



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 10:47 am BST

PDB ID : 6NYA
Title : Crystal Structure of ubiquitin E1 (Uba1) in complex with Ubc3 (Cdc34) and ubiquitin
Authors : Olsen, S.K.; Williams, K.M.; Atkison, J.H.
Deposited on : 2019-02-11
Resolution : 2.06 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.11
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) : 2.11

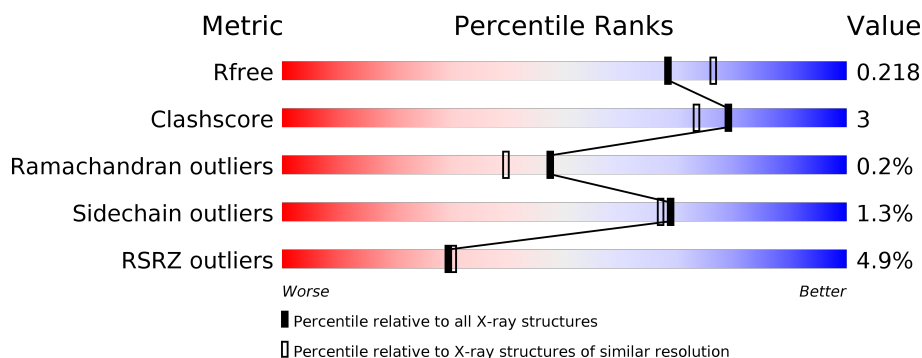
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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 on 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	1017	<div> <div>2%</div> <div>89%</div> <div>8%</div> <div>•</div> </div>
1	D	1017	<div> <div>5%</div> <div>90%</div> <div>6%</div> <div>•</div> </div>
2	B	85	<div> <div>82%</div> <div>8%</div> <div>•</div> <div>8%</div> </div>
2	E	85	<div> <div>5%</div> <div>76%</div> <div>13%</div> <div>•</div> <div>9%</div> </div>
3	C	197	<div> <div>10%</div> <div>78%</div> <div>8%</div> <div>14%</div> </div>
3	F	197	<div> <div>12%</div> <div>72%</div> <div>13%</div> <div>15%</div> </div>

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
6	SO4	A	1104	-	-	-	X
6	SO4	D	1204	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 20705 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 Ubiquitin-activating enzyme E1 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	987	Total	C	N	O	S	0	0	0
			7800	4979	1288	1510	23			
1	D	987	Total	C	N	O	S	0	0	0
			7796	4977	1288	1508	23			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	GLY	-	expression tag	UNP P22515
A	9	ALA	-	expression tag	UNP P22515
A	10	MET	-	expression tag	UNP P22515
D	8	GLY	-	expression tag	UNP P22515
D	9	ALA	-	expression tag	UNP P22515
D	10	MET	-	expression tag	UNP P22515

- Molecule 2 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	78	Total	C	N	O	S	0	0	0
			622	380	121	120	1			
2	E	77	Total	C	N	O	S	0	0	0
			618	378	120	119	1			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	MET	-	initiating methionine	UNP A0A1D6RLC6
B	-7	HIS	-	expression tag	UNP A0A1D6RLC6
B	-6	HIS	-	expression tag	UNP A0A1D6RLC6
B	-5	HIS	-	expression tag	UNP A0A1D6RLC6
B	-4	HIS	-	expression tag	UNP A0A1D6RLC6
B	-3	HIS	-	expression tag	UNP A0A1D6RLC6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	expression tag	UNP A0A1D6RLC6
B	-1	GLY	-	expression tag	UNP A0A1D6RLC6
B	0	ALA	-	expression tag	UNP A0A1D6RLC6
B	6	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
B	11	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
B	27	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
B	29	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
B	33	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
B	48	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
B	63	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
E	-8	MET	-	initiating methionine	UNP A0A1D6RLC6
E	-7	HIS	-	expression tag	UNP A0A1D6RLC6
E	-6	HIS	-	expression tag	UNP A0A1D6RLC6
E	-5	HIS	-	expression tag	UNP A0A1D6RLC6
E	-4	HIS	-	expression tag	UNP A0A1D6RLC6
E	-3	HIS	-	expression tag	UNP A0A1D6RLC6
E	-2	HIS	-	expression tag	UNP A0A1D6RLC6
E	-1	GLY	-	expression tag	UNP A0A1D6RLC6
E	0	ALA	-	expression tag	UNP A0A1D6RLC6
E	6	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
E	11	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
E	27	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
E	29	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
E	33	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
E	48	ARG	LYS	engineered mutation	UNP A0A1D6RLC6
E	63	ARG	LYS	engineered mutation	UNP A0A1D6RLC6

