wwPDB X-ray Structure Validation Summary Report (i)

Sep 5, 2023 – 08:18 PM EDT

PDB ID	:	4ERP
Title	:	Crystal structure of a gemcitabine-diphosphate inhibited E. coli class Ia ribonucleotide reductase complex
Authors	:	Zimanyi, C.M.; Drennan, C.L.
Deposited on	:	2012-04-20
Resolution	:	4.45 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

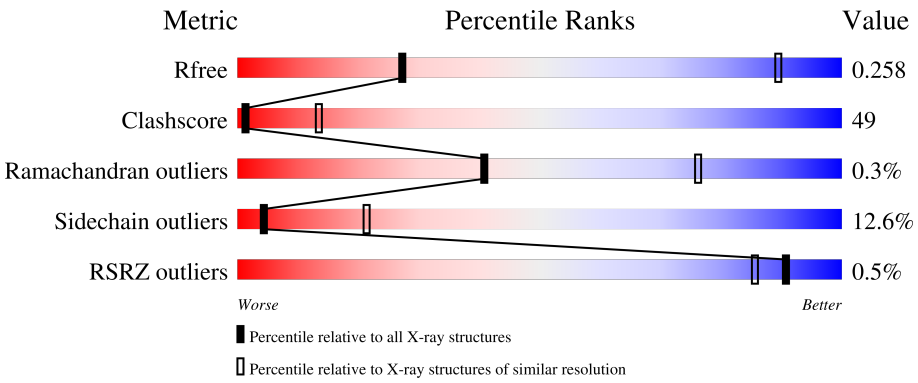
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 4.45 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	1051 (5.12-3.80)
Clashscore	141614	1119 (5.12-3.80)
Ramachandran outliers	138981	1065 (5.12-3.80)
Sidechain outliers	138945	1047 (5.12-3.80)
RSRZ outliers	127900	1099 (5.20-3.70)

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	761	36% 51% 9% •
1	B	761	% 36% 52% 8% •
1	C	761	39% 49% 8% •
1	D	761	35% 54% 9% •
2	E	375	% 39% 51% • 6%

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Mol	Chain	Length	Quality of chain
2	F	375	% 41% 50% 5% 5%
2	G	375	% 42% 48% 6% 5%
2	H	375	% 37% 52% 6% 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ATP	B	801	-	-	X	-
3	ATP	C	801	-	-	X	-
3	ATP	D	801	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 35205 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 Ribonucleoside-diphosphate reductase 1 subunit alpha.

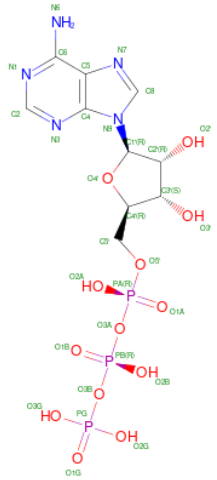
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	734	5845	3712	1004	1105	24	0	0	0
1	B	735	5850	3715	1005	1106	24	0	0	0
1	C	733	5841	3710	1003	1104	24	0	0	0
1	D	736	5859	3720	1007	1108	24	0	0	0

- Molecule 2 is a protein called Ribonucleoside-diphosphate reductase 1 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	354	2900	1850	480	557	13	0	0	0
2	F	358	2930	1867	486	564	13	0	0	0
2	G	357	2922	1863	483	563	13	0	0	0
2	H	356	2914	1857	483	561	13	0	0	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

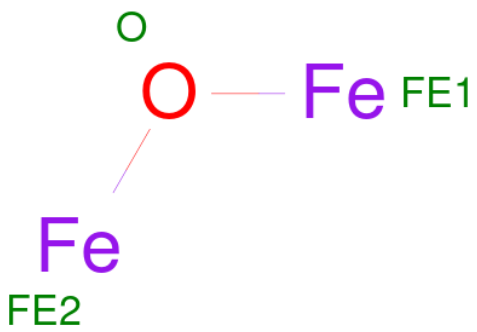
ATP



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

- Molecule 4 is MU-OXO-DIIRON (three-letter code: FEO) (formula: Fe_2O).

FEO



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	O		
4	E	1	3	2	1	0	0
4	F	1	3	2	1	0	0
4	G	1	3	2	1	0	0
4	H	1	3	2	1	0	0

- Molecule 5 is water.

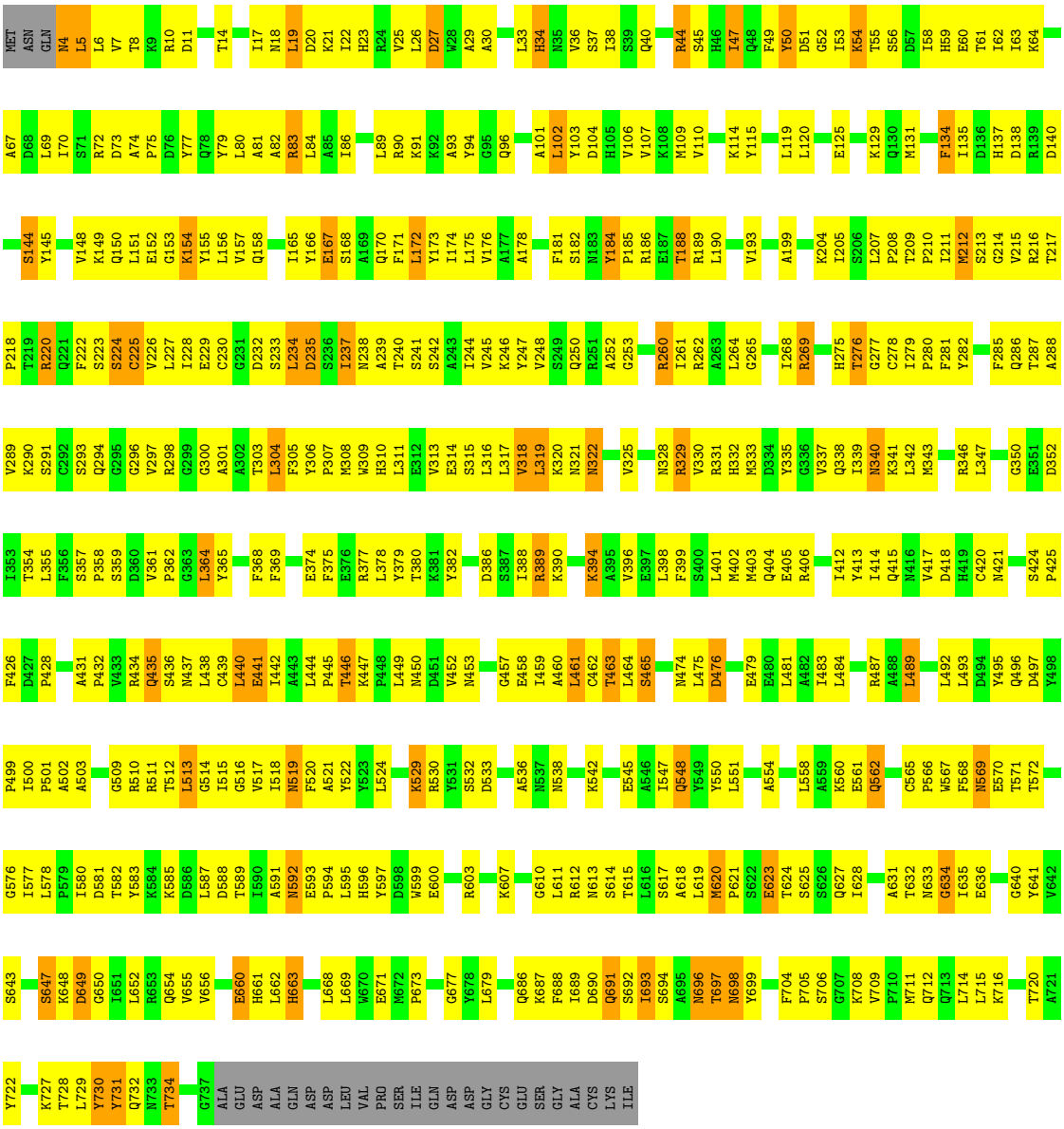
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	E	2	2	2	0	0
5	F	2	2	2	0	0
5	G	2	2	2	0	0
5	H	2	2	2	0	0

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.

