Full wwPDB X-ray Structure Validation Report (i)

Jun 13, 2024 – 04:05 PM EDT

PDB ID	:	6PXI
Title	:	The crystal structure of a singly capped HslUV complex with an axial pore plug and a HslU E257Q mutation
Authors	:	Baytshtok, V.; Grant, R.A.; Sauer, R.T.
Deposited on	:	2019-07-26
Resolution	:	3.45 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:

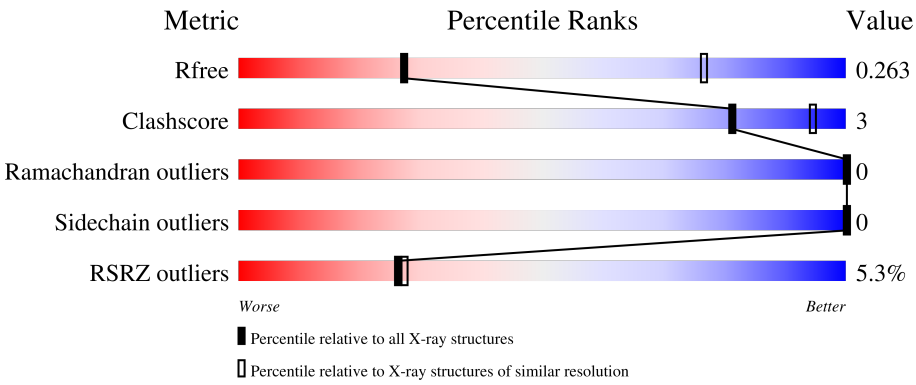
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 3.45 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	1278 (3.50-3.38)
Clashscore	141614	1361 (3.50-3.38)
Ramachandran outliers	138981	1327 (3.50-3.38)
Sidechain outliers	138945	1328 (3.50-3.38)
RSRZ outliers	127900	1192 (3.50-3.38)

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	174	6% 96% .
1	B	174	4% 95% 5%
1	C	174	5% 94% 6%
1	D	174	5% 94% 6%
2	E	448	3% 76% 7% 17%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	448	6% 75% 7% 18%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 11163 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 ATP-dependent protease subunit HslV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	174	1316	828	231	253	4	0	0	0
1	B	174	1316	828	231	253	4	0	0	0
1	C	174	1322	831	234	253	4	0	0	0
1	D	174	1316	828	231	253	4	0	0	0

- Molecule 2 is a protein called ATP-dependent protease ATPase subunit HslU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	374	2934	1835	521	568	10	0	0	0
2	F	367	2889	1806	516	554	13	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

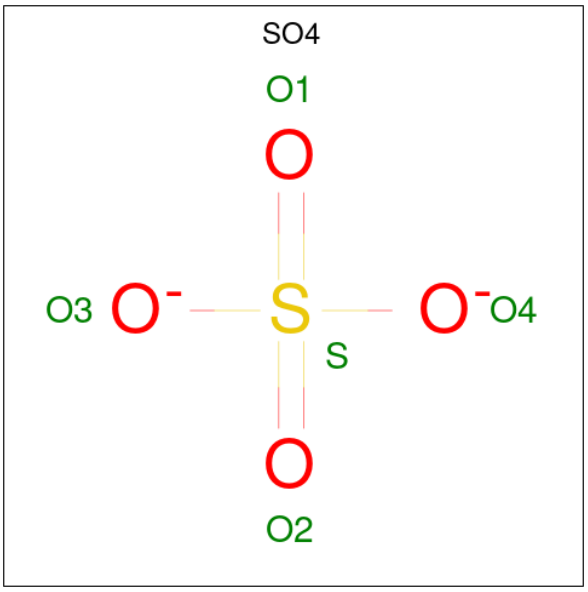
Chain	Residue	Modelled	Actual	Comment	Reference
E	-4	HIS	-	expression tag	UNP P0A6H5
E	-3	HIS	-	expression tag	UNP P0A6H5
E	-2	HIS	-	expression tag	UNP P0A6H5
E	-1	HIS	-	expression tag	UNP P0A6H5
E	0	HIS	-	expression tag	UNP P0A6H5
E	1	HIS	-	expression tag	UNP P0A6H5
E	257	GLN	GLU	engineered mutation	UNP P0A6H5
F	-4	HIS	-	expression tag	UNP P0A6H5
F	-3	HIS	-	expression tag	UNP P0A6H5
F	-2	HIS	-	expression tag	UNP P0A6H5
F	-1	HIS	-	expression tag	UNP P0A6H5
F	0	HIS	-	expression tag	UNP P0A6H5

Continued on next page...