- Molecule 3 is a protein called Ubiquitin-conjugating enzyme E2-34 kDa.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	170	Total	C	N	O	S	0	0	0
			1381	881	235	260	5			
3	F	167	Total	C	N	O	S	0	0	0
			1356	868	229	254	5			

There are 8 discrepancies between the modelled and reference sequences:

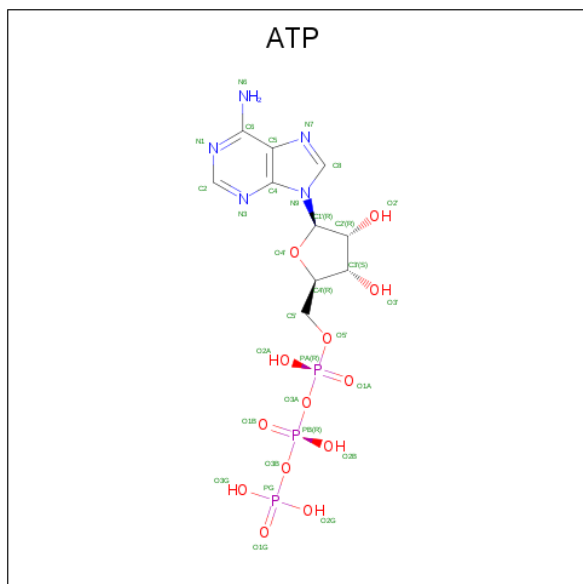
Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLY	-	expression tag	UNP P14682
C	0	ALA	-	expression tag	UNP P14682
C	1	MET	-	expression tag	UNP P14682
C	2	ALA	-	expression tag	UNP P14682

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	GLY	-	expression tag	UNP P14682
F	0	ALA	-	expression tag	UNP P14682
F	1	MET	-	expression tag	UNP P14682
F	2	ALA	-	expression tag	UNP P14682

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



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

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		
5	D	1	Total	Mg	0	0
			1	1		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

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

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0

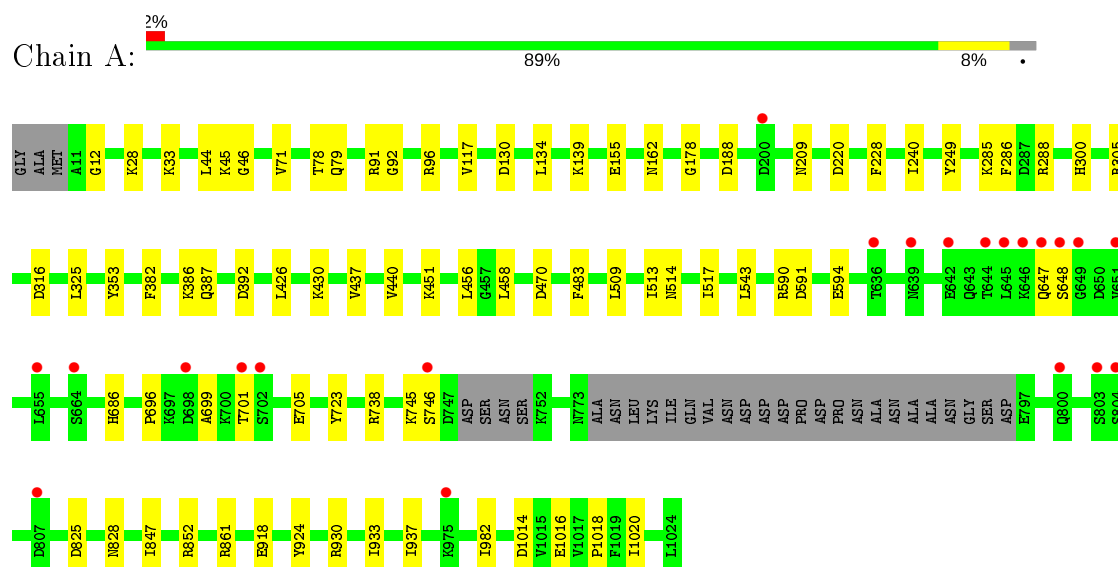
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	471	Total O 471 471	0	0
8	B	29	Total O 29 29	0	0
8	C	9	Total O 9 9	0	0
8	D	373	Total O 373 373	0	0
8	E	21	Total O 21 21	0	0
8	F	6	Total O 6 6	0	0

