Full wwPDB X-ray Structure Validation Report (i)

Nov 20, 2023 – 08:18 PM JST

PDB ID	:	7DC8
Title	:	Crystal structure of Switch Ab Fab and hIL6R in complex with ATP
Authors	:	Kadono, S.; Fukami, T.A.; Kawauchi, H.; Torizawa, T.; Mimoto, F.
Deposited on	:	2020-10-23
Resolution	:	2.76 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 (i) 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 (i)) were used in the production of this report:

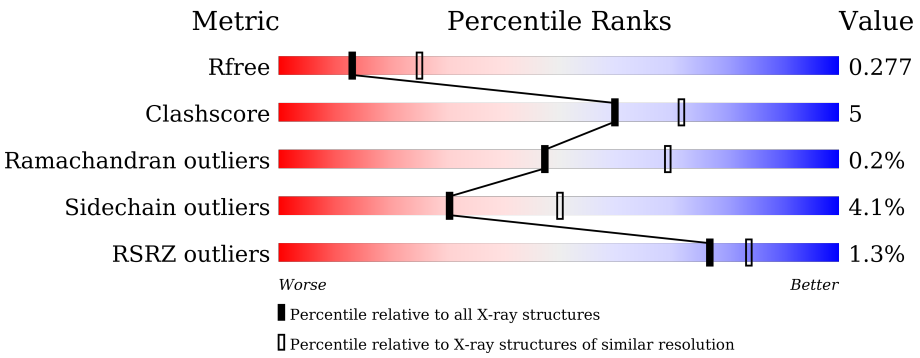
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.76 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}	130704	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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 <=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	216	85% 13% •
1	D	216	2% 89% 8% • •
2	B	230	% 77% 14% 9%
2	E	230	77% 14% 9%
3	C	218	2% 72% 13% 15%
3	F	218	2% 71% 12% • 16%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 9244 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 Switch Ab Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	212	1514	956	243	310	5	0	0	0
1	D	212	1536	969	251	311	5	0	0	0

- Molecule 2 is a protein called Switch Ab Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	209	1573	1004	259	304	6	0	0	0
2	E	209	1573	1006	257	304	6	0	1	0

- Molecule 3 is a protein called Interleukin-6 receptor subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	186	1439	920	243	267	9	0	0	0
3	F	184	1434	920	239	266	9	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	193	SER	CYS	engineered mutation	UNP P08887
C	321	ASP	-	expression tag	UNP P08887
C	322	TYR	-	expression tag	UNP P08887
C	323	LYS	-	expression tag	UNP P08887
C	324	ASP	-	expression tag	UNP P08887
C	325	ASP	-	expression tag	UNP P08887
C	326	ASP	-	expression tag	UNP P08887
C	327	ASP	-	expression tag	UNP P08887

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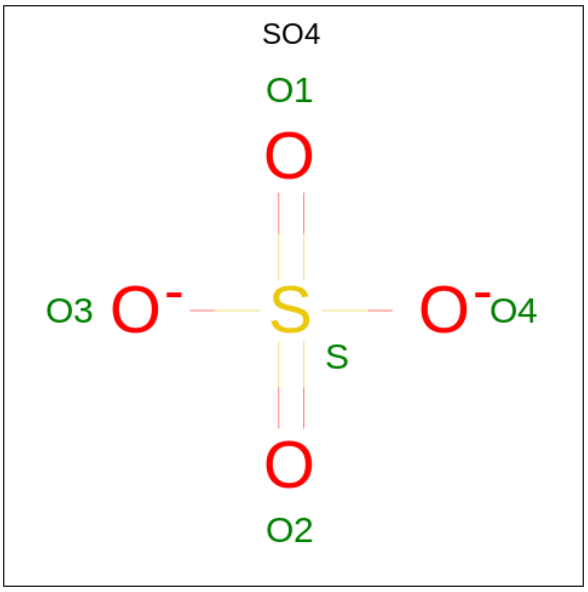
Chain	Residue	Modelled	Actual	Comment	Reference
C	328	LYS	-	expression tag	UNP P08887
F	193	SER	CYS	engineered mutation	UNP P08887
F	321	ASP	-	expression tag	UNP P08887
F	322	TYR	-	expression tag	UNP P08887
F	323	LYS	-	expression tag	UNP P08887
F	324	ASP	-	expression tag	UNP P08887
F	325	ASP	-	expression tag	UNP P08887
F	326	ASP	-	expression tag	UNP P08887
F	327	ASP	-	expression tag	UNP P08887
F	328	LYS	-	expression tag	UNP P08887