Continued from previous page...

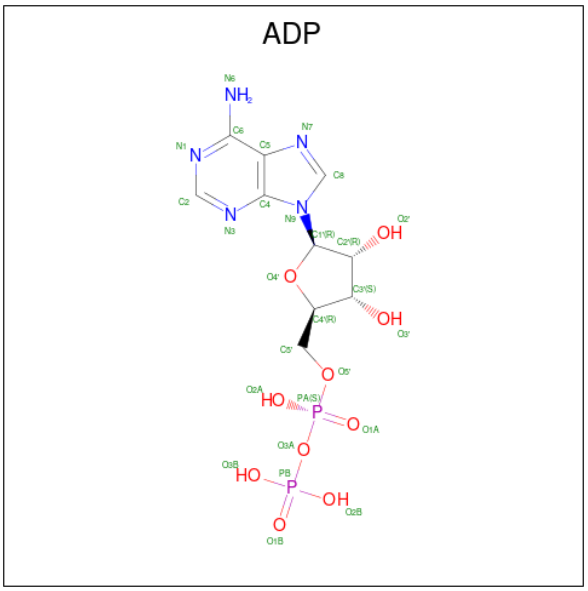
Chain	Residue	Modelled	Actual	Comment	Reference
F	1	HIS	-	expression tag	UNP P0A6H5
F	257	GLN	GLU	engineered mutation	UNP P0A6H5

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 5 is water.

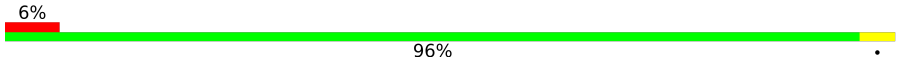
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	1	Total	O	0	0
			1	1		

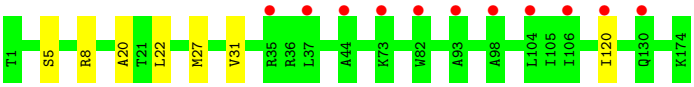
3 Residue-property plots (i)

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: ATP-dependent protease subunit HslV

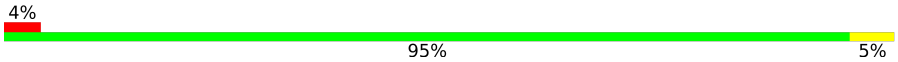
Chain A:

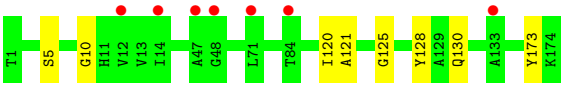




• Molecule 1: ATP-dependent protease subunit HslV

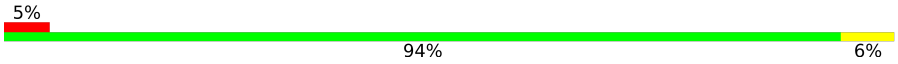
Chain B:

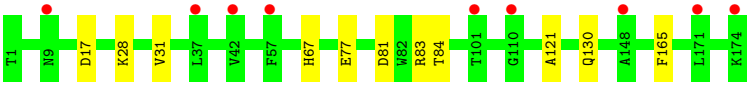




• Molecule 1: ATP-dependent protease subunit HslV

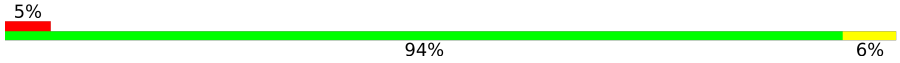
Chain C:

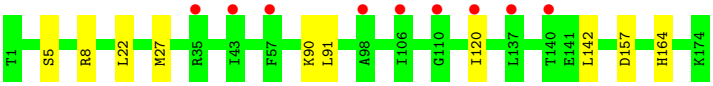




• Molecule 1: ATP-dependent protease subunit HslV

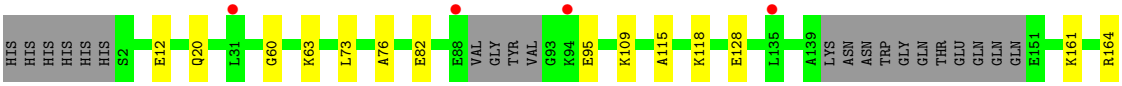
Chain D:

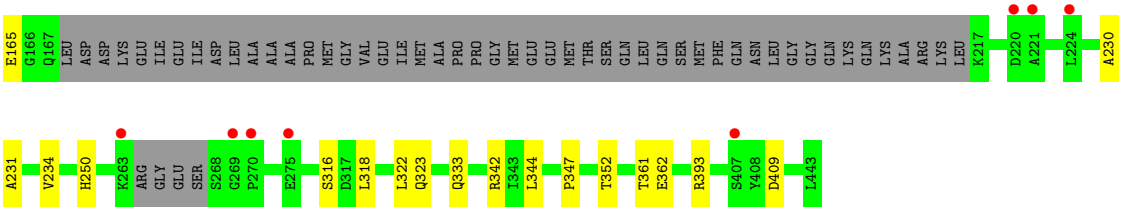




• Molecule 2: ATP-dependent protease ATPase subunit HslU

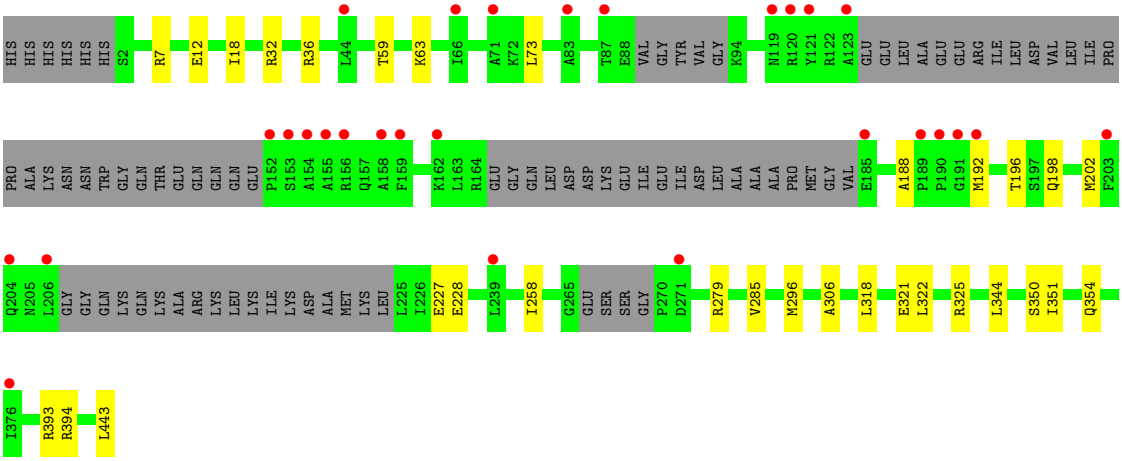
Chain E:





- Molecule 2: ATP-dependent protease ATPase subunit HslU

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α, β, γ	168.60Å 168.60Å 162.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.67 – 3.45 48.67 – 3.45	Depositor EDS
% Data completeness (in resolution range)	81.0 (48.67-3.45) 64.7 (48.67-3.45)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.90 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.10_2155	Depositor
R, R_{free}	0.257 , 0.285 0.244 , 0.263	Depositor DCC
R_{free} test set	1998 reflections (6.84%)	wwPDB-VP
Wilson B-factor (Å^2)	75.4	Xtriage
Anisotropy	0.207	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 35.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.368 for -h,-k,l	Xtriage
Reported twinning fraction	0.450 for -h,-k,l	Depositor
Outliers	0 of 29212 reflections	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	11163	wwPDB-VP
Average B, all atoms (Å^2)	111.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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: SO4, ADP

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	0.23	0/1333	0.42	0/1803
1	B	0.24	0/1333	0.42	0/1803
1	C	0.24	0/1339	0.42	0/1810
1	D	0.23	0/1333	0.42	0/1803
2	E	0.23	0/2967	0.38	0/3999
2	F	0.23	0/2922	0.38	0/3932
All	All	0.23	0/11227	0.40	0/15150

There are no bond length outliers.

There are no bond angle outliers.

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	1316	0	1326	4	0
1	B	1316	0	1326	4	0
1	C	1322	0	1337	9	0
1	D	1316	0	1326	6	0
2	E	2934	0	2990	21	0
2	F	2889	0	2948	23	0
3	A	10	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	5	0	0	0	0
4	E	27	0	12	2	0
4	F	27	0	12	3	0
5	E	1	0	0	0	0
All	All	11163	0	11277	59	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 3.

