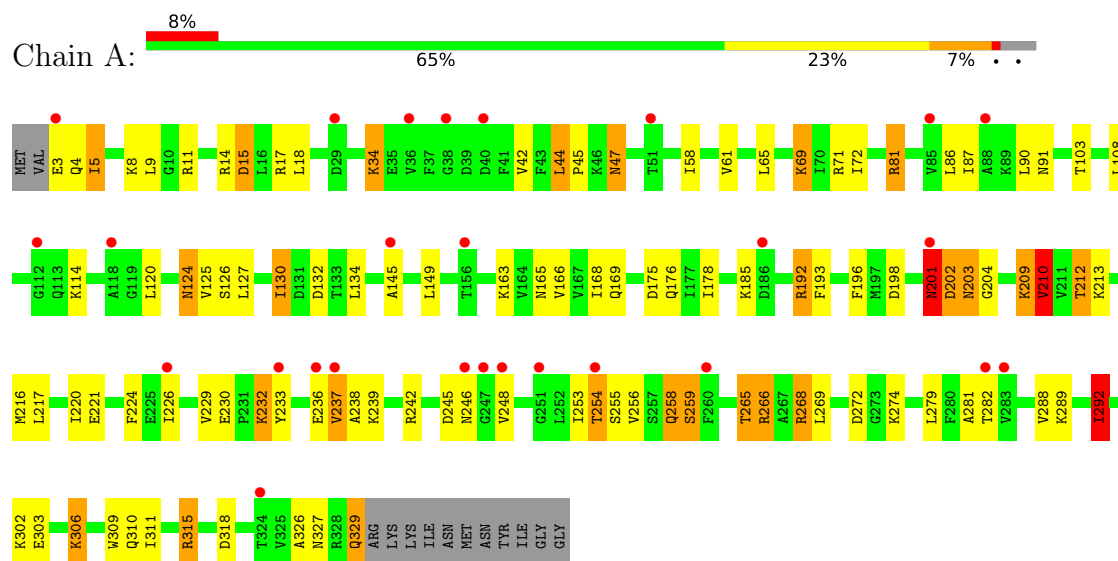
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	94	Total 94	O 94	0	0
8	B	33	Total 33	O 33	0	0

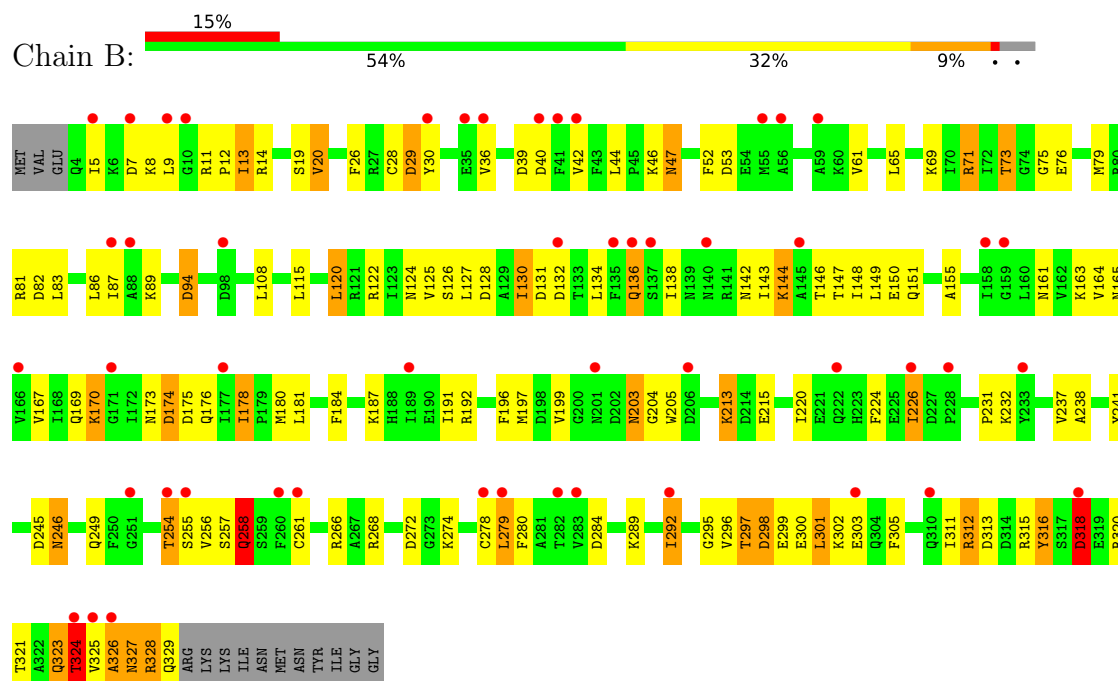
3 Residue-property plots

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: Molybdenum cofactor biosynthesis protein A



• Molecule 1: Molybdenum cofactor biosynthesis protein A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.02Å 103.45Å 191.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.35 20.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	91.1 (20.00-2.35) 90.9 (20.00-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.220 , 0.271 0.215 , 0.266	Depositor DCC
R_{free} test set	1859 reflections (4.56%)	wwPDB-VP
Wilson B-factor (Å ²)	56.5	Xtriage
Anisotropy	0.559	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 77.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5518	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% 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: 5AD, POP, GTP, SF4, SO4

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	1.31	7/2684 (0.3%)	1.23	15/3613 (0.4%)
1	B	1.17	22/2675 (0.8%)	1.07	7/3601 (0.2%)
All	All	1.24	29/5359 (0.5%)	1.16	22/7214 (0.3%)

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	1	0
1	B	0	1
All	All	1	1

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	329	GLN	C-O	24.21	1.72	1.23
1	A	329	GLN	CD-NE2	20.80	1.76	1.33
1	B	318	ASP	CG-OD2	19.18	1.61	1.25
1	A	329	GLN	CD-OE1	13.99	1.50	1.23
1	B	323	GLN	C-N	12.99	1.50	1.33
1	B	327	ASN	CG-ND2	12.75	1.60	1.33
1	B	11	ARG	CZ-NH1	9.46	1.46	1.32
1	B	323	GLN	CG-CD	8.97	1.74	1.52
1	B	316	TYR	C-O	8.24	1.33	1.24
1	B	323	GLN	C-O	7.66	1.32	1.24
1	B	323	GLN	CD-NE2	7.33	1.48	1.33
1	B	318	ASP	CB-CG	7.19	1.70	1.52
1	B	312	ARG	CZ-NH1	6.95	1.42	1.32
1	B	323	GLN	CD-OE1	6.94	1.36	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	326	ALA	C-O	6.92	1.32	1.24
1	B	215	GLU	CD-OE2	6.81	1.38	1.25
1	B	327	ASN	CG-OD1	6.17	1.35	1.23
1	B	328	ARG	CZ-NH1	6.10	1.41	1.32
1	B	203	ASN	C-N	6.07	1.41	1.33
1	B	324	THR	C-O	5.99	1.30	1.24
1	B	329	GLN	CD-NE2	5.70	1.45	1.33
1	B	325	VAL	C-O	5.67	1.31	1.24
1	B	203	ASN	C-O	5.58	1.31	1.24
1	A	306	LYS	N-CA	-5.36	1.40	1.46
1	A	292	ILE	CA-CB	5.21	1.60	1.54
1	A	42	VAL	CA-CB	5.12	1.59	1.53
1	B	326	ALA	CA-C	5.09	1.59	1.52
1	A	81	ARG	CA-C	5.05	1.58	1.52
1	B	325	VAL	N-CA	5.03	1.52	1.46