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

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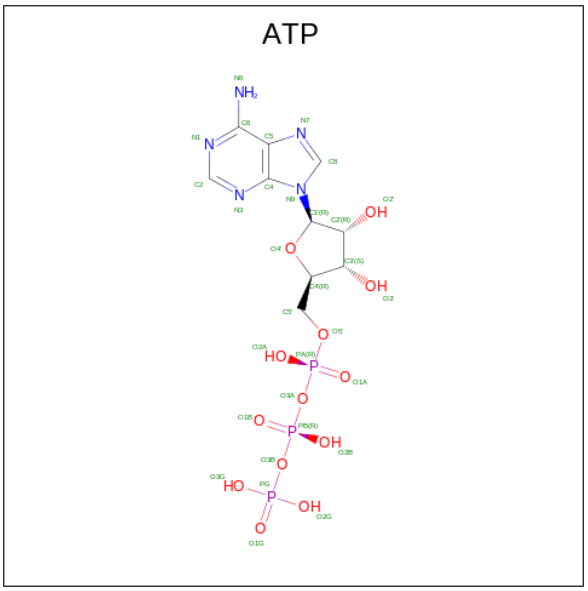
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	D	1	5	4	1	0	0
			Total	O	S		
4	E	1	5	4	1	0	0
			Total	O	S		
4	F	1	5	4	1	0	0
			Total	O	S		
4	F	1	5	4	1	0	0

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	B	1	31	10	5	13	3	0	0
			Total	C	N	O	P		
5	E	1	31	10	5	13	3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	4	4	4	0	0
			Total	O		
6	B	6	6	6	0	0
			Total	O		
6	C	9	9	9	0	0

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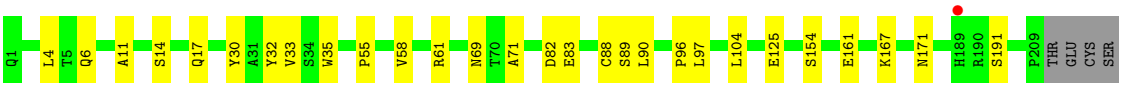
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	D	12	12	12	0	0
			Total	O		
6	E	22	22	22	0	0
			Total	O		
6	F	10	10	10	0	0

3 Residue-property plots (i)

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.