All (59) 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:81:ASP:HA	1:C:84:THR:HG22	1.59	0.84
2:F:59:THR:OG1	2:F:393:ARG:NH2	2.21	0.71
2:F:188:ALA:HB1	2:F:192:MET:HG3	1.75	0.68
1:C:83:ARG:NH1	1:D:90:LYS:O	2.32	0.63
1:C:81:ASP:HA	1:C:84:THR:CG2	2.29	0.62
1:A:8:ARG:HD3	3:A:202:SO4:O2	2.01	0.60
2:E:109:LYS:HB2	2:F:296:MET:HG2	1.83	0.59
2:E:231:ALA:HA	2:E:234:VAL:HG12	1.84	0.59
2:E:362:GLU:OE2	2:F:32:ARG:NE	2.34	0.58
2:F:63:LYS:N	4:F:501:ADP:O3B	2.36	0.56
1:C:81:ASP:CA	1:C:84:THR:HG22	2.36	0.54
2:F:18:ILE:N	4:F:501:ADP:N1	2.53	0.53
2:E:230:ALA:O	2:E:234:VAL:HG12	2.10	0.51
2:E:115:ALA:O	2:E:118:LYS:HG2	2.10	0.51
2:F:12:GLU:HG2	2:F:73:LEU:HD13	1.92	0.50
2:E:20:GLN:NE2	2:E:333:GLN:O	2.43	0.49
2:E:60:GLY:HA2	4:E:501:ADP:H5'2	1.95	0.48
2:E:361:THR:HG21	2:F:36:ARG:HA	1.95	0.48
2:E:12:GLU:HG2	2:E:73:LEU:HD13	1.96	0.48
2:E:82:GLU:HG3	2:F:279:ARG:HB3	1.96	0.47
2:E:409:ASP:OD1	2:F:7:ARG:NH2	2.48	0.47
2:E:63:LYS:N	4:E:501:ADP:O3B	2.44	0.47
2:E:318:LEU:HD22	2:E:322:LEU:HD23	1.96	0.46
1:A:5:SER:HB3	1:A:120:ILE:HB	1.97	0.46
1:C:121:ALA:HB3	1:C:130:GLN:HB2	1.97	0.46
2:F:344:LEU:HD23	2:F:351:ILE:HD11	1.98	0.46
2:F:188:ALA:HB2	2:F:196:THR:HG21	1.98	0.46
1:B:121:ALA:HB3	1:B:130:GLN:HB2	1.98	0.46
2:E:316:SER:O	2:E:323:GLN:NE2	2.49	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:393:ARG:NH2	2:F:321:GLU:HG3	2.32	0.45
1:A:22:LEU:HB2	1:A:27:MET:HE2	1.98	0.44
1:B:10:GLY:HA2	1:B:173:TYR:CE2	2.53	0.44
2:F:18:ILE:O	4:F:501:ADP:N6	2.49	0.44
1:B:125:GLY:HA2	1:B:128:TYR:CD2	2.53	0.43
2:E:344:LEU:O	2:E:352:THR:OG1	2.19	0.43
2:F:318:LEU:HD22	2:F:322:LEU:HD23	2.00	0.43
1:C:28:LYS:HD3	1:C:31:VAL:HG22	2.01	0.43
2:F:59:THR:HG1	2:F:393:ARG:HH21	1.58	0.43
2:F:198:GLN:O	2:F:202:MET:HG2	2.19	0.43
1:C:67:HIS:CE1	1:C:77:GLU:HG3	2.53	0.42
2:E:76:ALA:HB1	2:E:250:HIS:O	2.18	0.42
2:E:95:GLU:OE1	2:E:95:GLU:N	2.53	0.42
2:E:128:GLU:OE1	2:E:164:ARG:NH2	2.53	0.42
1:D:157:ASP:OD1	1:D:164:HIS:NE2	2.51	0.42
2:E:342:ARG:O	2:E:347:PRO:HD3	2.19	0.42
1:D:22:LEU:HB2	1:D:27:MET:HE2	2.01	0.42
1:C:83:ARG:HD3	1:D:91:LEU:HA	2.02	0.41
2:F:285:VAL:HG12	2:F:325:ARG:HE	1.85	0.41
2:E:161:LYS:HE2	2:E:165:GLU:OE2	2.20	0.41
2:F:285:VAL:HG11	2:F:325:ARG:HB3	2.03	0.41
2:F:350:SER:O	2:F:354:GLN:HG3	2.20	0.41
2:F:394:ARG:NH1	2:F:443:LEU:O	2.51	0.41
1:A:20:ALA:HB2	1:A:31:VAL:HG21	2.03	0.41
1:B:5:SER:HB3	1:B:120:ILE:HB	2.03	0.40
1:C:17:ASP:HA	1:C:165:PHE:O	2.21	0.40
1:D:8:ARG:NH1	1:D:142:LEU:O	2.52	0.40
2:F:258:ILE:HG21	2:F:306:ALA:HB1	2.03	0.40
1:D:5:SER:HB3	1:D:120:ILE:HB	2.04	0.40
2:F:227:GLU:HG2	2:F:228:GLU:N	2.37	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	172/174 (99%)	170 (99%)	2 (1%)	0	100	100
1	B	172/174 (99%)	169 (98%)	3 (2%)	0	100	100
1	C	172/174 (99%)	169 (98%)	3 (2%)	0	100	100
1	D	172/174 (99%)	170 (99%)	2 (1%)	0	100	100
2	E	364/448 (81%)	359 (99%)	5 (1%)	0	100	100
2	F	355/448 (79%)	350 (99%)	5 (1%)	0	100	100
All	All	1407/1592 (88%)	1387 (99%)	20 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	134/136 (98%)	134 (100%)	0	100	100
1	B	134/136 (98%)	134 (100%)	0	100	100
1	C	135/136 (99%)	135 (100%)	0	100	100
1	D	134/136 (98%)	134 (100%)	0	100	100
2	E	318/382 (83%)	318 (100%)	0	100	100
2	F	315/382 (82%)	315 (100%)	0	100	100
All	All	1170/1308 (89%)	1170 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	139	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	166	HIS
1	B	139	ASN
1	B	166	HIS
2	E	75	ASN
2	E	114	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)