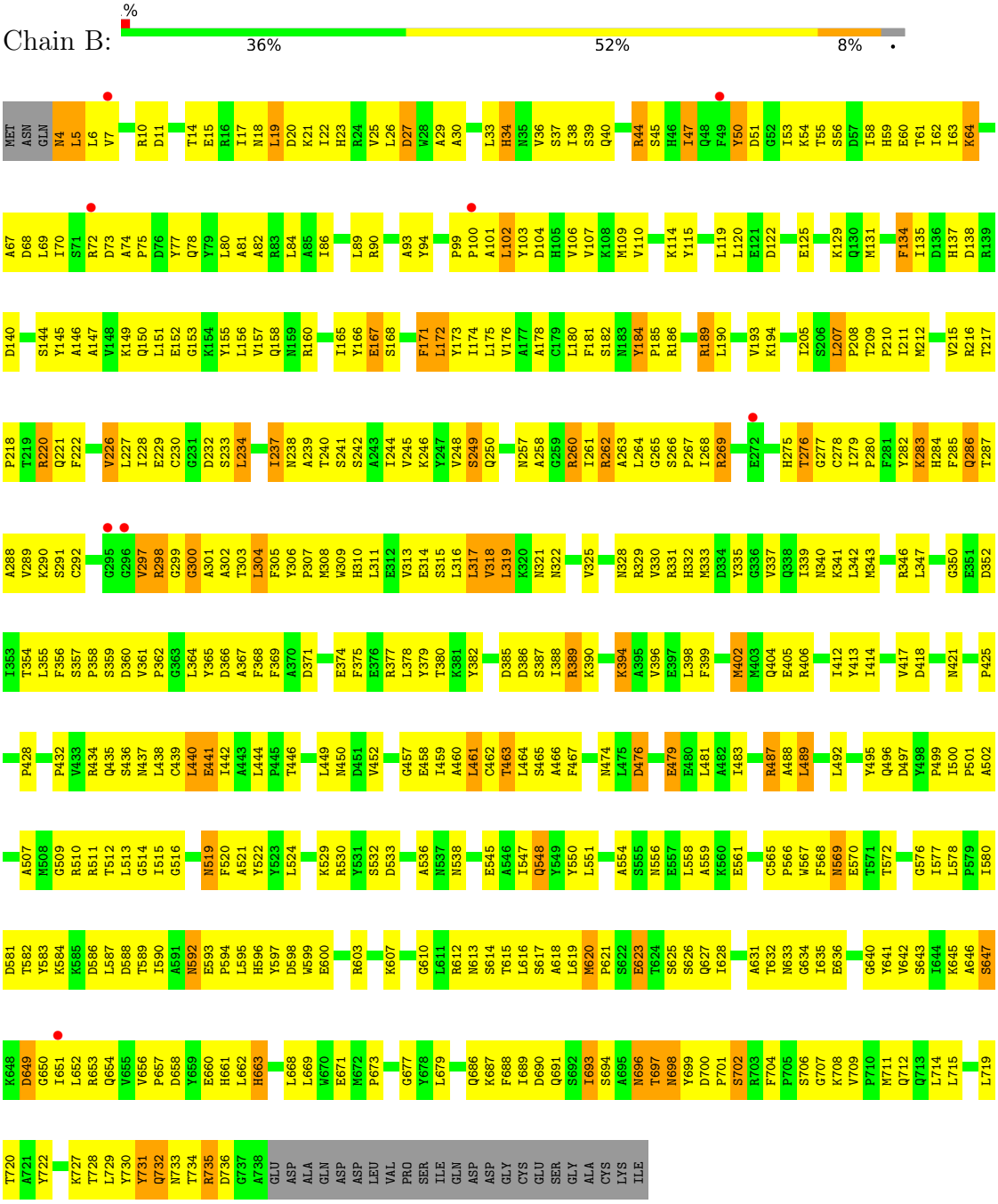
• Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha

Chain A: 36% 51% 9% •



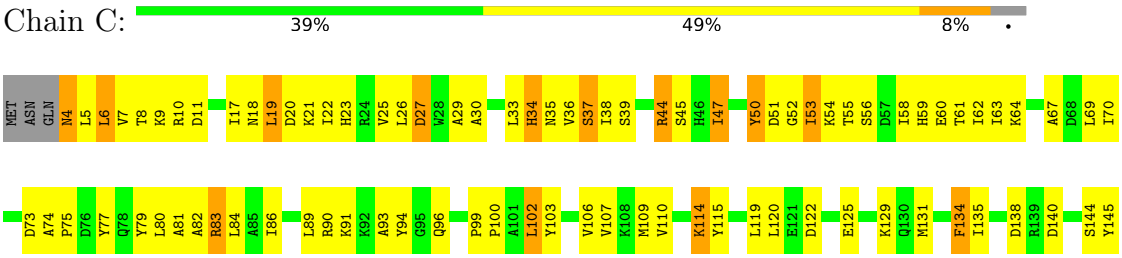
• Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha

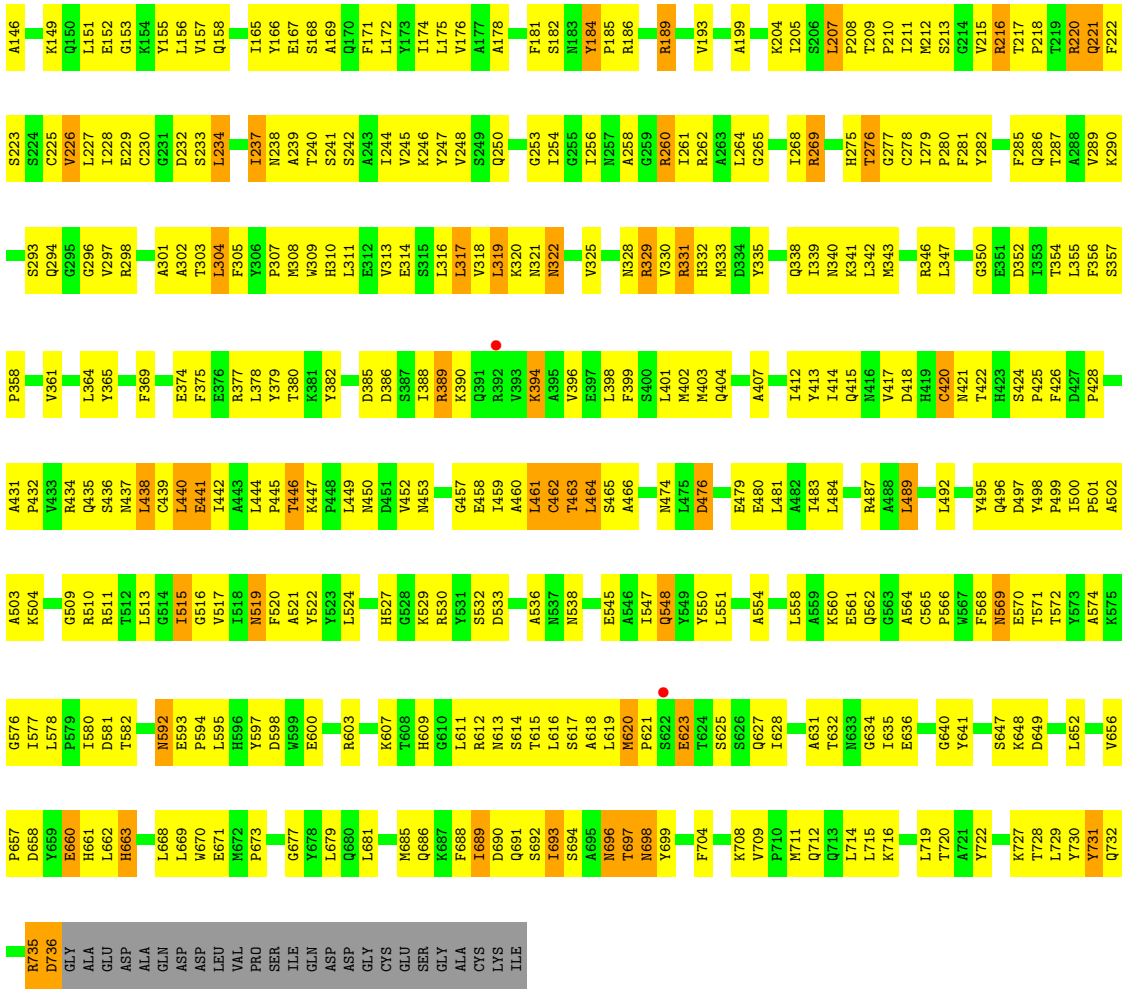
Chain B:



• Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha

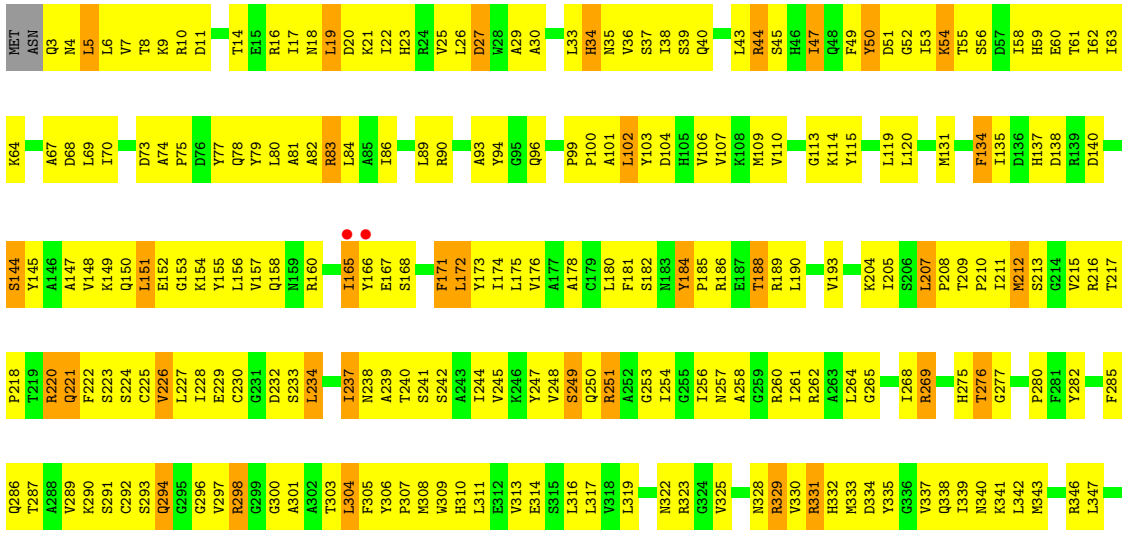
Chain C:

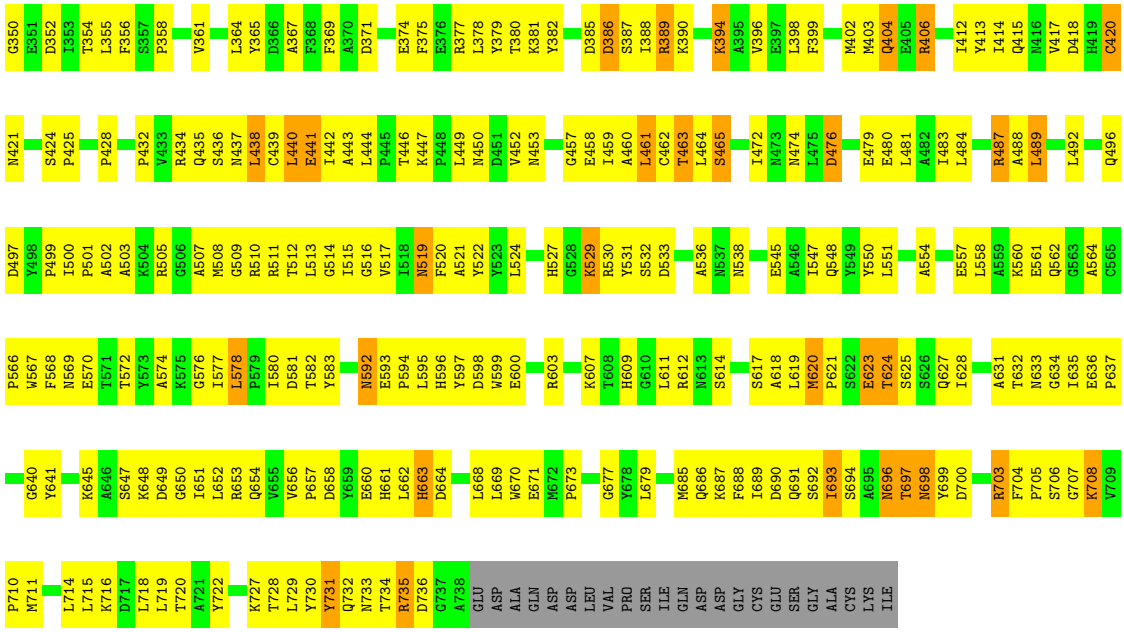




• Molecule 1: Ribonucleoside-diphosphate reductase 1 subunit alpha

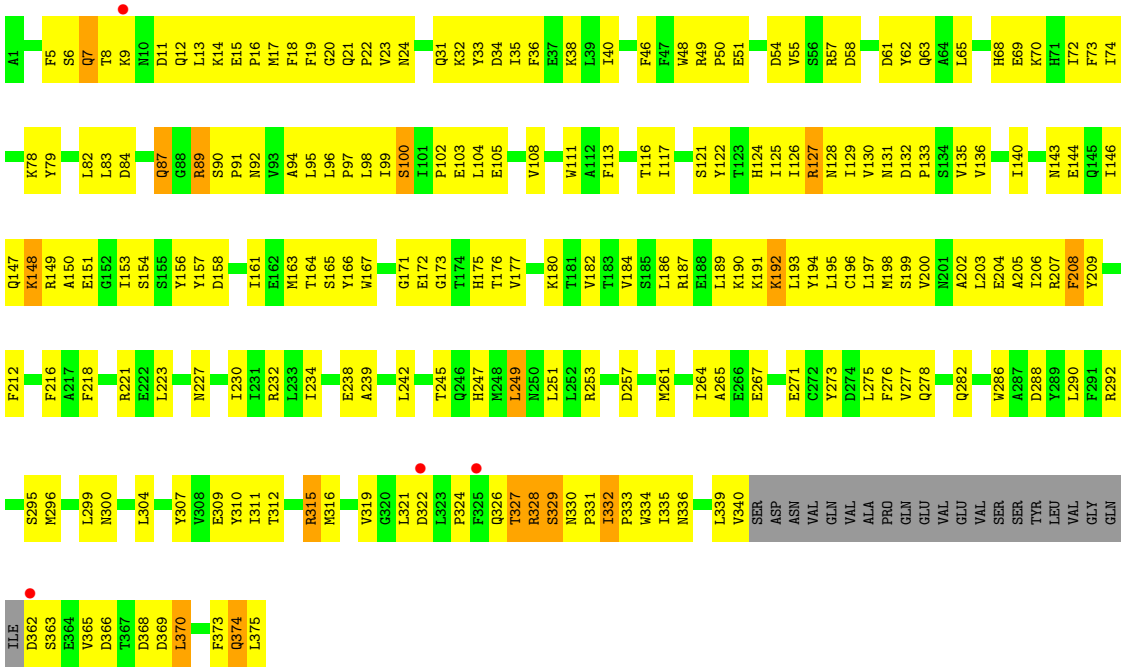
Chain D: 35% 54% 9% •





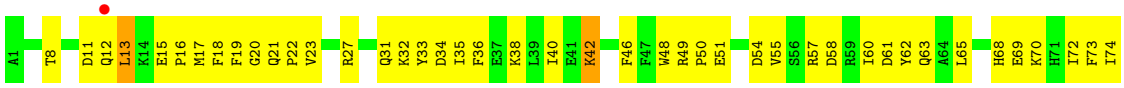
• Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta

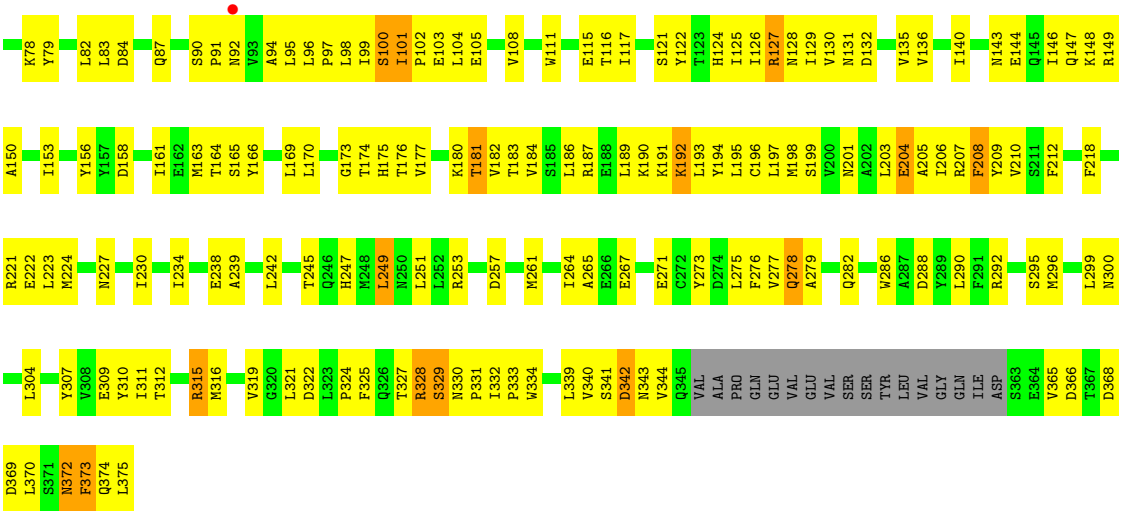
Chain E:



• Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta

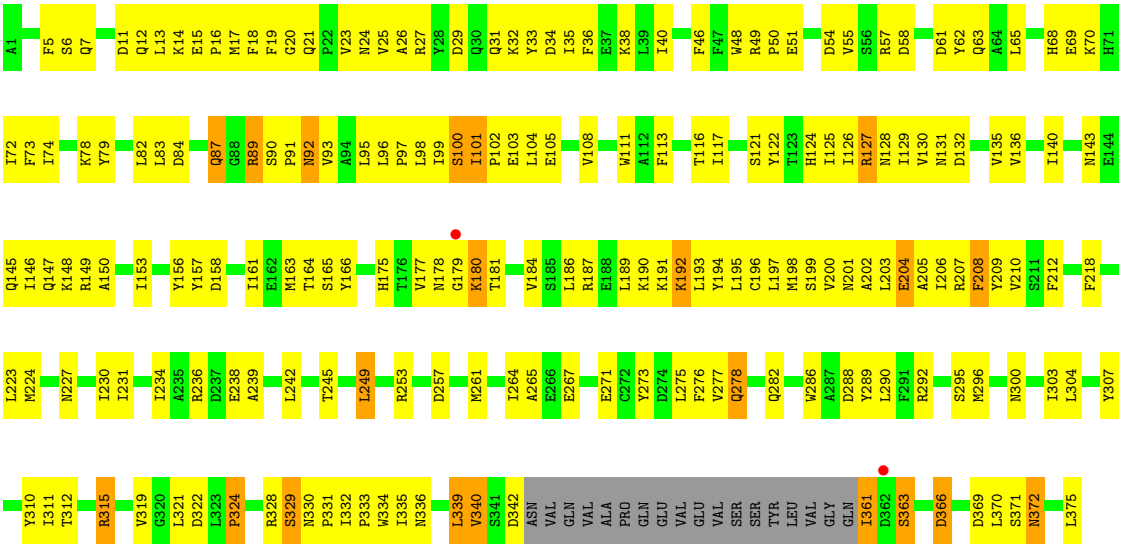
Chain F:





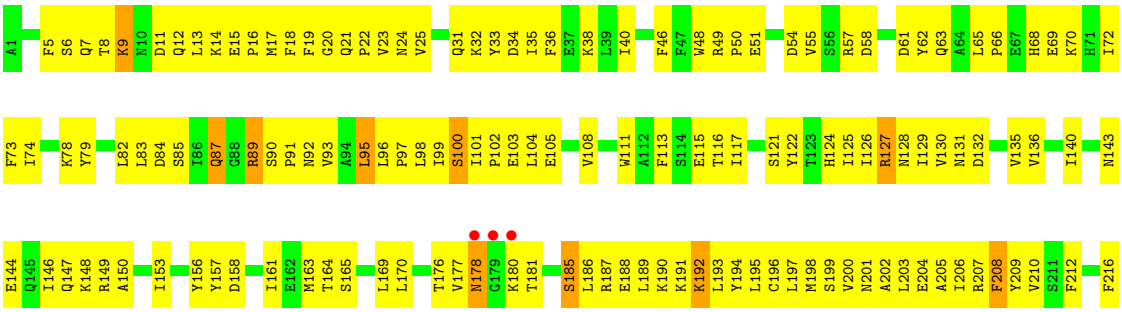
• Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta

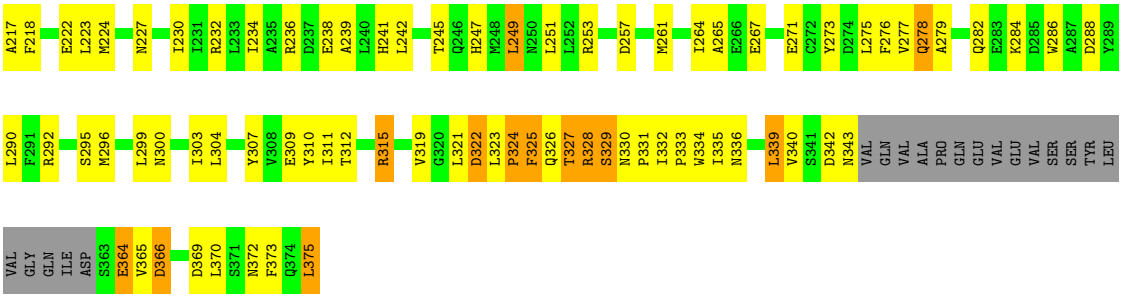
Chain G:



• Molecule 2: Ribonucleoside-diphosphate reductase 1 subunit beta

Chain H:




A217 F218 E222 L223 M224 N227 I230 I231 R232 L233 I234 A235 R236 D237 E238 A239 L240 H241 L242 T245 Q246 H247 M248 L249 N250 L251 L252 R253 D257 M261 I264 A265 E266 E267 E271 C272 Y273 D274 L275 F276 V277 Q278 A279 Q282 E283 K284 D285 W286 A287 D288 Y289
L290 F291 R292 S295 M296 L299 N300 I303 L304 Y307 V308 E309 Y310 I311 T312 R315 V319 G320 L321 D322 L323 P324 F325 Q326 T327 R328 S329 N330 P331 I332 P333 W334 I335 N336 L339 V340 S341 D342 N343 VAL GLN VAL ALA PRO GLN GLU VAL GLU VAL SER SER TYR LEU
VAL GLY GLN ILE ASP S363 E364 V365 D366 D369 L370 S371 N372 F373 Q374 L375