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	204	GLY	N-CA-C	-8.33	102.79	112.79
1	B	323	GLN	O-C-N	7.75	130.46	122.09
1	A	329	GLN	CA-C-O	-7.42	108.19	120.80
1	A	209	LYS	CA-C-N	7.38	134.99	121.70
1	A	209	LYS	C-N-CA	7.38	134.99	121.70
1	A	329	GLN	OE1-CD-NE2	7.00	129.60	122.60
1	A	201	ASN	CA-C-N	6.99	134.28	121.70
1	A	201	ASN	C-N-CA	6.99	134.28	121.70
1	A	108	LEU	N-CA-C	6.86	118.41	111.07
1	A	292	ILE	CB-CA-C	-6.64	103.47	111.97
1	A	15	ASP	CB-CA-C	-6.36	97.22	109.37
1	B	13	ILE	CB-CA-C	-6.21	102.48	110.98
1	B	323	GLN	CA-C-O	-6.17	114.34	120.70
1	A	292	ILE	N-CA-CB	6.14	117.73	110.55
1	A	329	GLN	CG-CD-NE2	-5.83	107.65	116.40
1	B	94	ASP	N-CA-C	5.62	119.86	112.89
1	B	73	THR	N-CA-C	5.56	117.08	109.18
1	A	210	VAL	N-CA-C	5.30	125.83	111.00
1	A	11	ARG	N-CA-C	5.29	116.32	109.65
1	B	316	TYR	N-CA-C	5.19	117.61	111.33
1	A	44	LEU	N-CA-C	5.18	116.22	109.64
1	B	20	VAL	CB-CA-C	5.06	115.61	110.65

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	210	VAL	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	318	ASP	Sidechain

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	2641	0	2637	106	0
1	B	2632	0	2631	105	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
3	A	9	0	8	2	0
3	B	9	0	8	2	0
4	A	16	0	0	0	0
4	B	16	0	0	0	0
5	A	32	0	11	3	0
6	A	17	0	9	1	0
7	B	9	0	0	0	0
8	A	94	0	0	13	0
8	B	33	0	0	7	0
All	All	5518	0	5304	208	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