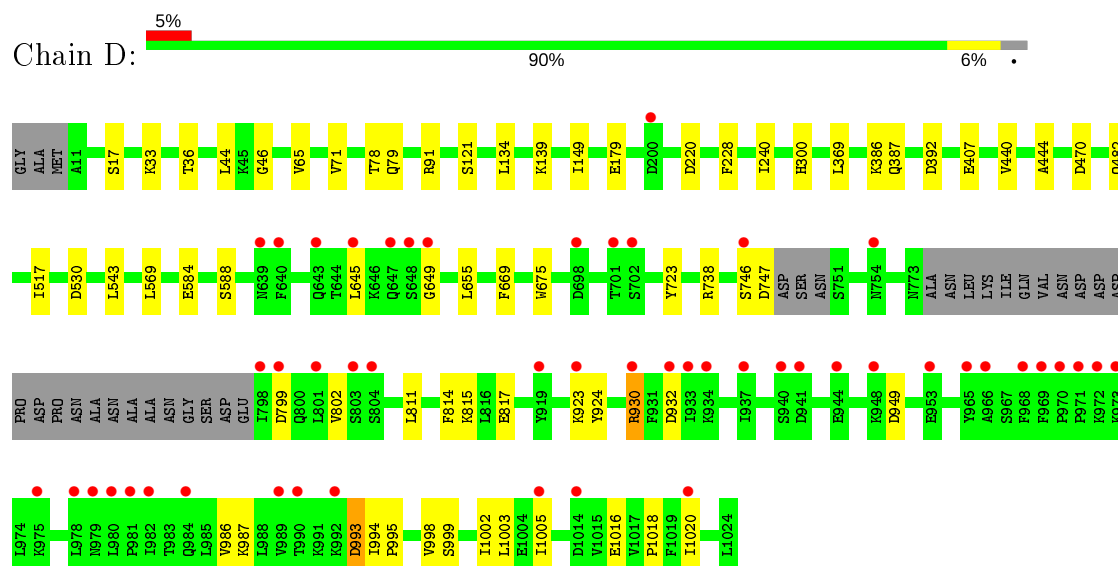
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Ubiquitin-activating enzyme E1 1



- Molecule 1: Ubiquitin-activating enzyme E1 1




- Molecule 2: Ubiquitin

Chain B:  82% 8% 8%




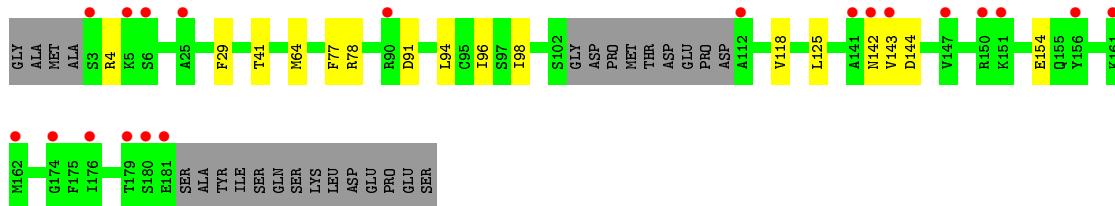
• Molecule 2: Ubiquitin

Chain E:  5% 76% 13% 9%




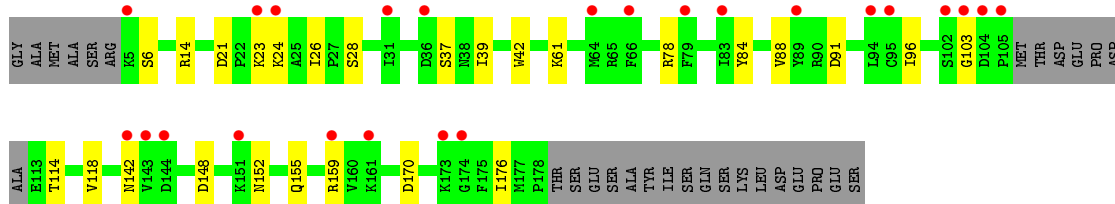
• Molecule 3: Ubiquitin-conjugating enzyme E2-34 kDa

Chain C:  10% 78% 8% 14%



• Molecule 3: Ubiquitin-conjugating enzyme E2-34 kDa

Chain F:  12% 72% 13% 15%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	126.44Å 68.54Å 171.72Å 90.00° 110.72° 90.00°	Depositor
Resolution (Å)	117.03 – 2.06 117.03 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.0 (117.03-2.06) 89.4 (117.03-2.07)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.88 (at 2.07Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155)	Depositor
R, R_{free}	0.187 , 0.217 0.187 , 0.218	Depositor DCC
R_{free} test set	2005 reflections (1.20%)	wwPDB-VP
Wilson B-factor (Å ²)	27.1	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20705	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.85% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SO4, ATP, EDO