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	128.67Å 398.91Å 319.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 4.45 49.54 – 4.44	Depositor EDS
% Data completeness (in resolution range)	82.3 (50.00-4.45) 81.8 (49.54-4.44)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.75 (at 4.45Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.233 , 0.267 0.226 , 0.258	Depositor DCC
R_{free} test set	2334 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	108.8	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 137.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.85	EDS
Total number of atoms	35205	wwPDB-VP
Average B, all atoms (Å^2)	143.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.38% of the height of the origin peak. No significant pseudotranslation is detected.*

[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, FEO

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	0.31	0/5973	0.51	0/8090
1	B	0.31	0/5978	0.54	1/8097 (0.0%)
1	C	0.31	0/5969	0.55	0/8085
1	D	0.31	0/5987	0.53	0/8109
2	E	0.32	0/2964	0.49	1/4019 (0.0%)
2	F	0.34	0/2994	0.51	2/4060 (0.0%)
2	G	0.34	0/2986	0.51	2/4049 (0.0%)
2	H	0.33	0/2978	0.48	0/4038
All	All	0.32	0/35829	0.52	6/48547 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	324	PRO	N-CA-C	5.82	127.23	112.10
2	G	92	ASN	N-CA-C	5.57	126.03	111.00
1	B	360	ASP	O-C-N	-5.35	114.14	122.70
2	E	362	ASP	CB-CG-OD2	5.17	122.95	118.30
2	F	342	ASP	CB-CG-OD2	5.14	122.92	118.30

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	5845	0	5770	637	0
1	B	5850	0	5774	647	0
1	C	5841	0	5767	626	0
1	D	5859	0	5783	649	0
2	E	2900	0	2826	238	0
2	F	2930	0	2854	232	0
2	G	2922	0	2846	239	0
2	H	2914	0	2837	275	0
3	A	31	0	12	4	0
3	B	31	0	12	9	0
3	C	31	0	11	15	0
3	D	31	0	12	10	0
4	E	3	0	0	0	0
4	F	3	0	0	0	0
4	G	3	0	0	0	0
4	H	3	0	0	0	0
5	E	2	0	0	1	0
5	F	2	0	0	1	0
5	G	2	0	0	1	0
5	H	2	0	0	0	0
All	All	35205	0	34504	3414	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 49.

The worst 5 of 3414 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:115:TYR:CE1	1:C:216:ARG:HD2	1.42	1.53
1:C:442:ILE:HD12	1:C:462:CYS:SG	1.48	1.51
1:D:114:LYS:HG3	1:D:166:TYR:CE2	1.45	1.50
1:B:222:PHE:CD2	1:B:492:LEU:HD11	1.44	1.49
1:A:5:LEU:HD12	1:A:17:ILE:CG1	1.41	1.49

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	732/761 (96%)	672 (92%)	57 (8%)	3 (0%)	34	72
1	B	733/761 (96%)	679 (93%)	50 (7%)	4 (0%)	29	68
1	C	731/761 (96%)	681 (93%)	48 (7%)	2 (0%)	41	76
1	D	734/761 (96%)	673 (92%)	59 (8%)	2 (0%)	41	76
2	E	350/375 (93%)	325 (93%)	25 (7%)	0	100	100
2	F	354/375 (94%)	326 (92%)	28 (8%)	0	100	100
2	G	353/375 (94%)	328 (93%)	25 (7%)	0	100	100
2	H	352/375 (94%)	327 (93%)	24 (7%)	1 (0%)	41	76
All	All	4339/4544 (96%)	4011 (92%)	316 (7%)	12 (0%)	41	76

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	731	TYR
1	C	731	TYR
1	D	731	TYR
1	B	300	GLY
2	H	324	PRO

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	629/651 (97%)	532 (85%)	97 (15%)	2	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	629/651 (97%)	545 (87%)	84 (13%)	4	20
1	C	629/651 (97%)	542 (86%)	87 (14%)	3	19
1	D	630/651 (97%)	537 (85%)	93 (15%)	3	17
2	E	321/340 (94%)	292 (91%)	29 (9%)	9	32
2	F	325/340 (96%)	297 (91%)	28 (9%)	10	35
2	G	324/340 (95%)	295 (91%)	29 (9%)	9	32
2	H	323/340 (95%)	289 (90%)	34 (10%)	7	26
All	All	3810/3964 (96%)	3329 (87%)	481 (13%)	4	21

5 of 481 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	404	GLN
2	G	363	SER
1	D	171	PHE
2	G	329	SER
2	H	327	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 123 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	250	GLN
2	F	372	ASN
1	C	613	ASN
2	F	278	GLN
2	H	76	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

8 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	FEO	F	501	5,2	0,2,2	-	-	-		
3	ATP	C	801	-	26,33,33	2.02	6 (23%)	31,52,52	1.75	7 (22%)
4	FEO	H	501	5,2	0,2,2	-	-	-		
4	FEO	G	501	5,2	0,2,2	-	-	-		
3	ATP	D	801	-	26,33,33	2.06	6 (23%)	31,52,52	1.76	4 (12%)
4	FEO	E	501	5,2	0,2,2	-	-	-		
3	ATP	B	801	-	26,33,33	2.12	6 (23%)	31,52,52	1.72	7 (22%)
3	ATP	A	801	-	26,33,33	2.12	6 (23%)	31,52,52	1.72	7 (22%)

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	ATP	B	801	-	-	4/18/38/38	0/3/3/3
3	ATP	D	801	-	-	5/18/38/38	0/3/3/3
3	ATP	C	801	-	-	6/18/38/38	0/3/3/3
3	ATP	A	801	-	-	4/18/38/38	0/3/3/3

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	801	ATP	O4'-C1'	5.55	1.48	1.41
3	D	801	ATP	O4'-C1'	5.47	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	801	ATP	O4'-C1'	5.43	1.48	1.41
3	A	801	ATP	O4'-C1'	5.40	1.48	1.41
3	D	801	ATP	C6-N6	4.40	1.50	1.34

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	801	ATP	N3-C2-N1	-4.75	121.25	128.68
3	B	801	ATP	N3-C2-N1	-4.64	121.43	128.68
3	A	801	ATP	N3-C2-N1	-4.63	121.44	128.68
3	D	801	ATP	N3-C2-N1	-4.63	121.44	128.68
3	D	801	ATP	PB-O3B-PG	-4.57	117.16	132.83

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	801	ATP	PB-O3A-PA-O5'
3	B	801	ATP	PB-O3A-PA-O5'
3	C	801	ATP	C5'-O5'-PA-O2A
3	C	801	ATP	C5'-O5'-PA-O3A
3	D	801	ATP	C5'-O5'-PA-O1A

There are no ring outliers.