All (208) 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:323:GLN:CD	1:B:323:GLN:CG	1.74	1.58
1:A:329:GLN:CD	1:A:329:GLN:NE2	1.76	1.42
1:A:329:GLN:O	1:A:329:GLN:C	1.72	1.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:ARG:HD2	5:A:404:GTP:O6	1.38	1.21
1:A:245:ASP:HB2	1:A:246:ASN:HB3	1.28	1.12
1:A:245:ASP:CB	1:A:246:ASN:HB3	1.78	1.12
1:A:201:ASN:HB3	1:A:202:ASP:HB3	1.15	1.10
1:A:246:ASN:HD21	1:A:248:VAL:HG23	1.28	0.96
1:B:292:ILE:HD11	1:B:301:LEU:HD21	1.50	0.94
1:A:201:ASN:CB	1:A:202:ASP:HB3	1.98	0.94
1:A:201:ASN:HB3	1:A:202:ASP:CB	1.98	0.94
1:A:34:LYS:HD2	8:A:584:HOH:O	1.70	0.90
1:A:237:VAL:HG23	1:A:238:ALA:H	1.37	0.90
1:B:30:TYR:CD1	1:B:196:PHE:HE1	1.91	0.88
1:B:178:ILE:H	1:B:178:ILE:HD12	1.41	0.85
3:A:500:MET:SD	6:A:501:5AD:C4'	2.67	0.83
1:B:124:ASN:HB3	1:B:165:ASN:ND2	1.95	0.81
1:A:245:ASP:CB	1:A:246:ASN:CB	2.58	0.80
1:B:261:CYS:HB2	1:B:318:ASP:OD2	1.84	0.76
1:A:81:ARG:HD3	8:A:525:HOH:O	1.84	0.76
1:A:315:ARG:NH2	1:B:9:LEU:O	2.19	0.76
1:A:329:GLN:HA	1:B:14:ARG:NH2	2.02	0.75
1:A:9:LEU:O	1:B:315:ARG:NH2	2.20	0.74
1:B:268:ARG:HD2	1:B:279:LEU:HD23	1.70	0.74
1:B:301:LEU:HD22	1:B:305:PHE:CE1	2.22	0.74
1:A:303:GLU:HG2	8:A:552:HOH:O	1.86	0.73
1:A:58:ILE:HD13	1:A:269:LEU:HD11	1.71	0.72
1:B:266:ARG:HD3	8:B:510:HOH:O	1.88	0.72
1:A:266:ARG:CD	5:A:404:GTP:O6	2.30	0.71
1:A:245:ASP:HB3	1:A:246:ASN:CB	2.20	0.71
1:A:245:ASP:HB3	1:A:246:ASN:HB3	1.71	0.71
1:A:202:ASP:CG	1:A:203:ASN:HA	2.17	0.70
1:A:237:VAL:HG23	1:A:238:ALA:N	2.06	0.70
1:A:81:ARG:CD	8:A:525:HOH:O	2.37	0.69
1:B:128:ASP:O	1:B:173:ASN:ND2	2.25	0.69
1:A:69:LYS:HD3	8:A:539:HOH:O	1.93	0.69
1:A:224:PHE:HB2	1:A:226:ILE:HD11	1.75	0.68
1:B:30:TYR:CD1	1:B:196:PHE:CE1	2.78	0.68
1:B:87:ILE:CD1	1:B:115:LEU:HD22	2.23	0.68
1:B:199:VAL:HG13	1:B:204:GLY:O	1.94	0.68
1:B:324:THR:O	1:B:328:ARG:HG2	1.95	0.66
1:B:292:ILE:HD11	1:B:301:LEU:CD2	2.26	0.66
1:B:197:MET:HE1	1:B:280:PHE:CZ	2.29	0.66
1:B:87:ILE:HD12	1:B:115:LEU:CD2	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:LYS:NZ	1:A:239:LYS:HG3	2.10	0.66
1:A:14:ARG:NE	8:A:579:HOH:O	2.30	0.64
1:A:126:SER:HB3	2:A:403:SO4:O1	1.96	0.64
1:B:124:ASN:HB3	1:B:165:ASN:HD21	1.62	0.64
1:B:87:ILE:HD12	1:B:115:LEU:HD22	1.78	0.64
1:B:323:GLN:CD	1:B:323:GLN:CB	2.69	0.64
1:B:124:ASN:HD21	1:B:192:ARG:NH2	1.97	0.64
1:A:17:ARG:HD3	1:A:71:ARG:HB3	1.80	0.63
1:A:229:VAL:HG12	1:A:230:GLU:O	1.99	0.63
1:B:146:THR:HG22	1:B:150:GLU:OE2	1.98	0.63
1:A:8:LYS:HE2	1:A:310:GLN:O	1.99	0.63
1:A:47:ASN:ND2	1:A:47:ASN:H	1.95	0.63
1:A:202:ASP:OD1	1:A:203:ASN:HA	1.99	0.62
1:A:163:LYS:NZ	5:A:404:GTP:O3G	2.33	0.62
1:B:71:ARG:NH2	1:B:124:ASN:OD1	2.33	0.61
1:B:161:ASN:HD21	1:B:163:LYS:HE2	1.67	0.60
1:A:14:ARG:HB2	1:A:265:THR:HG23	1.83	0.60
1:B:71:ARG:HD3	8:B:531:HOH:O	2.00	0.60
1:A:14:ARG:HB2	1:A:265:THR:CG2	2.32	0.59
1:A:169:GLN:HE21	1:A:209:LYS:NZ	2.00	0.59
1:B:132:ASP:OD2	1:B:144:LYS:HB3	2.04	0.58
1:B:124:ASN:HD21	1:B:192:ARG:HH22	1.50	0.58
1:A:237:VAL:CG2	1:A:238:ALA:H	2.12	0.58
1:B:30:TYR:HD1	1:B:196:PHE:HE1	1.47	0.58
1:A:329:GLN:NE2	1:A:329:GLN:CG	2.66	0.57
1:B:46:LYS:HG2	8:B:529:HOH:O	2.03	0.57
1:B:205:TRP:CZ2	1:B:320:ARG:HB2	2.39	0.57
1:B:237:VAL:HG23	1:B:238:ALA:H	1.69	0.57
1:A:237:VAL:HG12	8:A:594:HOH:O	2.04	0.56
1:B:130:ILE:HG22	1:B:176:GLN:OE1	2.06	0.56
1:A:246:ASN:ND2	1:A:248:VAL:HG23	2.10	0.56
1:A:259:SER:HB2	1:A:318:ASP:OD1	2.06	0.55
1:B:205:TRP:CD2	1:B:256:VAL:HG13	2.42	0.55
1:A:71:ARG:NH1	1:A:124:ASN:ND2	2.56	0.54
1:A:268:ARG:HH11	1:A:268:ARG:CG	2.20	0.54
1:B:184:PHE:CD1	1:B:191:ILE:HD12	2.43	0.54
1:B:170:LYS:O	1:B:174:ASP:HB2	2.07	0.54
1:A:3:GLU:OE2	1:A:3:GLU:O	2.26	0.54
1:B:181:LEU:HD11	1:B:220:ILE:HG12	1.90	0.54
1:A:5:ILE:HD13	1:A:65:LEU:HD22	1.90	0.53
1:A:169:GLN:HA	1:A:209:LYS:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:197:MET:CE	1:B:280:PHE:CZ	2.92	0.53
1:A:47:ASN:H	1:A:47:ASN:HD22	1.57	0.53
1:B:205:TRP:CE2	1:B:320:ARG:HB2	2.43	0.53
1:A:14:ARG:CD	8:A:579:HOH:O	2.56	0.52
1:A:4:GLN:HG3	1:A:14:ARG:NH2	2.23	0.52
1:B:266:ARG:NH2	8:B:524:HOH:O	2.42	0.52
1:A:72:ILE:CD1	1:A:87:ILE:CD1	2.88	0.52
1:B:231:PRO:O	1:B:232:LYS:C	2.53	0.51
1:A:202:ASP:N	1:A:203:ASN:HB3	2.25	0.51
1:B:127:LEU:HD13	1:B:148:ILE:CG2	2.40	0.51
1:B:184:PHE:HD1	1:B:191:ILE:HD12	1.74	0.51
1:B:53:ASP:HA	1:B:89:LYS:HE2	1.91	0.51
1:B:169:GLN:H	1:B:173:ASN:HB3	1.74	0.51
1:B:280:PHE:CD2	1:B:316:TYR:CE2	2.99	0.51
1:B:30:TYR:CE1	1:B:196:PHE:CE1	2.98	0.51
1:B:318:ASP:O	1:B:321:THR:HB	2.11	0.50
1:A:202:ASP:OD2	1:A:327:ASN:ND2	2.44	0.50
1:B:144:LYS:HD2	8:B:533:HOH:O	2.11	0.50
1:B:7:ASP:HB2	1:B:312:ARG:O	2.11	0.50
1:A:165:ASN:HD21	1:A:192:ARG:HH11	1.60	0.50