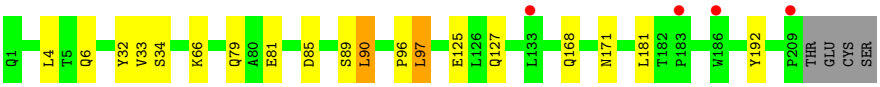
• Molecule 1: Switch Ab Fab light chain

Chain A: 85% 13%



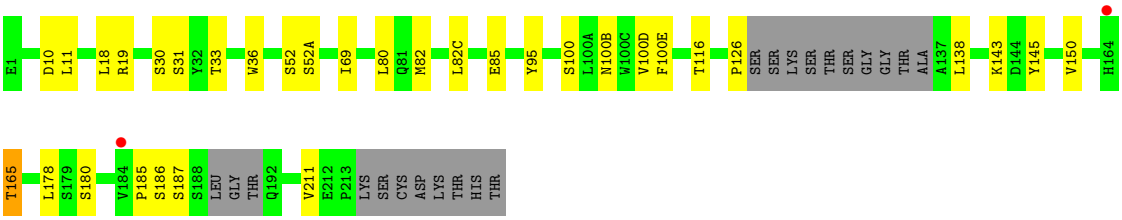
• Molecule 1: Switch Ab Fab light chain

Chain D: 2% 89% 8%



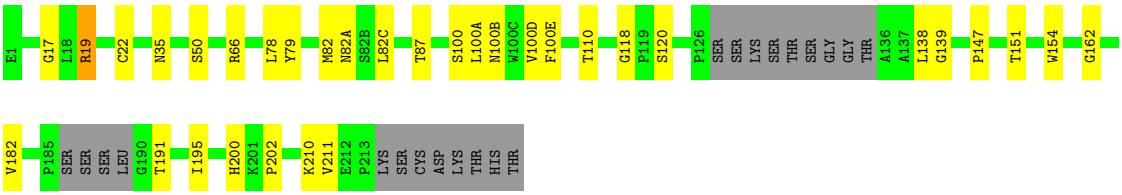
• Molecule 2: Switch Ab Fab heavy chain

Chain B: % 77% 14% 9%



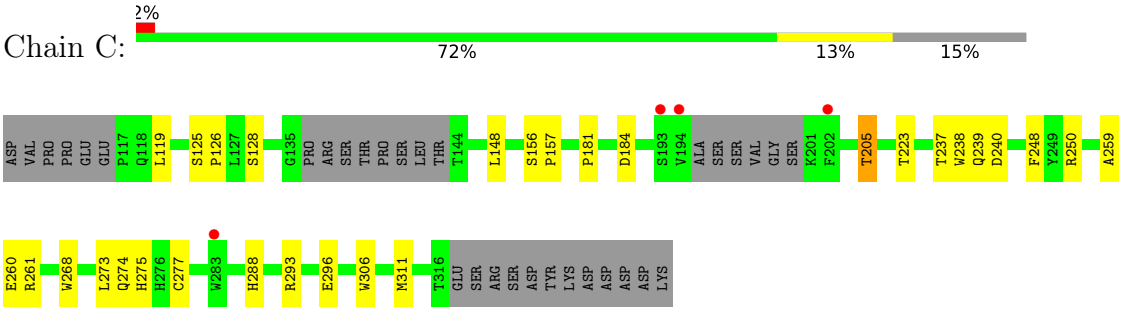
• Molecule 2: Switch Ab Fab heavy chain

Chain E: 77% 14% 9%



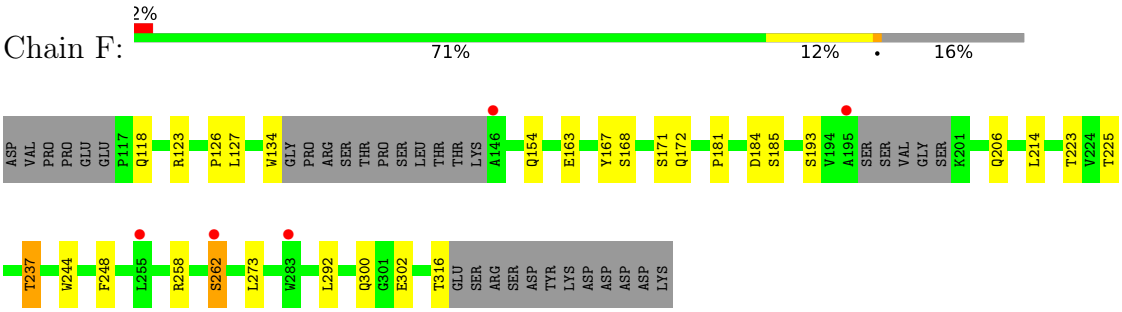
• Molecule 3: Interleukin-6 receptor subunit alpha

Chain C:



- Molecule 3: Interleukin-6 receptor subunit alpha

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	103.04Å 185.61Å 152.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.09 – 2.76 90.09 – 2.76	Depositor EDS
% Data completeness (in resolution range)	99.9 (90.09-2.76) 100.0 (90.09-2.76)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.19 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.14rc2_3184	Depositor
R, R_{free}	0.207 , 0.278 0.207 , 0.277	Depositor DCC
R_{free} test set	1959 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å^2)	59.6	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 50.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.000 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.022 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	9244	wwPDB-VP
Average B, all atoms (Å^2)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.14 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.4892e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, 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	0.39	0/1557	0.57	0/2143
1	D	0.46	0/1579	0.62	1/2167 (0.0%)
2	B	0.42	0/1614	0.62	0/2205
2	E	0.47	0/1617	0.65	0/2210
3	C	0.40	0/1485	0.56	0/2030
3	F	0.44	0/1481	0.60	1/2025 (0.0%)
All	All	0.43	0/9333	0.61	2/12780 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	97	LEU	CA-CB-CG	5.73	128.48	115.30
3	F	292	LEU	CA-CB-CG	5.09	127.01	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1514	0	1400	15	0
1	D	1536	0	1457	6	0
2	B	1573	0	1495	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	1573	0	1493	20	0
3	C	1439	0	1294	17	0
3	F	1434	0	1288	16	0
4	A	5	0	0	0	0
4	B	10	0	0	0	0
4	C	10	0	0	0	0
4	D	10	0	0	0	0
4	E	5	0	0	0	0
4	F	10	0	0	0	0
5	B	31	0	12	0	0
5	E	31	0	12	0	0
6	A	4	0	0	0	0
6	B	6	0	0	0	0
6	C	9	0	0	1	0
6	D	12	0	0	0	0
6	E	22	0	0	0	0
6	F	10	0	0	0	0
All	All	9244	0	8451	81	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 5.