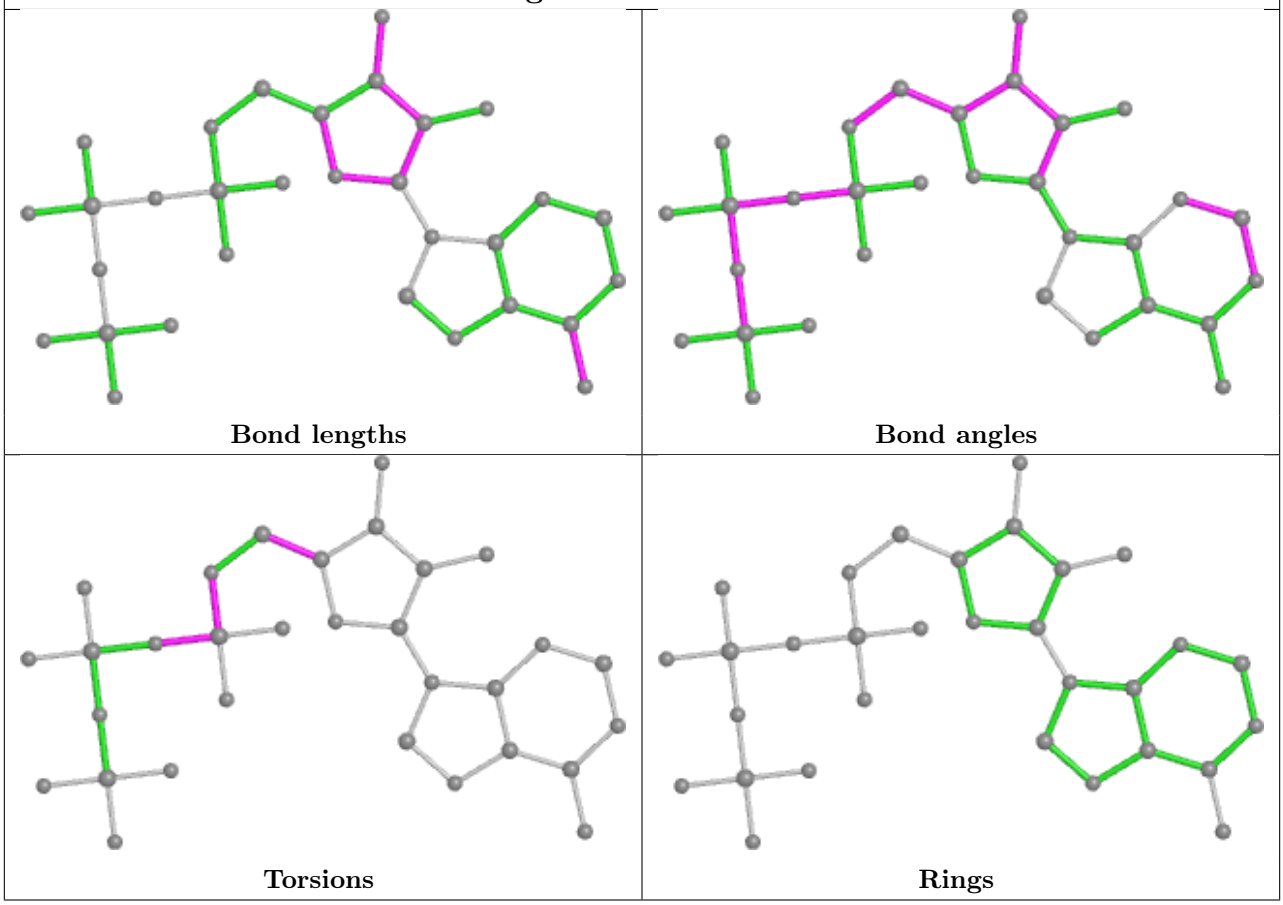
4 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	801	ATP	15	0
3	D	801	ATP	10	0
3	B	801	ATP	9	0
3	A	801	ATP	4	0

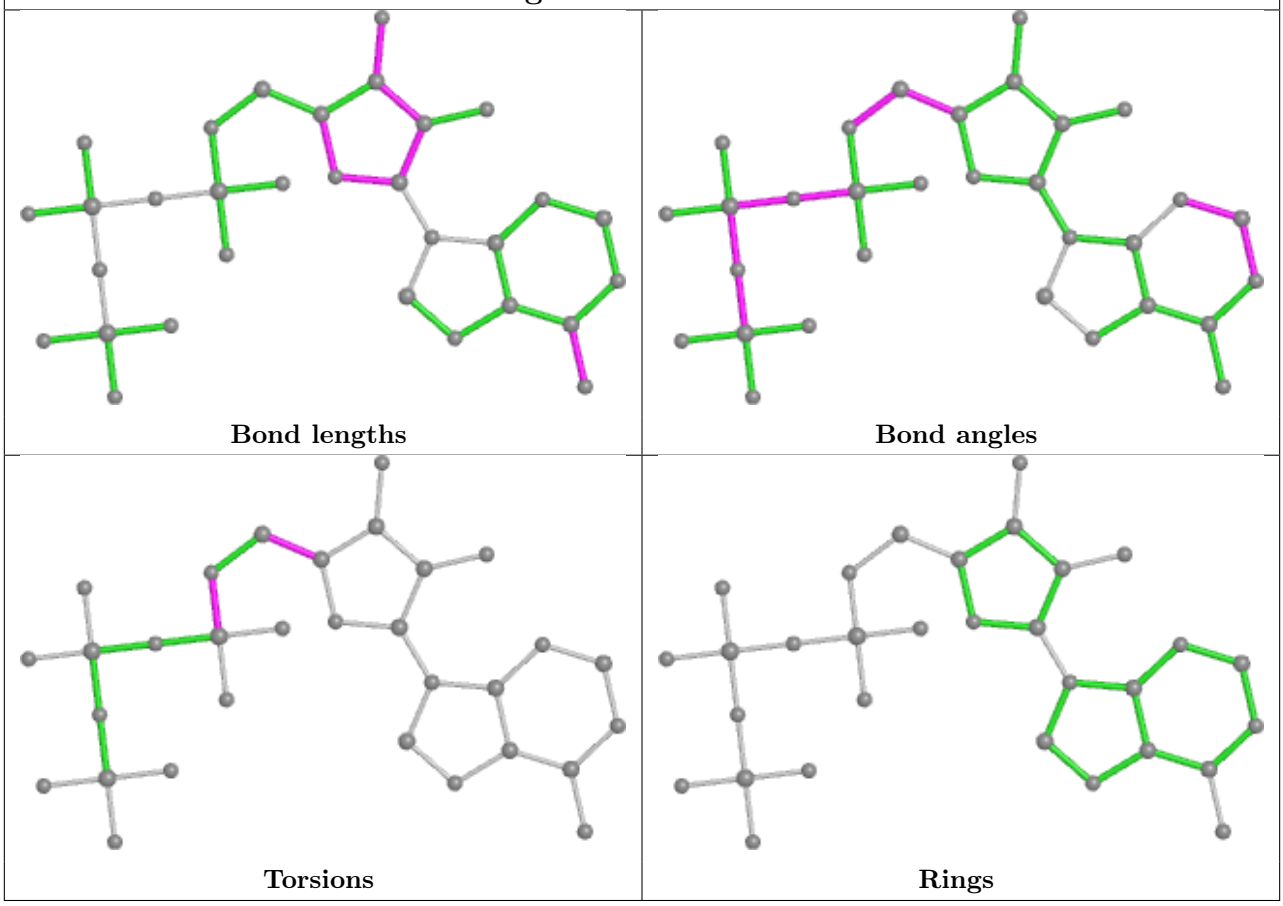
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