1:B:29:ASP:OD1	1:B:29:ASP:N	2.44	0.50
1:B:197:MET:CE	1:B:280:PHE:HZ	2.24	0.50
1:A:268:ARG:CG	1:A:268:ARG:NH1	2.75	0.49
1:A:5:ILE:HG22	1:A:309:TRP:HD1	1.77	0.49
1:A:254:THR:OG1	1:A:258:GLN:HB3	2.11	0.49
1:B:75:GLY:O	3:B:501:MET:HG3	2.13	0.49
1:B:316:TYR:O	1:B:320:ARG:HG2	2.12	0.49
1:A:288:VAL:O	1:A:292:ILE:HG12	2.12	0.49
1:B:300:GLU:O	1:B:303:GLU:HG2	2.13	0.49
1:A:201:ASN:CA	1:A:202:ASP:HB3	2.43	0.49
1:B:5:ILE:H	1:B:5:ILE:HD12	1.77	0.49
1:A:4:GLN:HG3	1:A:14:ARG:HH21	1.78	0.48
1:A:71:ARG:HH12	1:A:124:ASN:ND2	2.10	0.48
1:B:203:ASN:O	1:B:320:ARG:HD3	2.13	0.48
1:B:323:GLN:O	1:B:326:ALA:HB3	2.13	0.48
1:A:268:ARG:HE	1:A:279:LEU:HD23	1.77	0.48
1:A:233:TYR:O	1:A:236:GLU:HB2	2.14	0.48
1:B:5:ILE:HG12	1:B:65:LEU:HD22	1.95	0.48
1:B:241:TYR:O	1:B:249:GLN:HG2	2.13	0.48
1:A:242:ARG:HD2	8:A:567:HOH:O	2.13	0.47
1:B:254:THR:HB	1:B:258:GLN:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:ARG:HH11	1:A:268:ARG:HG3	1.78	0.47
1:A:196:PHE:CE2	1:A:198:ASP:HB2	2.49	0.47
3:A:500:MET:SD	3:A:500:MET:C	2.97	0.47
1:A:220:ILE:HG22	1:A:226:ILE:CD1	2.45	0.47
1:A:268:ARG:NH2	1:A:279:LEU:HG	2.29	0.47
1:B:47:ASN:HD22	1:B:47:ASN:C	2.21	0.47
1:A:315:ARG:HD2	8:A:588:HOH:O	2.15	0.47
1:B:127:LEU:HD13	1:B:148:ILE:HG21	1.96	0.47
1:B:224:PHE:HB2	1:B:226:ILE:HD13	1.96	0.47
1:B:274:LYS:NZ	1:B:284:ASP:HB3	2.30	0.46
1:B:61:VAL:CG1	1:B:302:LYS:HA	2.45	0.46
1:B:131:ASP:HB2	1:B:176:GLN:HE22	1.80	0.46
1:A:14:ARG:HD2	8:A:579:HOH:O	2.16	0.46
1:A:213:LYS:HZ1	1:A:239:LYS:HG3	1.80	0.46
1:B:122:ARG:HD2	8:B:515:HOH:O	2.14	0.46
1:B:132:ASP:O	1:B:136:GLN:HB2	2.15	0.46
1:B:197:MET:HE1	1:B:280:PHE:HZ	1.80	0.46
1:A:5:ILE:HG22	1:A:309:TRP:CD1	2.51	0.45
1:A:272:ASP:OD2	1:A:274:LYS:CE	2.64	0.45
1:A:185:LYS:NZ	1:A:245:ASP:OD2	2.37	0.45
1:A:127:LEU:O	1:A:166:VAL:HG22	2.16	0.45
1:B:184:PHE:HA	1:B:187:LYS:HB2	1.98	0.45
1:A:169:GLN:NE2	1:A:209:LYS:NZ	2.65	0.45
1:A:132:ASP:OD1	1:A:145:ALA:N	2.50	0.45
1:B:125:VAL:O	1:B:164:VAL:HA	2.16	0.45
1:A:114:LYS:HE3	8:A:510:HOH:O	2.17	0.45
1:A:329:GLN:HA	1:B:14:ARG:CZ	2.47	0.44
1:B:254:THR:HG22	1:B:257:SER:OG	2.16	0.44
1:B:26:PHE:HZ	1:B:148:ILE:HD11	1.80	0.44
1:A:72:ILE:CD1	1:A:87:ILE:HD11	2.47	0.44
1:A:245:ASP:HB3	1:A:246:ASN:HB2	1.95	0.44
1:A:326:ALA:HB2	1:B:12:PRO:HD3	1.99	0.44
1:B:237:VAL:HG23	1:B:238:ALA:N	2.33	0.44
1:A:217:LEU:O	1:A:221:GLU:HG2	2.18	0.44
1:B:115:LEU:O	1:B:120:LEU:HB2	2.18	0.44
1:B:44:LEU:HD11	1:B:272:ASP:HB3	1.99	0.44
1:A:232:LYS:HB3	1:A:233:TYR:HD2	1.83	0.43
1:B:213:LYS:HB3	1:B:254:THR:HG23	2.01	0.43
1:A:5:ILE:HG12	1:A:306:LYS:HG3	2.00	0.43
1:B:278:CYS:C	1:B:280:PHE:H	2.25	0.43
1:A:212:THR:O	1:A:216:MET:HE3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:ILE:HB	1:B:180:MET:HG2	2.00	0.43
1:B:130:ILE:HD11	1:B:149:LEU:HD21	1.99	0.43
1:B:298:ASP:C	1:B:300:GLU:H	2.27	0.43
1:B:323:GLN:O	1:B:327:ASN:N	2.49	0.43
1:A:130:ILE:HG22	1:A:176:GLN:OE1	2.19	0.43
1:A:265:THR:HG23	1:A:265:THR:O	2.18	0.43
1:B:178:ILE:H	1:B:178:ILE:CD1	2.13	0.43
1:A:221:GLU:OE2	1:A:226:ILE:HB	2.19	0.42
1:A:268:ARG:NE	1:A:279:LEU:HD23	2.34	0.42
1:B:167:VAL:HG11	8:B:522:HOH:O	2.17	0.42
1:A:272:ASP:OD2	1:A:274:LYS:HE3	2.20	0.42
1:B:246:ASN:HD22	1:B:246:ASN:H	1.68	0.42
1:A:114:LYS:HB3	1:A:114:LYS:HE2	1.81	0.42
1:B:76:GLU:HB3	1:B:79:MET:CG	2.49	0.42
1:A:81:ARG:HD2	8:A:525:HOH:O	2.14	0.42
1:A:289:LYS:HE2	1:A:289:LYS:HB3	1.60	0.42
1:B:297:THR:OG1	1:B:300:GLU:HB2	2.20	0.42
1:B:108:LEU:HD13	1:B:155:ALA:HB2	2.02	0.41
1:A:169:GLN:HE21	1:A:209:LYS:HZ1	1.65	0.41
1:A:103:THR:O	1:A:125:VAL:HA	2.20	0.41
1:A:202:ASP:H	1:A:203:ASN:HB3	1.86	0.41
1:A:238:ALA:HB2	1:A:253:ILE:HG12	2.02	0.41
1:B:8:LYS:HB2	1:B:313:ASP:HB3	2.01	0.41
1:B:126:SER:HB2	3:B:501:MET:O	2.21	0.41
1:A:61:VAL:HG13	1:A:302:LYS:HG3	2.02	0.41
1:A:86:LEU:O	1:A:90:LEU:HG	2.20	0.41
1:A:168:ILE:HD11	1:A:193:PHE:CD2	2.56	0.41
1:A:145:ALA:O	1:A:149:LEU:HG	2.21	0.41
1:B:124:ASN:HB3	1:B:165:ASN:HD22	1.79	0.41
1:B:81:ARG:O	1:B:82:ASP:HB2	2.20	0.41
1:B:124:ASN:HA	1:B:163:LYS:O	2.20	0.41
1:B:28:CYS:HA	1:B:138:ILE:O	2.20	0.41
1:B:147:THR:O	1:B:151:GLN:HG2	2.21	0.41
1:B:279:LEU:H	1:B:279:LEU:HG	1.77	0.41
1:A:237:VAL:CG2	1:A:238:ALA:N	2.75	0.40
1:B:301:LEU:CD2	1:B:305:PHE:CE1	2.99	0.40
1:A:71:ARG:HH12	1:A:124:ASN:HD22	1.70	0.40
1:B:52:PHE:CD2	1:B:86:LEU:HB2	2.56	0.40
1:A:44:LEU:HA	1:A:45:PRO:HD3	1.99	0.40
1:B:254:THR:HB	1:B:258:GLN:CB	2.51	0.40
1:B:205:TRP:CE3	1:B:256:VAL:HG13	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	325/340 (96%)	296 (91%)	22 (7%)	7 (2%)	5	3
1	B	324/340 (95%)	297 (92%)	23 (7%)	4 (1%)	10	8
All	All	649/680 (95%)	593 (91%)	45 (7%)	11 (2%)	7	5