All (81) 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)
3:F:258:ARG:HD2	3:F:262:SER:HB2	1.61	0.81
2:E:87:THR:HG23	2:E:110:THR:HA	1.72	0.70
1:D:79:GLN:NE2	1:D:81:GLU:OE1	2.25	0.70
1:A:14:SER:N	1:A:17:GLN:OE1	2.27	0.68
3:F:168:SER:HB3	3:F:171:SER:HB2	1.79	0.64
3:C:156:SER:HB2	3:C:157:PRO:HD2	1.81	0.63
3:C:293:ARG:HD3	3:C:306:TRP:CE2	2.33	0.61
3:F:181:PRO:HG2	3:F:184:ASP:HB2	1.82	0.61
1:A:69:ASN:O	1:A:69:ASN:ND2	2.32	0.61
3:C:277:CYS:SG	6:C:507:HOH:O	2.57	0.60
3:C:156:SER:OG	3:F:154:GLN:O	2.11	0.59
2:E:118:GLY:HA2	2:E:200:HIS:HD2	1.68	0.59
3:F:123:ARG:NH1	3:F:126:PRO:O	2.36	0.58
2:B:126:PRO:HG3	2:B:138:LEU:HD23	1.86	0.58
3:F:167:TYR:OH	3:F:172:GLN:HA	2.04	0.57
1:A:61:ARG:NH1	1:A:82:ASP:OD1	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:118:GLN:HA	3:F:134:TRP:HE1	1.70	0.56
2:B:18:LEU:HB2	2:B:82:MET:HE3	1.87	0.55
2:B:165:THR:HB	2:B:180:SER:OG	2.07	0.54
1:A:32:TYR:CE1	2:B:100(B):ASN:HB2	2.43	0.54
2:B:10:ASP:OD1	2:B:11:LEU:N	2.39	0.54
1:D:32:TYR:CE1	2:E:100(B):ASN:HB2	2.43	0.53
2:E:118:GLY:HA2	2:E:200:HIS:CD2	2.44	0.53
2:B:100(B):ASN:O	2:B:100(D):VAL:HG23	2.10	0.52
2:E:100(B):ASN:O	2:E:100(D):VAL:HG23	2.10	0.51
2:B:185:PRO:O	2:B:187:SER:N	2.44	0.51
2:E:19:ARG:HE	2:E:79:TYR:HB3	1.76	0.50
1:A:55:PRO:HD2	1:A:58:VAL:HG21	1.94	0.50
2:E:195:ILE:HG22	2:E:210:LYS:HA	1.93	0.50
2:B:82:MET:HB3	2:B:82(C):LEU:HD21	1.94	0.50
1:D:4:LEU:HD11	1:D:90:LEU:HG	1.93	0.50
3:F:223:THR:HG23	3:F:225:THR:HG23	1.94	0.49
1:A:33:VAL:HG21	1:A:71:ALA:HB2	1.94	0.49
3:C:148:LEU:HB3	3:F:163:GLU:HB2	1.94	0.49
2:E:35:ASN:OD1	2:E:50:SER:HB3	2.12	0.48
1:A:4:LEU:HD11	1:A:90:LEU:HG	1.95	0.48
1:A:125:GLU:OE1	2:B:143:LYS:NZ	2.41	0.48
1:A:30:TYR:HA	1:A:90:LEU:HD22	1.96	0.47
3:C:240:ASP:OD1	3:C:275:HIS:NE2	2.39	0.47
3:C:223:THR:OG1	3:C:237:THR:HB	2.14	0.47
1:D:96:PRO:HG2	2:E:100(E):PHE:CE2	2.49	0.47
3:C:259:ALA:C	3:C:261:ARG:H	2.18	0.47
1:A:167:LYS:HE2	1:A:171:ASN:O	2.15	0.47
3:C:238:TRP:O	3:C:275:HIS:HB3	2.15	0.47
2:E:17:GLY:HA2	2:E:82:MET:O	2.15	0.46
3:F:214:LEU:HD23	3:F:300:GLN:HG2	1.97	0.46
1:A:11:ALA:O	1:A:104:LEU:HA	2.16	0.46
2:B:85:GLU:H	2:B:85:GLU:CD	2.19	0.46
2:E:139:GLY:HA2	2:E:154:TRP:CH2	2.51	0.46
2:E:195:ILE:HD12	2:E:195:ILE:O	2.17	0.45
3:C:126:PRO:HD3	3:F:244:TRP:CH2	2.51	0.44
1:D:181:LEU:HD11	1:D:192:TYR:CE2	2.52	0.44
3:C:288:HIS:O	3:C:311:MET:HA	2.17	0.44
2:B:30:SER:O	2:B:52(A):SER:HB2	2.18	0.44
3:C:250:ARG:CZ	3:C:273:LEU:HD13	2.48	0.44
3:F:127:LEU:HD23	3:F:127:LEU:HA	1.81	0.44
1:A:89:SER:HA	1:A:97:LEU:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:126:PRO:HD3	3:F:244:TRP:CZ3	2.53	0.43
2:E:162:GLY:O	2:E:182:VAL:HA	2.17	0.43
3:C:119:LEU:HD23	3:F:206:GLN:HG3	1.99	0.43
2:E:200:HIS:ND1	2:E:202:PRO:HD2	2.34	0.43
2:B:165:THR:HA	2:B:180:SER:HA	2.01	0.42
2:E:147:PRO:O	2:E:200:HIS:HE1	2.02	0.42
3:F:223:THR:HB	3:F:237:THR:HB	2.00	0.42
3:C:181:PRO:HG2	3:C:184:ASP:HB2	2.02	0.42
1:A:4:LEU:HD23	1:A:4:LEU:HA	1.91	0.42
1:A:96:PRO:HG2	2:B:100(E):PHE:CE2	2.54	0.42
2:B:150:VAL:CG2	2:B:178:LEU:HD21	2.50	0.41
2:E:82(C):LEU:HD23	2:E:82(C):LEU:HA	1.88	0.41
2:B:36:TRP:NE1	2:B:80:LEU:HB2	2.35	0.41
2:E:22:CYS:HB3	2:E:78:LEU:HB3	2.03	0.41
2:B:145:TYR:CE1	2:B:150:VAL:HG13	2.56	0.41
1:A:35:TRP:CZ3	1:A:88:CYS:HB3	2.55	0.41
2:B:33:THR:OG1	2:B:52:SER:HA	2.20	0.41
2:E:138:LEU:HB2	2:E:211:VAL:HG11	2.03	0.41
3:C:205:THR:OG1	3:F:302:GLU:OE1	2.30	0.40
2:E:66:ARG:HB3	2:E:82(A):ASN:O	2.21	0.40
2:E:100:SER:O	2:E:100(A):LEU:HD12	2.22	0.40
2:B:69:ILE:HD13	2:B:69:ILE:HG21	1.82	0.40
1:D:33:VAL:HA	1:D:89:SER:O	2.21	0.40
3:C:274:GLN:H	3:C:274:GLN:HG2	1.68	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	210/216 (97%)	200 (95%)	10 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	210/216 (97%)	201 (96%)	9 (4%)	0	100	100
2	B	203/230 (88%)	191 (94%)	11 (5%)	1 (0%)	29	47
2	E	204/230 (89%)	194 (95%)	10 (5%)	0	100	100
3	C	180/218 (83%)	172 (96%)	7 (4%)	1 (1%)	25	42
3	F	178/218 (82%)	170 (96%)	8 (4%)	0	100	100
All	All	1185/1328 (89%)	1128 (95%)	55 (5%)	2 (0%)	47	69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	186	SER
3	C	260	GLU