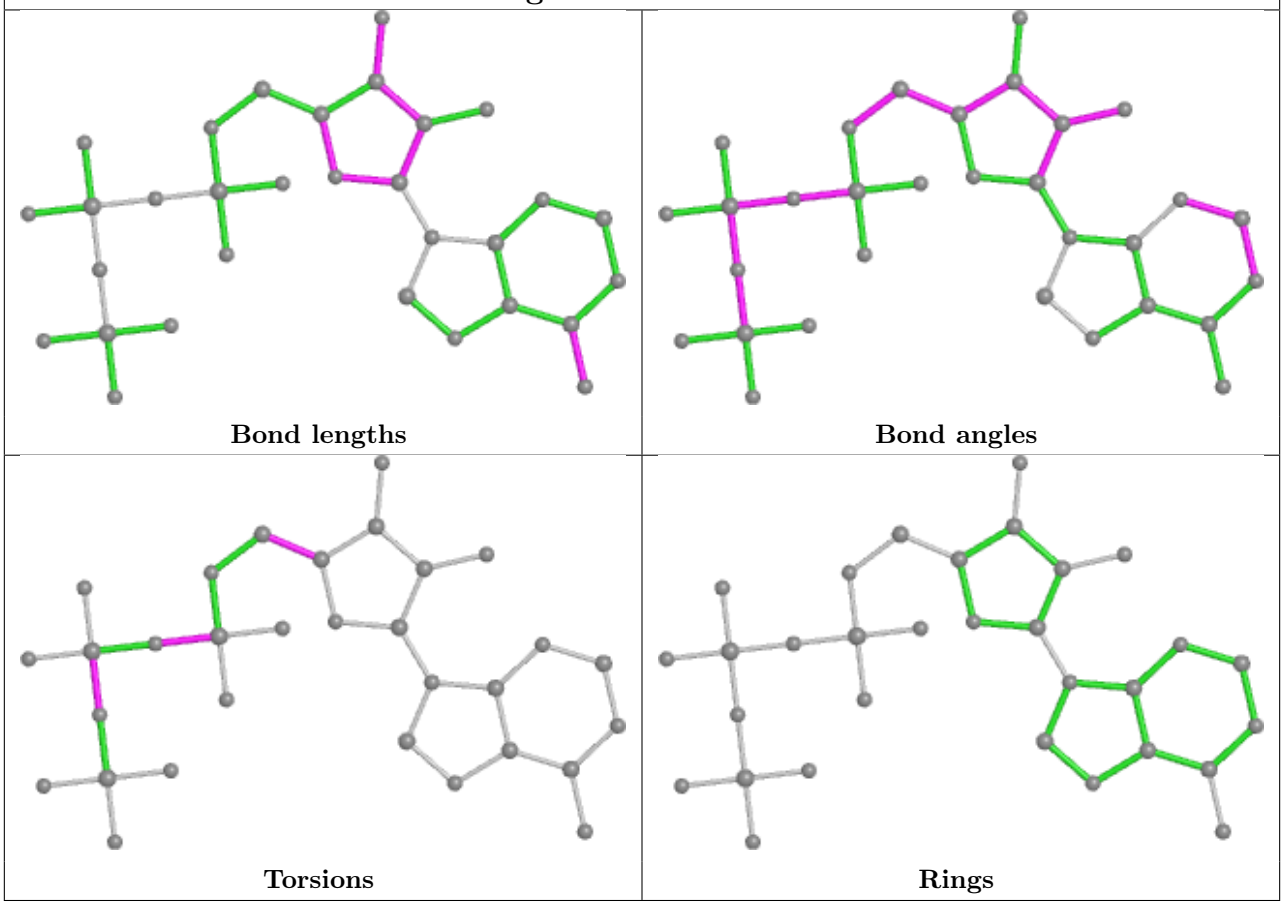
Ligand ATP C 801



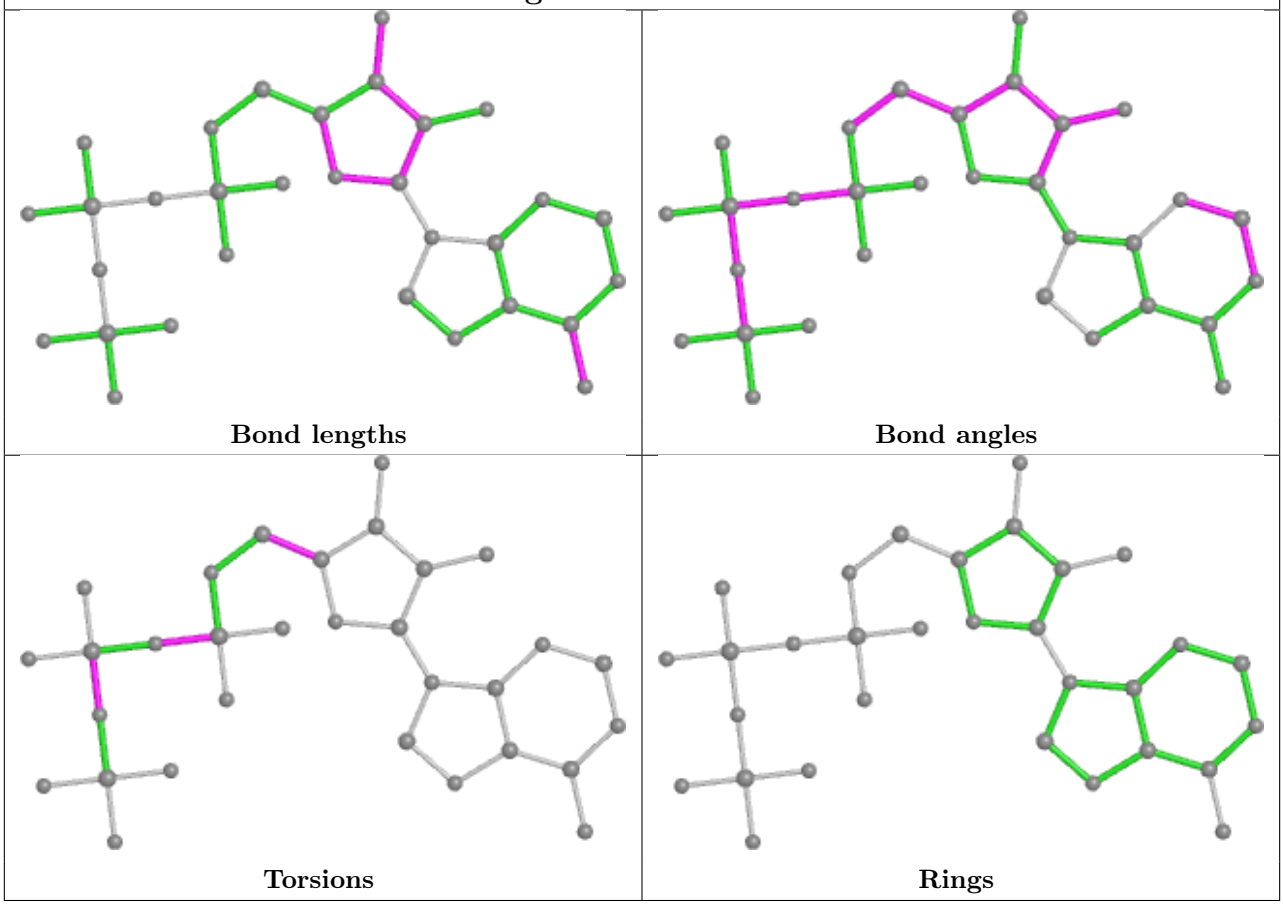
Ligand ATP D 801



Ligand ATP B 801



Ligand ATP A 801



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	734/761 (96%)	-0.29	0	100	100	62, 120, 165, 251	0
1	B	735/761 (96%)	-0.04	8 (1%)	80	72	76, 152, 200, 256	0
1	C	733/761 (96%)	-0.24	2 (0%)	94	90	63, 128, 171, 261	0
1	D	736/761 (96%)	-0.16	2 (0%)	94	90	68, 133, 187, 253	0
2	E	354/375 (94%)	-0.06	4 (1%)	80	72	77, 152, 210, 243	0
2	F	358/375 (95%)	-0.02	2 (0%)	89	84	74, 151, 209, 256	0
2	G	357/375 (95%)	-0.17	2 (0%)	89	84	96, 162, 207, 255	0
2	H	356/375 (94%)	-0.07	3 (0%)	86	79	117, 172, 208, 267	0
All	All	4363/4544 (96%)	-0.15	23 (0%)	91	85	62, 141, 198, 267	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	322	ASP	3.5
1	D	166	TYR	3.4
1	B	295	GLY	3.3
2	F	92	ASN	3.1
2	H	178	ASN	3.1

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)

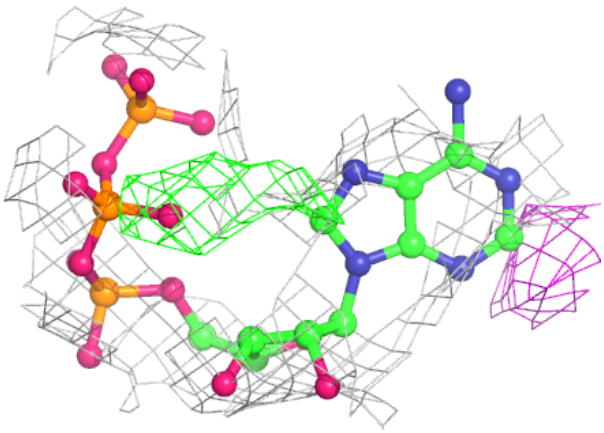
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