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	201	ASN
1	A	202	ASP
1	A	237	VAL
1	B	36	VAL
1	B	170	LYS
1	B	258	GLN
1	A	281	ALA
1	A	212	THR
1	A	258	GLN
1	B	295	GLY
1	A	210	VAL

5.3.2 Protein sidechains [i](#)

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	291/302 (96%)	263 (90%)	28 (10%)	8	7
1	B	290/302 (96%)	250 (86%)	40 (14%)	3	2
All	All	581/604 (96%)	513 (88%)	68 (12%)	5	4

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	A	15	ASP
1	A	18	LEU
1	A	34	LYS
1	A	47	ASN
1	A	69	LYS
1	A	91	ASN
1	A	120	LEU
1	A	124	ASN
1	A	130	ILE
1	A	134	LEU
1	A	175	ASP
1	A	178	ILE
1	A	192	ARG
1	A	203	ASN
1	A	210	VAL
1	A	232	LYS
1	A	254	THR
1	A	255	SER
1	A	256	VAL
1	A	259	SER
1	A	265	THR
1	A	266	ARG
1	A	268	ARG
1	A	282	THR
1	A	292	ILE
1	A	311	ILE
1	A	315	ARG
1	B	13	ILE
1	B	19	SER
1	B	20	VAL
1	B	29	ASP
1	B	39	ASP
1	B	40	ASP
1	B	42	VAL

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Mol	Chain	Res	Type
1	B	47	ASN
1	B	69	LYS
1	B	71	ARG
1	B	73	THR
1	B	83	LEU
1	B	94	ASP
1	B	120	LEU
1	B	130	ILE
1	B	134	LEU
1	B	136	GLN
1	B	142	ASN
1	B	143	ILE
1	B	144	LYS
1	B	174	ASP
1	B	175	ASP
1	B	178	ILE
1	B	213	LYS
1	B	226	ILE
1	B	245	ASP
1	B	246	ASN
1	B	254	THR
1	B	255	SER
1	B	258	GLN
1	B	279	LEU
1	B	289	LYS
1	B	292	ILE
1	B	296	VAL
1	B	297	THR
1	B	298	ASP
1	B	299	GLU
1	B	301	LEU
1	B	311	ILE
1	B	324	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	47	ASN
1	A	91	ASN
1	A	92	GLN
1	A	124	ASN

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Mol	Chain	Res	Type
1	A	136	GLN
1	A	165	ASN
1	A	169	GLN
1	A	203	ASN
1	A	246	ASN
1	A	258	GLN
1	B	47	ASN
1	B	136	GLN
1	B	161	ASN
1	B	243	HIS
1	B	246	ASN
1	B	258	GLN

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](#)

11 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	MET	B	501	4	7,8,8	0.94	0	5,9,9	1.04	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MET	A	500	4	7,8,8	1.93	1 (14%)	5,9,9	0.84	0
4	SF4	A	402	1,5	0,12,12	-	-	-		
4	SF4	B	402	1	0,12,12	-	-	-		
2	SO4	B	403	-	4,4,4	0.35	0	6,6,6	0.31	0
5	GTP	A	404	4	33,34,34	1.22	3 (9%)	50,54,54	1.84	14 (28%)
6	5AD	A	501	-	19,19,20	1.09	1 (5%)	27,28,30	2.62	13 (48%)
4	SF4	B	401	1,3	0,12,12	-	-	-		
2	SO4	A	403	-	4,4,4	0.42	0	6,6,6	1.15	1 (16%)
7	POP	B	404	-	6,8,8	0.62	0	12,13,13	1.07	0
4	SF4	A	401	1,3	0,12,12	-	-	-		

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	MET	B	501	4	-	3/8/8/8	-
3	MET	A	500	4	-	0/8/8/8	-
4	SF4	A	402	1,5	-	-	0/6/5/5
4	SF4	B	402	1	-	-	0/6/5/5
6	5AD	A	501	-	-	0/4/17/20	0/3/3/3
5	GTP	A	404	4	-	8/22/38/38	0/3/3/3
4	SF4	B	401	1,3	-	-	0/6/5/5
7	POP	B	404	-	-	2/6/6/6	-
4	SF4	A	401	1,3	-	-	0/6/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	MET	OXT-C	4.72	1.45	1.30
5	A	404	GTP	C2-N3	3.57	1.41	1.33
5	A	404	GTP	PA-O3A	3.03	1.62	1.59
5	A	404	GTP	PB-O3A	2.85	1.62	1.59
6	A	501	5AD	C8-N7	2.60	1.36	1.31