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	160/181 (88%)	155 (97%)	5 (3%)	40	60
1	D	167/181 (92%)	157 (94%)	10 (6%)	19	33
2	B	171/196 (87%)	164 (96%)	7 (4%)	30	50
2	E	169/196 (86%)	165 (98%)	4 (2%)	49	68
3	C	149/198 (75%)	142 (95%)	7 (5%)	26	45
3	F	149/198 (75%)	142 (95%)	7 (5%)	26	45
All	All	965/1150 (84%)	925 (96%)	40 (4%)	30	50

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	83	GLU
1	A	154	SER
1	A	161	GLU

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Mol	Chain	Res	Type
1	A	191	SER
2	B	19	ARG
2	B	31	SER
2	B	95	TYR
2	B	100	SER
2	B	116	THR
2	B	165	THR
2	B	211	VAL
3	C	125	SER
3	C	128	SER
3	C	205	THR
3	C	239	GLN
3	C	248	PHE
3	C	268	TRP
3	C	296	GLU
1	D	6	GLN
1	D	34	SER
1	D	66	LYS
1	D	85	ASP
1	D	90	LEU
1	D	97	LEU
1	D	125	GLU
1	D	127	GLN
1	D	168	GLN
1	D	171	ASN
2	E	19	ARG
2	E	120	SER
2	E	151	THR
2	E	191	THR
3	F	185	SER
3	F	193	SER
3	F	237	THR
3	F	248	PHE
3	F	262	SER
3	F	273	LEU
3	F	316	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	171	ASN
2	B	199	ASN

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Mol	Chain	Res	Type
1	D	79	GLN
1	D	127	GLN
1	D	168	GLN
2	E	200	HIS
3	F	215	GLN
3	F	230	ASN
3	F	274	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

12 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	$\#\|Z\| > 2$
4	SO4	F	401	-	4,4,4	0.23	0	6,6,6	0.72	0
4	SO4	A	301	-	4,4,4	0.15	0	6,6,6	0.14	0
4	SO4	E	302	-	4,4,4	0.14	0	6,6,6	0.29	0
4	SO4	D	302	-	4,4,4	0.18	0	6,6,6	0.32	0
4	SO4	F	402	-	4,4,4	0.18	0	6,6,6	0.29	0
5	ATP	E	301	-	26,33,33	1.05	1 (3%)	31,52,52	1.51	6 (19%)
4	SO4	B	303	-	4,4,4	0.16	0	6,6,6	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	SO4	C	401	-	4,4,4	0.21	0	6,6,6	0.25	0
4	SO4	B	302	-	4,4,4	0.13	0	6,6,6	0.17	0
5	ATP	B	301	-	26,33,33	0.95	1 (3%)	31,52,52	1.44	5 (16%)
4	SO4	C	402	-	4,4,4	0.14	0	6,6,6	0.37	0
4	SO4	D	301	-	4,4,4	0.20	0	6,6,6	0.32	0

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
5	ATP	B	301	-	-	3/18/38/38	0/3/3/3
5	ATP	E	301	-	-	0/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	301	ATP	C5-C4	2.75	1.48	1.40
5	B	301	ATP	C5-C4	2.58	1.47	1.40