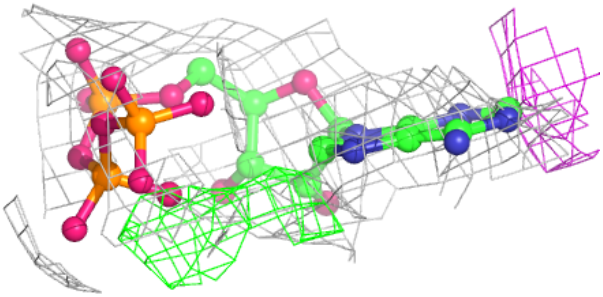
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ATP	C	801	31/31	0.80	0.31	138,138,138,138	0
3	ATP	D	801	31/31	0.83	0.42	195,195,195,195	0
3	ATP	B	801	31/31	0.88	0.56	225,225,225,225	0
3	ATP	A	801	31/31	0.91	0.35	126,126,126,126	0
4	FEO	E	501	3/3	0.97	0.10	119,119,119,119	0
4	FEO	G	501	3/3	0.98	0.13	124,124,124,124	0
4	FEO	F	501	3/3	0.99	0.19	106,106,106,106	0
4	FEO	H	501	3/3	0.99	0.09	133,133,133,133	0

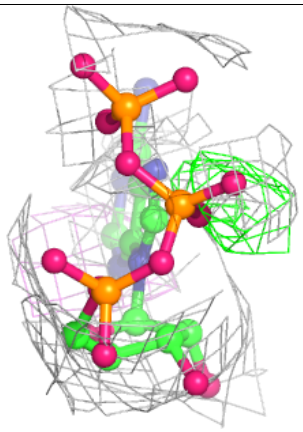
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ATP C 801:

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

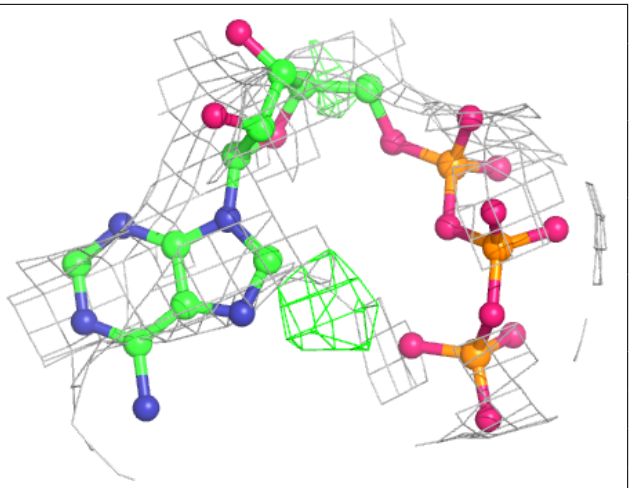


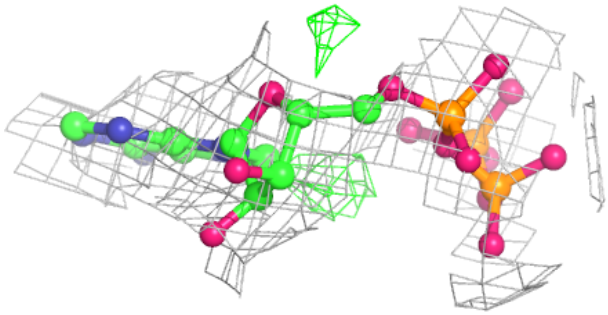


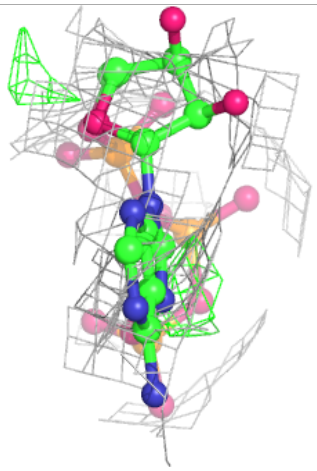


Electron density around ATP D 801:

$2mF_o$-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 B 801:

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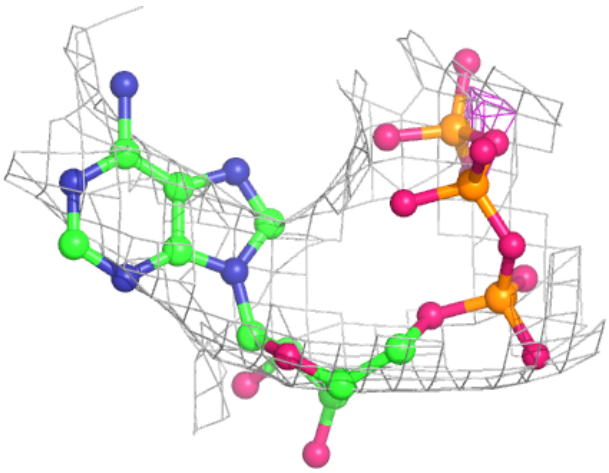
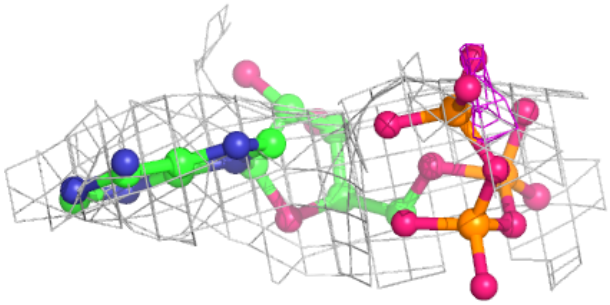
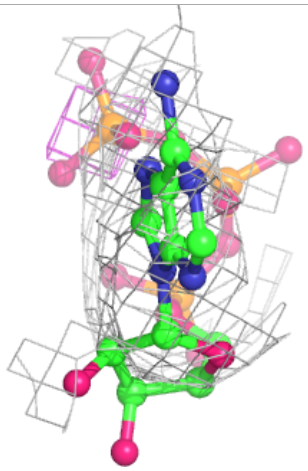
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

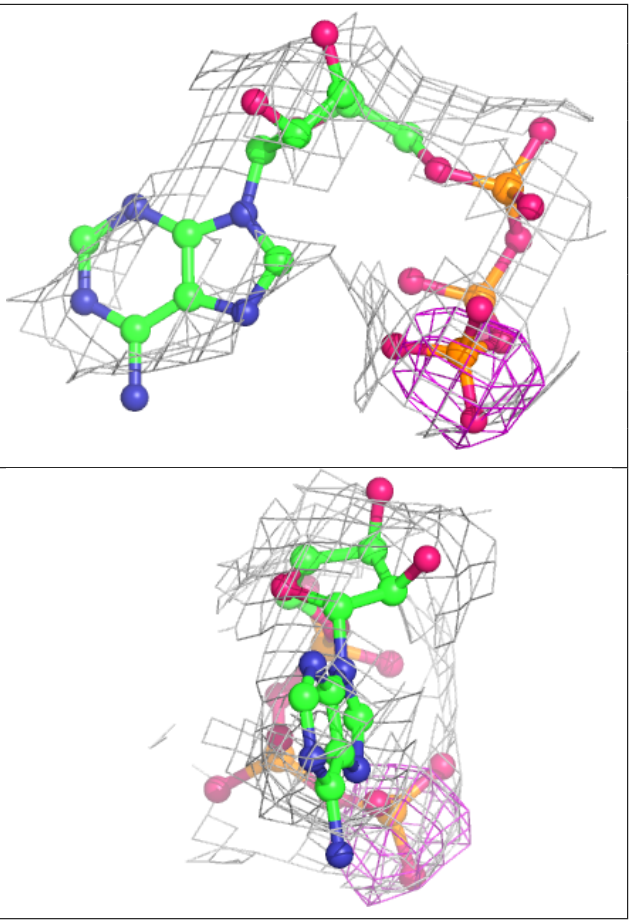






Electron density around ATP A 801:

$2mF_o$-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.