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	501	5AD	C5-C4-N3	-5.93	118.56	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	501	5AD	O2'-C2'-C3'	-5.11	99.85	111.97
5	A	404	GTP	C5-C4-N3	-5.04	120.36	128.39
5	A	404	GTP	C2-N3-C4	4.66	120.32	112.30
6	A	501	5AD	N3-C2-N1	-4.44	121.87	128.58
5	A	404	GTP	C2'-C1'-N9	-4.18	101.60	113.25
5	A	404	GTP	N9-C4-N3	4.07	134.09	125.95
6	A	501	5AD	C2-N3-C4	3.68	120.83	111.83
6	A	501	5AD	N9-C8-N7	-3.65	108.76	113.94
6	A	501	5AD	C4-C5-N7	-3.64	106.42	110.58
6	A	501	5AD	N3-C4-N9	3.48	133.09	127.17
6	A	501	5AD	C5-N7-C8	3.25	108.56	103.45
5	A	404	GTP	O3G-PG-O3B	3.19	115.35	104.64
5	A	404	GTP	O6-C6-C5	-3.04	118.50	126.53
5	A	404	GTP	C5-C6-N1	2.89	120.62	113.25
6	A	501	5AD	C3'-C2'-C1'	2.69	104.53	101.76
5	A	404	GTP	N1-C2-N3	-2.61	118.54	123.32
5	A	404	GTP	N9-C8-N7	-2.50	108.77	113.40
6	A	501	5AD	C4'-C3'-C2'	2.40	105.46	101.63
6	A	501	5AD	C5-C4-N9	2.33	108.35	105.81
5	A	404	GTP	C8-N7-C5	2.27	108.30	104.26
6	A	501	5AD	O3'-C3'-C2'	-2.27	106.96	111.43
5	A	404	GTP	C2-N1-C6	-2.26	121.02	125.11
5	A	404	GTP	O3B-PG-O1G	-2.23	99.30	111.04
5	A	404	GTP	C3'-C2'-C1'	2.19	105.60	101.46
2	A	403	SO4	O3-S-O1	-2.18	98.14	109.56
3	B	501	MET	OXT-C-O	-2.09	119.33	124.08
6	A	501	5AD	C4-N9-C8	2.06	107.90	105.74
5	A	404	GTP	O4'-C1'-N9	2.01	112.92	108.36

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	501	MET	O-C-CA-N
5	A	404	GTP	PB-O3B-PG-O3G
5	A	404	GTP	C5'-O5'-PA-O3A
5	A	404	GTP	C5'-O5'-PA-O2A
7	B	404	POP	P1-O-P2-O6
3	B	501	MET	OXT-C-CA-N
5	A	404	GTP	PB-O3B-PG-O1G
5	A	404	GTP	PB-O3A-PA-O5'
3	B	501	MET	C-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
7	B	404	POP	P1-O-P2-O4
5	A	404	GTP	O4'-C4'-C5'-O5'
5	A	404	GTP	PB-O3A-PA-O1A
5	A	404	GTP	C3'-C4'-C5'-O5'

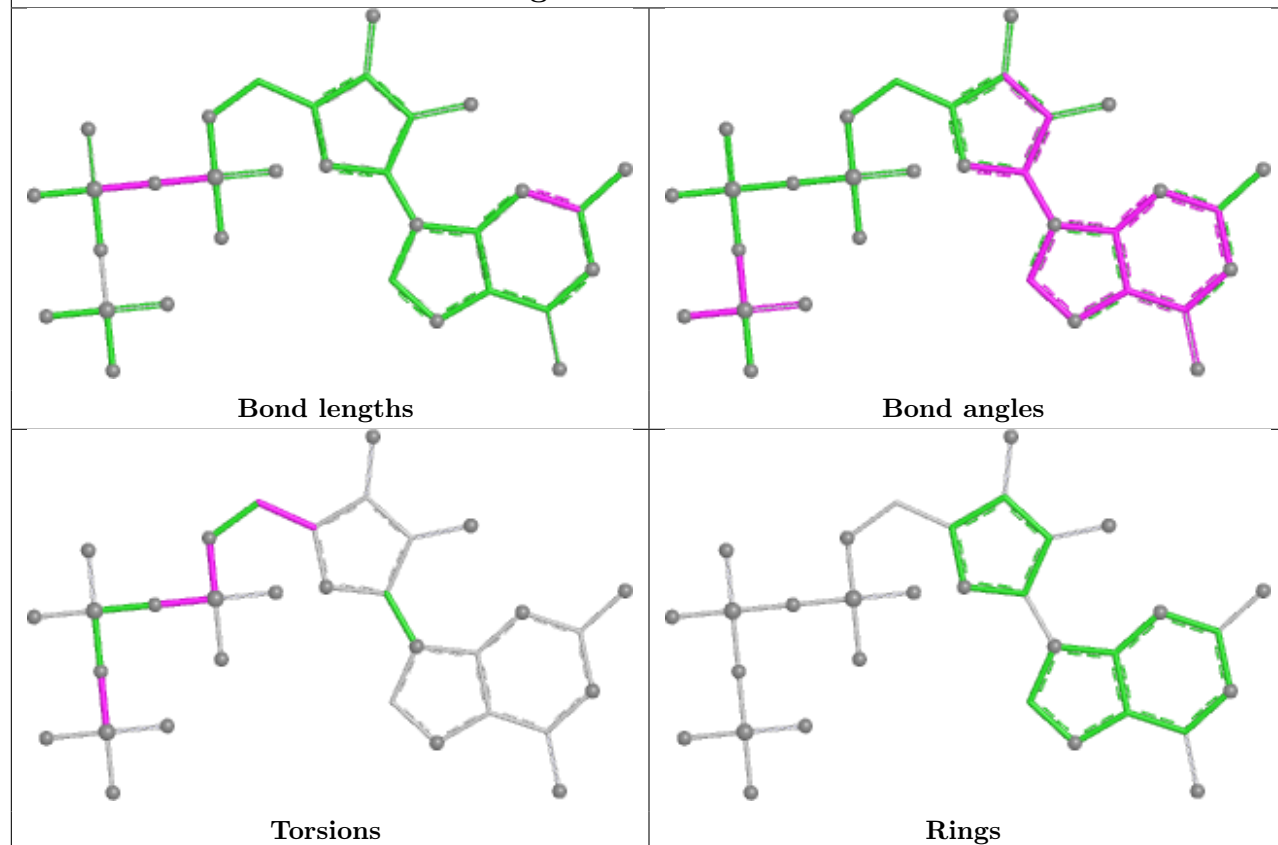
There are no ring outliers.