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	E	301	ATP	C1'-N9-C4	-3.28	120.88	126.64
5	E	301	ATP	N3-C2-N1	-3.11	123.81	128.68
5	B	301	ATP	N3-C2-N1	-2.91	124.14	128.68
5	E	301	ATP	O3'-C3'-C4'	-2.83	102.86	111.05
5	E	301	ATP	C4-C5-N7	-2.73	106.55	109.40
5	B	301	ATP	O3'-C3'-C4'	-2.70	103.26	111.05
5	B	301	ATP	PA-O3A-PB	-2.65	123.72	132.83
5	E	301	ATP	PA-O3A-PB	-2.42	124.52	132.83
5	E	301	ATP	C2-N1-C6	2.35	122.78	118.75
5	B	301	ATP	C1'-N9-C4	-2.33	122.55	126.64
5	B	301	ATP	C2-N1-C6	2.10	122.35	118.75

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	301	ATP	PG-O3B-PB-O2B

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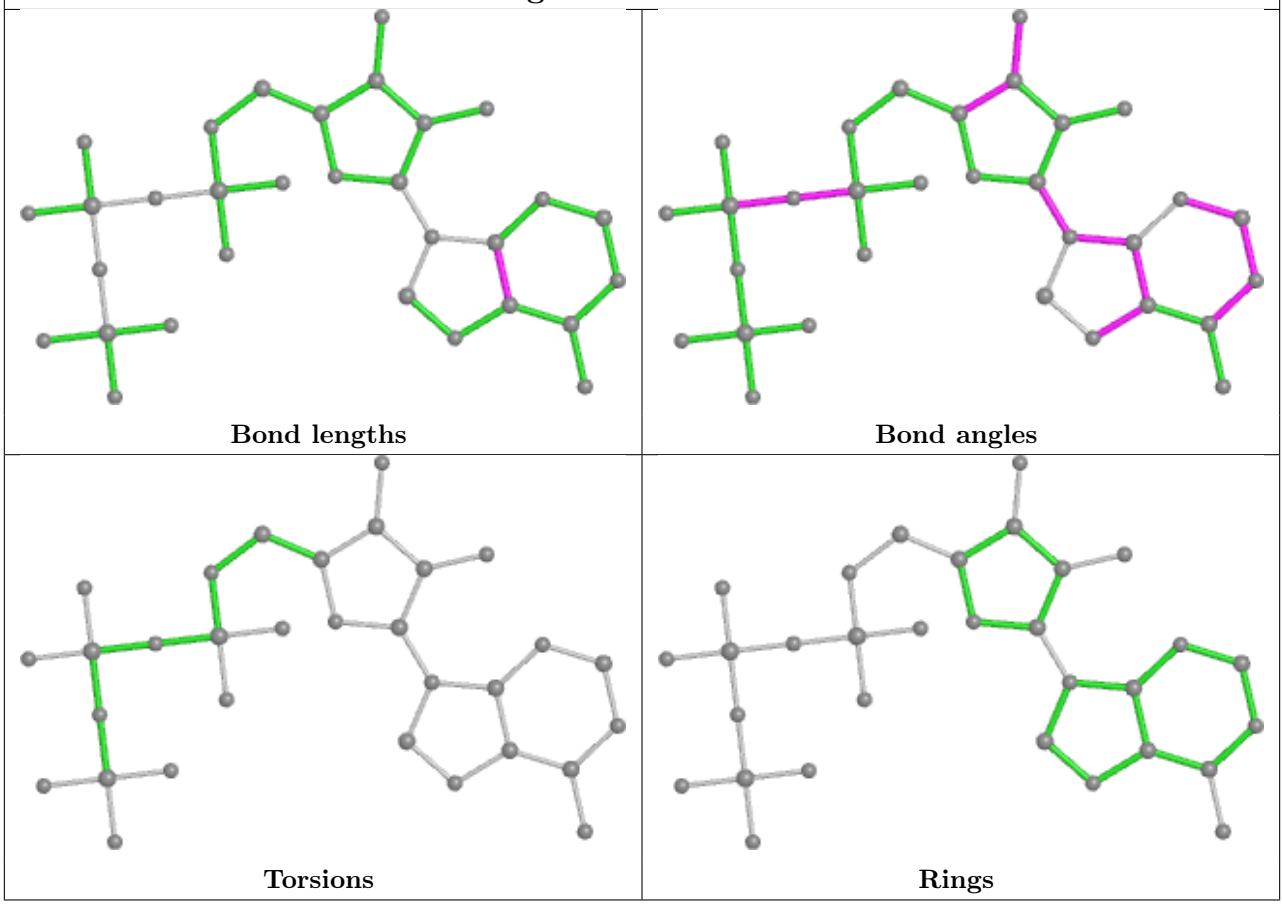
Mol	Chain	Res	Type	Atoms
5	B	301	ATP	PA-O3A-PB-O2B
5	B	301	ATP	PG-O3B-PB-O1B

There are no ring outliers.