5 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	ADP	F	501	-	24,29,29	0.95	1 (4%)	29,45,45	1.46	4 (13%)
3	SO4	A	202	-	4,4,4	0.20	0	6,6,6	0.16	0
3	SO4	A	201	-	4,4,4	0.15	0	6,6,6	0.07	0
4	ADP	E	501	-	24,29,29	0.97	1 (4%)	29,45,45	1.43	4 (13%)
3	SO4	C	201	-	4,4,4	0.16	0	6,6,6	0.06	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
4	ADP	F	501	-	-	5/12/32/32	0/3/3/3
4	ADP	E	501	-	-	4/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	501	ADP	C5-C4	2.52	1.47	1.40
4	E	501	ADP	C5-C4	2.52	1.47	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	F	501	ADP	C3'-C2'-C1'	3.46	106.18	100.98
4	E	501	ADP	C3'-C2'-C1'	3.44	106.16	100.98
4	F	501	ADP	PA-O3A-PB	-3.27	121.61	132.83
4	F	501	ADP	N3-C2-N1	-3.14	123.77	128.68
4	E	501	ADP	N3-C2-N1	-3.14	123.77	128.68
4	E	501	ADP	PA-O3A-PB	-3.00	122.52	132.83
4	F	501	ADP	C4-C5-N7	-2.61	106.68	109.40
4	E	501	ADP	C4-C5-N7	-2.54	106.75	109.40

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	501	ADP	C5'-O5'-PA-O2A
4	F	501	ADP	C5'-O5'-PA-O2A
4	F	501	ADP	O4'-C4'-C5'-O5'
4	E	501	ADP	C5'-O5'-PA-O3A
4	F	501	ADP	C5'-O5'-PA-O3A
4	F	501	ADP	C3'-C4'-C5'-O5'
4	E	501	ADP	O4'-C4'-C5'-O5'
4	E	501	ADP	C5'-O5'-PA-O1A
4	F	501	ADP	C5'-O5'-PA-O1A