5 monomers are involved in 8 short contacts:

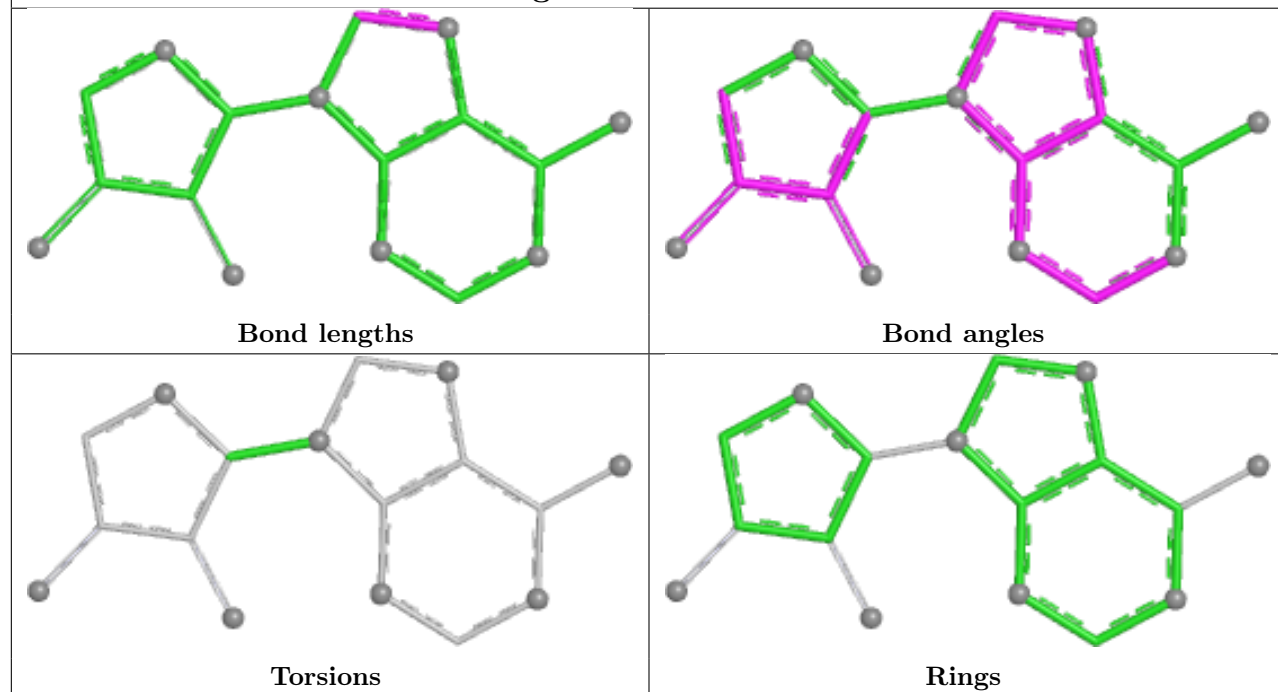
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	MET	2	0
3	A	500	MET	2	0
5	A	404	GTP	3	0
6	A	501	5AD	1	0
2	A	403	SO4	1	0

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.

Ligand GTP A 404



Ligand 5AD A 501



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	327/340 (96%)	0.94	27 (8%) 17 20	54, 63, 72, 83	0
1	B	326/340 (95%)	1.29	50 (15%) 5 6	54, 63, 71, 75	0
All	All	653/680 (96%)	1.11	77 (11%) 9 10	54, 63, 72, 83	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	325	VAL	5.0
1	B	251	GLY	4.2
1	B	206	ASP	4.1
1	B	171	GLY	4.1
1	B	261	CYS	4.1
1	B	254	THR	3.9
1	B	226	ILE	3.9
1	B	88	ALA	3.7
1	B	140	ASN	3.6
1	A	260	PHE	3.6
1	B	159	GLY	3.6
1	B	56	ALA	3.6
1	A	282	THR	3.5
1	B	35	GLU	3.5
1	B	135	PHE	3.5
1	B	282	THR	3.4
1	B	292	ILE	3.2
1	B	303	GLU	3.2
1	B	255	SER	3.1
1	B	98	ASP	3.1
1	B	283	VAL	3.1
1	B	30	TYR	3.1
1	B	222	GLN	3.0
1	A	88	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	201	ASN	2.9
1	A	233	TYR	2.8
1	B	189	ILE	2.7
1	A	247	GLY	2.7
1	A	236	GLU	2.7
1	A	51	THR	2.7
1	B	36	VAL	2.6
1	A	254	THR	2.6
1	B	278	CYS	2.6
1	A	226	ILE	2.5
1	B	10	GLY	2.5
1	B	260	PHE	2.5
1	B	5	ILE	2.5
1	B	132	ASP	2.5
1	B	59	ALA	2.5
1	A	38	GLY	2.5
1	B	324	THR	2.4
1	A	40	ASP	2.4
1	A	324	THR	2.4
1	A	237	VAL	2.4
1	B	9	LEU	2.4
1	B	233	TYR	2.4
1	A	246	ASN	2.4
1	B	7	ASP	2.4
1	B	201	ASN	2.4
1	B	145	ALA	2.4
1	A	36	VAL	2.4
1	A	248	VAL	2.4
1	B	41	PHE	2.4
1	B	87	ILE	2.4
1	A	29	ASP	2.3
1	B	228	PRO	2.3
1	B	137	SER	2.3
1	B	177	ILE	2.3
1	B	40	ASP	2.3
1	B	166	VAL	2.3
1	A	118	ALA	2.2
1	B	136	GLN	2.2
1	A	85	VAL	2.2
1	A	283	VAL	2.2
1	B	279	LEU	2.2
1	B	318	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	251	GLY	2.2
1	A	3	GLU	2.2
1	B	42	VAL	2.2
1	B	326	ALA	2.2
1	B	310	GLN	2.1
1	A	145	ALA	2.1
1	B	158	ILE	2.1
1	A	186	ASP	2.1
1	A	156	THR	2.0
1	B	55	MET	2.0
1	A	112	GLY	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](#)