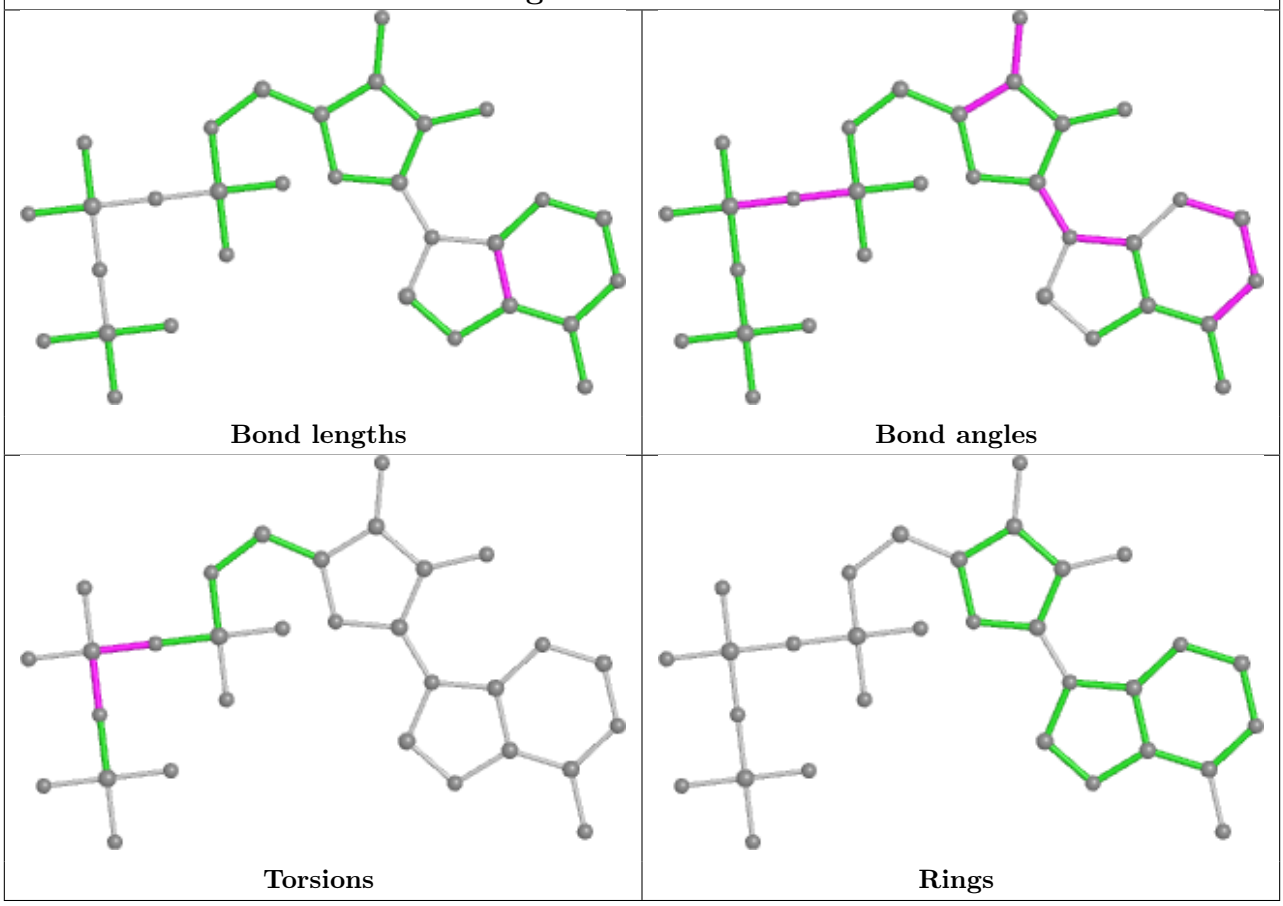
No monomer is involved in short contacts.

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 then 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 ATP E 301



Ligand ATP B 301



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 (i)

6.1 Protein, DNA and RNA chains (i)

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	212/216 (98%)	0.18	1 (0%)	91	94	41, 66, 87, 96	0
1	D	212/216 (98%)	0.11	4 (1%)	66	75	30, 43, 99, 109	0
2	B	209/230 (90%)	0.16	2 (0%)	82	87	39, 57, 81, 108	0
2	E	209/230 (90%)	0.12	0	100	100	29, 43, 80, 99	0
3	C	186/218 (85%)	0.34	4 (2%)	62	70	43, 60, 102, 140	0
3	F	184/218 (84%)	0.25	5 (2%)	54	63	34, 57, 90, 107	0
All	All	1212/1328 (91%)	0.19	16 (1%)	77	84	29, 57, 92, 140	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	255	LEU	3.3
3	C	194	VAL	3.1
1	D	209	PRO	3.1
3	F	283	TRP	3.0
3	F	195	ALA	2.8
2	B	184	VAL	2.6
3	F	146	ALA	2.5
3	C	193	SER	2.5
1	D	183	PRO	2.5
2	B	164	HIS	2.4
3	C	202	PHE	2.4
3	C	283	TRP	2.4
3	F	262	SER	2.3
1	D	133	LEU	2.3
1	A	189	HIS	2.1
1	D	186	TRP	2.1

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 monosaccharides in this entry.