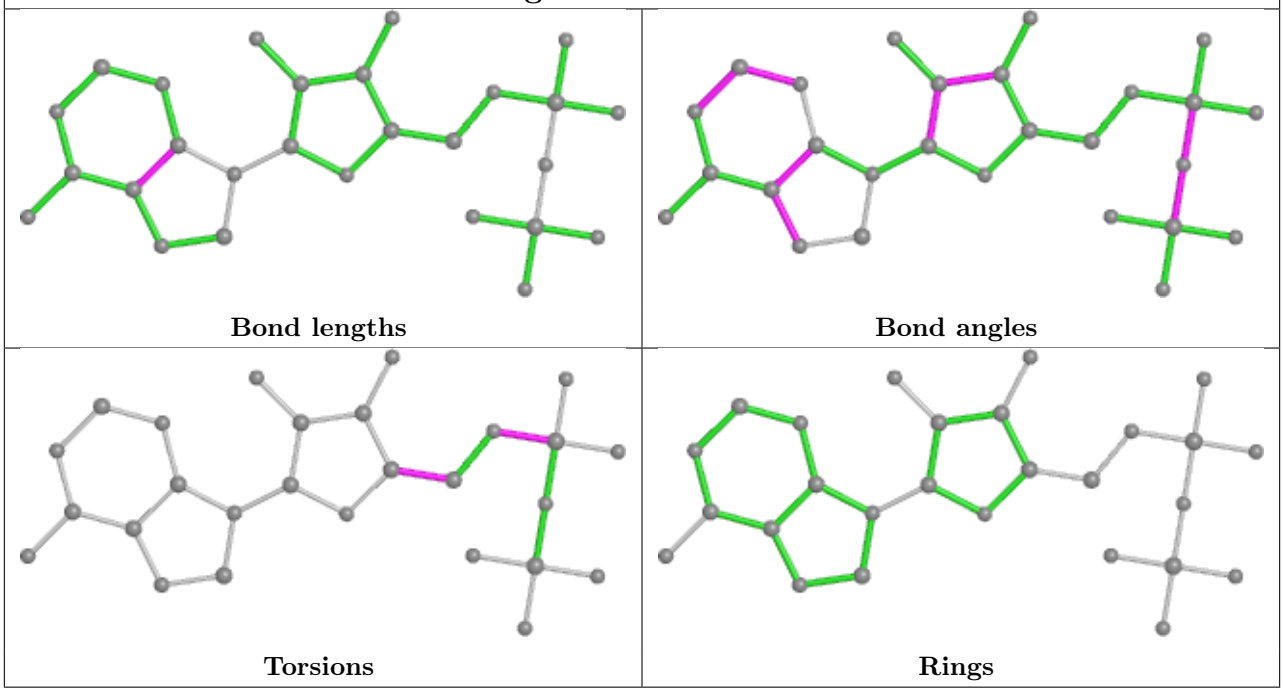
There are no ring outliers.

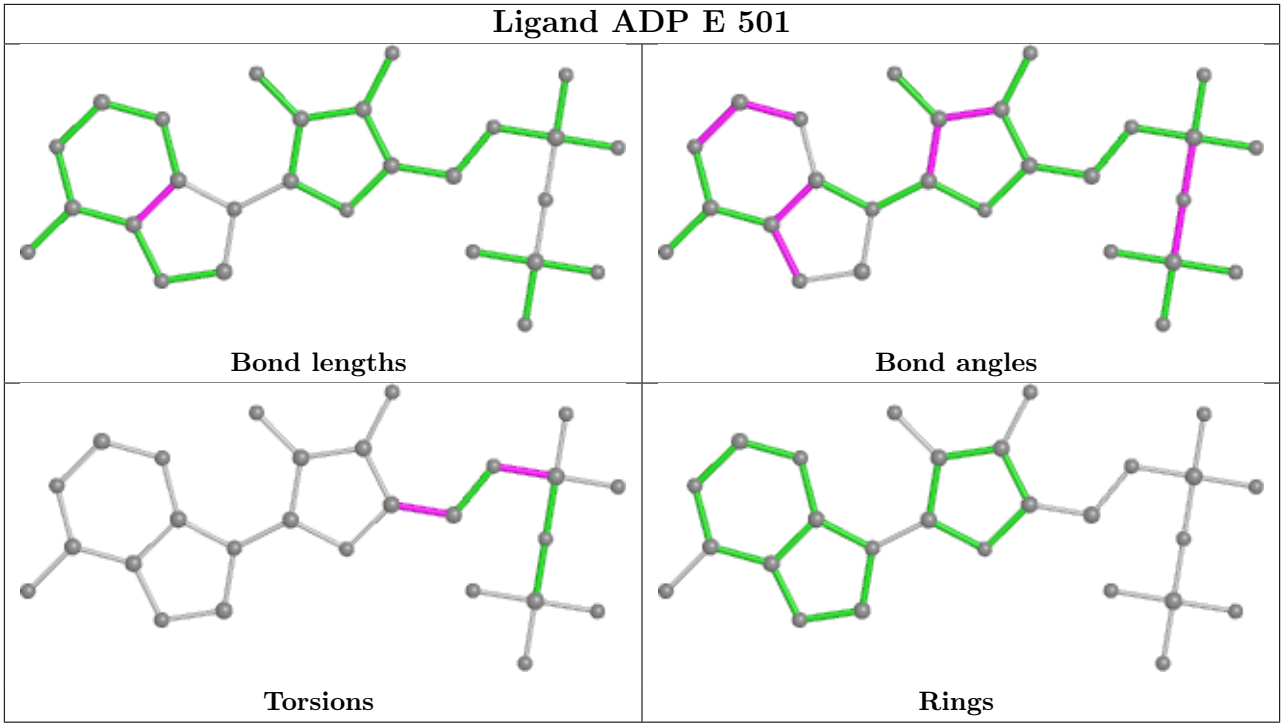
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	501	ADP	3	0
3	A	202	SO4	1	0
4	E	501	ADP	2	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 ADP F 501