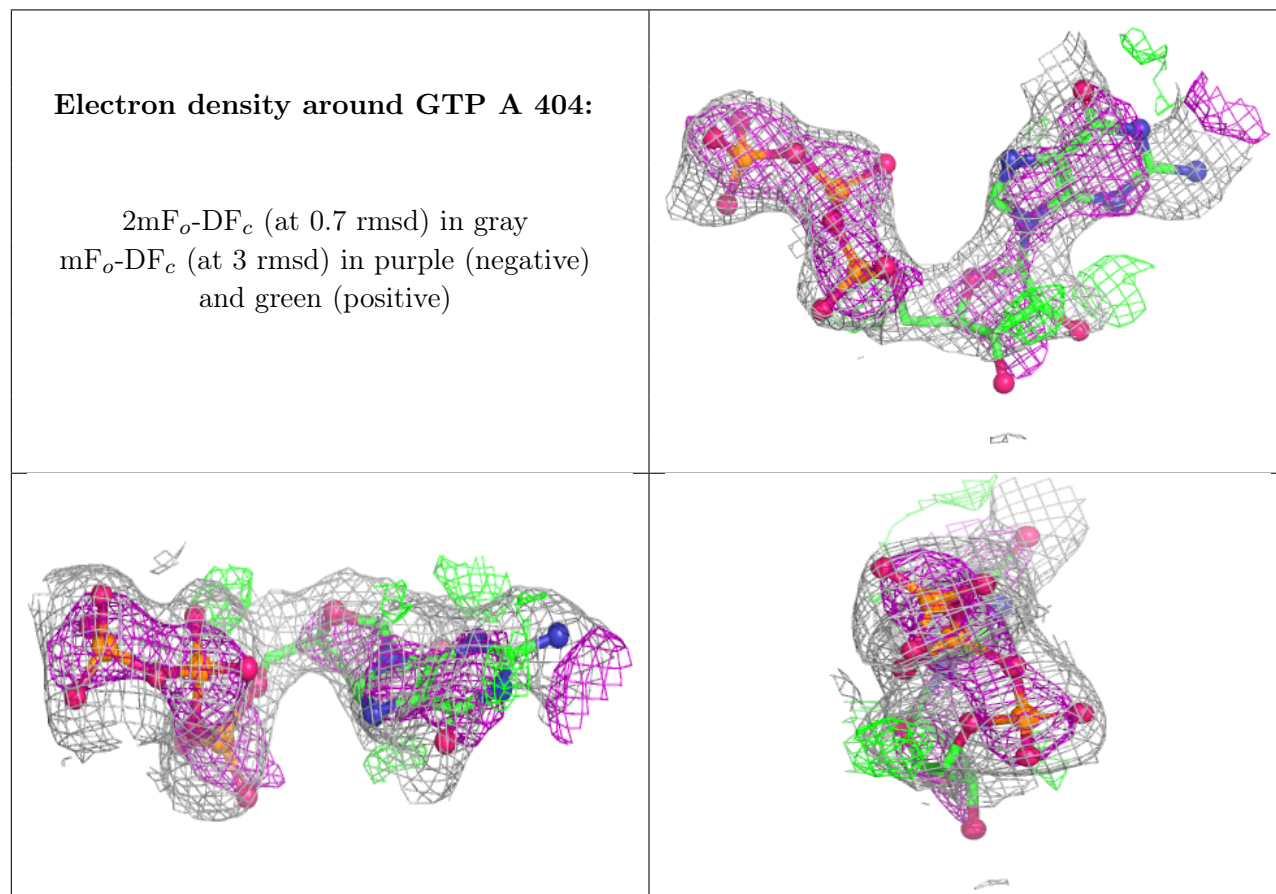
There are no oligosaccharides in this entry.

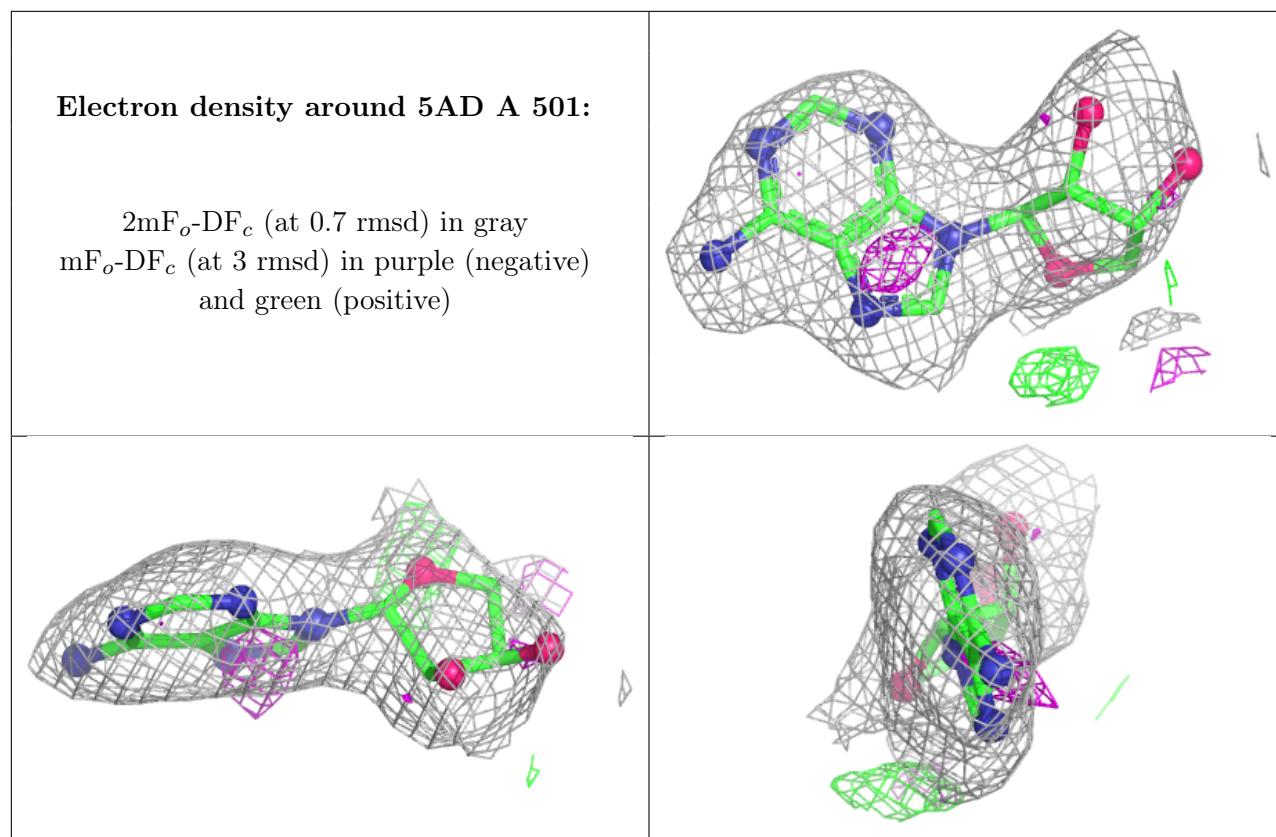
6.4 Ligands [i](#)

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
7	POP	B	404	9/9	0.47	0.16	114,115,116,117	0
3	MET	B	501	9/9	0.77	0.23	83,85,85,85	0
5	GTP	A	404	32/32	0.83	0.15	74,78,81,85	0
6	5AD	A	501	17/18	0.86	0.12	77,78,82,82	0
2	SO4	B	403	5/5	0.87	0.19	94,95,96,98	0
4	SF4	B	402	8/8	0.93	0.10	68,70,72,77	0
3	MET	A	500	9/9	0.94	0.20	49,55,60,60	0
2	SO4	A	403	5/5	0.95	0.25	65,66,67,72	0
4	SF4	B	401	8/8	0.95	0.09	64,67,68,69	0
4	SF4	A	402	8/8	0.98	0.10	52,53,54,61	0
4	SF4	A	401	8/8	0.99	0.10	42,46,48,48	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 [i](#)

There are no such residues in this entry.