6.4 Ligands (i)

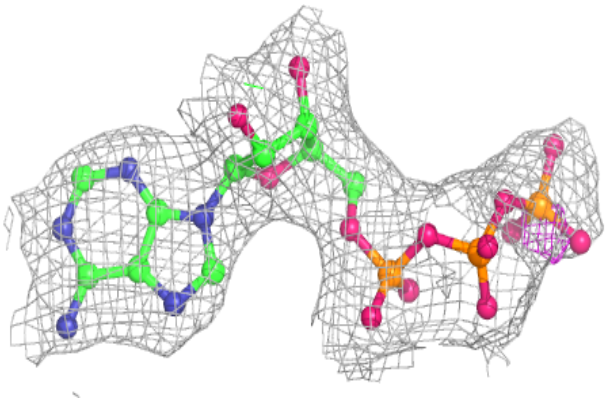
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

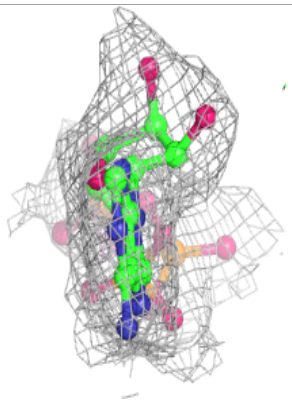
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	SO4	F	402	5/5	0.84	0.18	94,99,103,112	0
4	SO4	C	402	5/5	0.88	0.16	96,99,110,111	0
4	SO4	A	301	5/5	0.90	0.11	102,105,106,110	0
4	SO4	D	302	5/5	0.90	0.13	65,74,83,94	0
4	SO4	C	401	5/5	0.90	0.18	67,72,83,83	0
4	SO4	B	302	5/5	0.96	0.10	67,69,79,79	0
5	ATP	B	301	31/31	0.96	0.19	36,46,82,94	0
4	SO4	F	401	5/5	0.97	0.15	49,56,66,70	0
4	SO4	B	303	5/5	0.97	0.11	57,63,67,77	0
4	SO4	E	302	5/5	0.97	0.15	51,52,59,60	0
4	SO4	D	301	5/5	0.98	0.13	43,44,56,61	0
5	ATP	E	301	31/31	0.98	0.16	28,31,71,78	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ATP B 301:

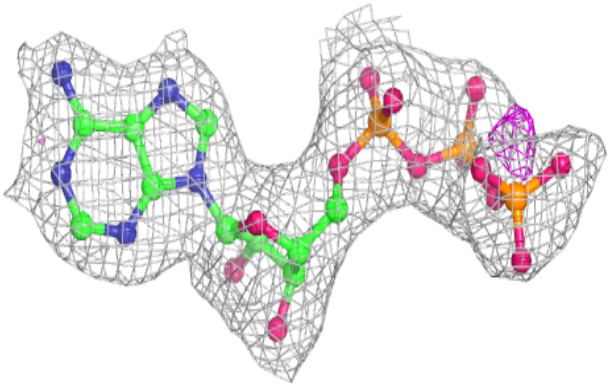
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

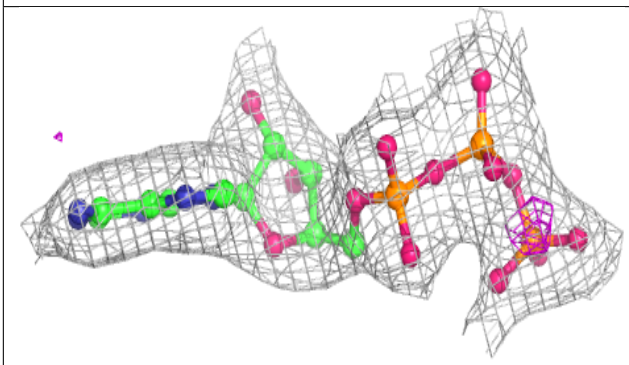


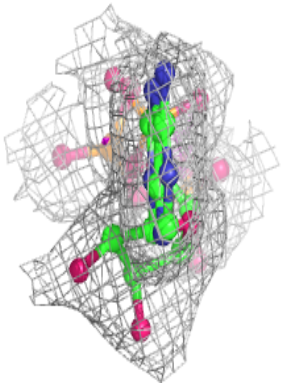


Electron density around ATP E 301:

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







6.5 Other polymers (i)

There are no such residues in this entry.