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	174/174 (100%)	0.64	11 (6%)	20	21	95, 126, 148, 159	0
1	B	174/174 (100%)	0.53	7 (4%)	38	37	81, 109, 136, 155	0
1	C	174/174 (100%)	0.57	9 (5%)	27	28	86, 118, 138, 146	0
1	D	174/174 (100%)	0.58	9 (5%)	27	28	83, 116, 140, 147	0
2	E	374/448 (83%)	0.50	12 (3%)	47	46	67, 97, 138, 166	0
2	F	367/448 (81%)	0.65	28 (7%)	13	16	65, 103, 150, 179	0
All	All	1437/1592 (90%)	0.58	76 (5%)	26	27	65, 110, 145, 179	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	269	GLY	6.8
2	F	152	PRO	6.2
2	F	190	PRO	5.9
2	E	270	PRO	5.3
2	F	119	ASN	5.1
2	F	191	GLY	5.1
2	E	220	ASP	5.0
1	A	98	ALA	4.7
2	F	154	ALA	4.4
2	F	153	SER	4.2
2	F	123	ALA	4.0
1	C	42	VAL	4.0
2	E	263	LYS	3.9
2	E	88	GLU	3.8
1	C	110	GLY	3.7
1	C	57	PHE	3.5
2	F	155	ALA	3.4
1	A	73	LYS	3.4
1	B	71	LEU	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	E	224	LEU	3.3
2	F	121	TYR	3.2
2	F	271	ASP	3.2
2	E	31	LEU	3.2
2	F	159	PHE	3.2
2	E	221	ALA	3.0
1	B	47	ALA	3.0
1	A	120	ILE	3.0
2	F	158	ALA	3.0
2	F	162	LYS	2.9
1	C	37	LEU	2.9
1	A	93	ALA	2.9
1	D	98	ALA	2.8
2	E	407	SER	2.8
2	F	206	LEU	2.8
1	C	174	LYS	2.8
1	D	140	THR	2.8
2	F	120	ARG	2.7
1	A	37	LEU	2.7
2	F	239	LEU	2.6
1	A	82	TRP	2.6
1	A	44	ALA	2.6
2	F	71	ALA	2.5
2	F	87	THR	2.5
1	B	12	VAL	2.5
1	C	171	LEU	2.5
1	A	104	LEU	2.5
2	F	192	MET	2.4
2	F	203	PHE	2.4
2	F	376	ILE	2.4
1	C	9	ASN	2.4
2	E	275	GLU	2.4
1	D	106	ILE	2.4
2	F	156	ARG	2.4
2	F	189	PRO	2.3
1	D	43	ILE	2.3
2	F	204	GLN	2.3
1	A	35	ARG	2.2
2	F	44	LEU	2.2
1	C	101	THR	2.2
1	D	120	ILE	2.2
2	F	66	ILE	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	F	185	GLU	2.2
1	B	48	GLY	2.2
2	E	94	LYS	2.2
1	D	137	LEU	2.1
2	E	135	LEU	2.1
1	B	84	THR	2.1
1	C	148	ALA	2.1
1	D	110	GLY	2.1
1	A	106	ILE	2.1
1	D	35	ARG	2.0
1	B	133	ALA	2.0
2	F	83	ALA	2.0
1	D	57	PHE	2.0
1	B	14	ILE	2.0
1	A	130	GLN	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 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.

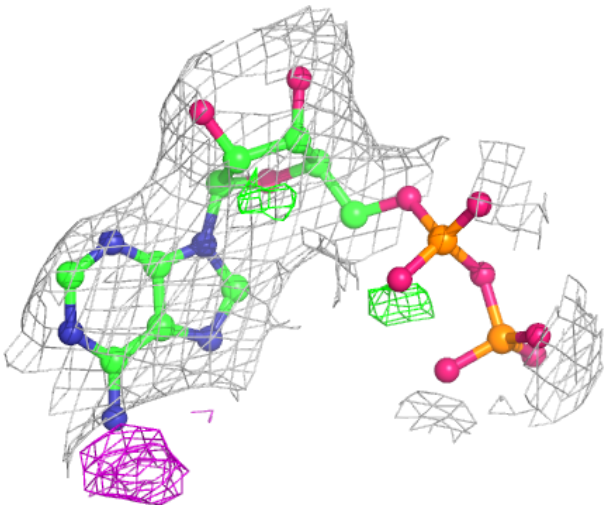
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	A	201	5/5	0.83	0.19	162,162,169,171	0
3	SO4	A	202	5/5	0.90	0.12	151,156,159,162	0
4	ADP	E	501	27/27	0.94	0.25	64,72,94,96	0
3	SO4	C	201	5/5	0.95	0.17	94,95,98,99	5
4	ADP	F	501	27/27	0.96	0.21	71,82,95,99	0

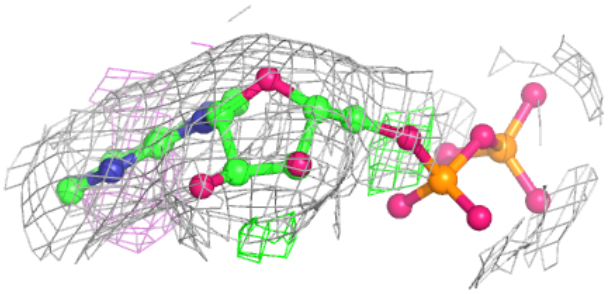
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

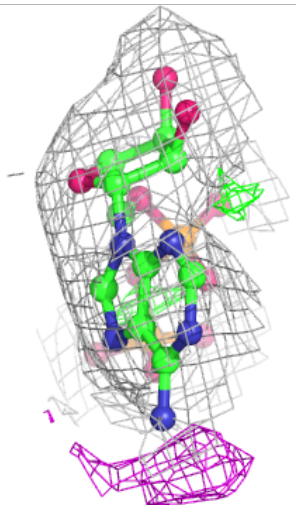
as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ADP E 501:

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

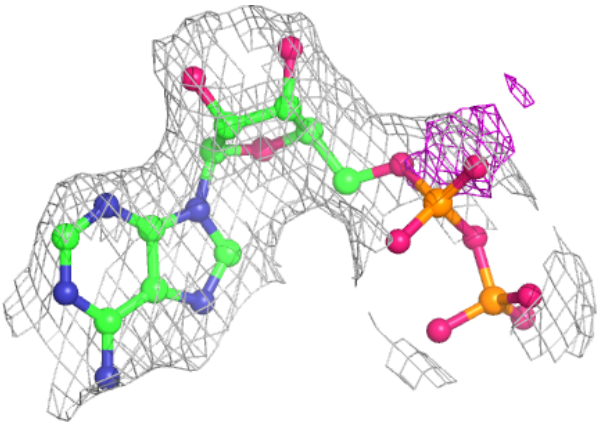


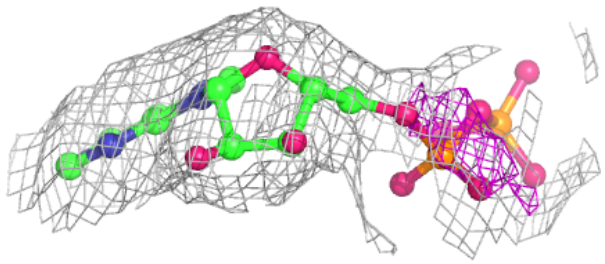


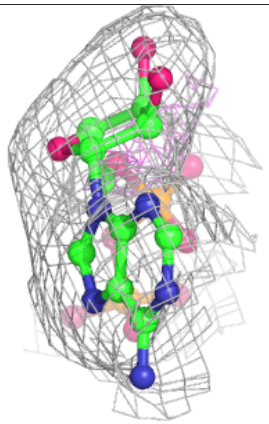


Electron density around ADP F 501:

$2mF_o$-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.