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	0.27	0/7962	0.44	0/10770
1	D	0.27	0/7958	0.43	0/10766
2	B	0.25	0/627	0.49	1/843 (0.1%)
2	E	0.23	0/623	0.48	1/838 (0.1%)
3	C	0.25	0/1417	0.40	0/1922
3	F	0.25	0/1393	0.40	0/1891
All	All	0.27	0/19980	0.43	2/27030 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	73	LEU	CA-CB-CG	-5.22	103.29	115.30
2	E	73	LEU	CA-CB-CG	-5.14	103.47	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	7800	0	7721	46	0
1	D	7796	0	7721	43	0
2	B	622	0	633	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	618	0	630	7	0
3	C	1381	0	1351	9	0
3	F	1356	0	1325	13	0
4	A	31	0	12	0	0
4	D	31	0	12	0	0
5	A	1	0	0	0	0
5	D	1	0	0	0	0
6	A	40	0	0	1	0
6	D	35	0	0	2	0
7	A	44	0	66	2	0
7	C	4	0	6	1	0
7	D	36	0	54	3	0
8	A	471	0	0	7	0
8	B	29	0	0	0	0
8	C	9	0	0	0	0
8	D	373	0	0	3	0
8	E	21	0	0	2	0
8	F	6	0	0	0	0
All	All	20705	0	19531	111	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 (111) 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:D:930:ARG:NH1	1:D:932:ASP:OD2	2.07	0.88
1:D:1016:GLU:OE2	3:F:14:ARG:NH2	2.21	0.73
3:F:84:TYR:OH	3:F:148:ASP:OD2	2.05	0.73
3:C:143:VAL:HB	3:C:144:ASP:HA	1.72	0.71
1:D:44:LEU:HD21	1:D:65:VAL:HB	1.76	0.66
1:D:811:LEU:HB3	1:D:814:PHE:HB3	1.80	0.61
1:A:71:VAL:HG22	1:A:91:ARG:HG2	1.84	0.60
1:D:655:LEU:HD13	1:D:802:VAL:HG12	1.85	0.58
1:D:71:VAL:HG22	1:D:91:ARG:HG2	1.86	0.58
1:D:1005:ILE:HD13	1:D:1020:ILE:HD11	1.86	0.57
1:A:96:ARG:HH21	7:A:1112:EDO:H11	1.70	0.57
3:F:78:ARG:NH1	3:F:91:ASP:O	2.38	0.57
1:D:17:SER:H	7:D:1212:EDO:H11	1.70	0.57
2:E:26:VAL:HG21	2:E:56:LEU:HD21	1.85	0.56
1:D:440:VAL:HG12	1:D:543:LEU:HD21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:142:ASN:ND2	3:C:143:VAL:O	2.39	0.54
1:A:117:VAL:HG21	1:D:723:TYR:HE2	1.72	0.53
1:A:44:LEU:HD12	1:A:92:GLY:HA2	1.90	0.53
1:A:1016:GLU:HG2	3:C:4:ARG:HE	1.74	0.52
1:D:987:LYS:HG2	1:D:993:ASP:HA	1.91	0.51
3:F:61:LYS:HE3	3:F:170:ASP:HB3	1.91	0.51
1:A:852:ARG:NH1	8:A:1213:HOH:O	2.43	0.51
1:A:745:LYS:HG2	1:A:746:SER:H	1.76	0.50
1:A:451:LYS:HG3	1:A:483:PHE:HZ	1.76	0.50
3:C:96:ILE:HG12	3:C:98:ILE:HG22	1.94	0.49
1:A:591:ASP:OD1	8:A:1201:HOH:O	2.19	0.49
1:A:440:VAL:HG12	1:A:543:LEU:HD21	1.94	0.49
1:A:45:LYS:NZ	8:A:1218:HOH:O	2.45	0.49
1:A:209:ASN:OD1	2:B:11:ARG:NH2	2.45	0.49
1:A:738:ARG:NH2	8:A:1217:HOH:O	2.45	0.48
2:B:26:VAL:HG21	2:B:56:LEU:HD21	1.94	0.48
1:D:930:ARG:HG2	6:D:1204:SO4:S	2.54	0.48
2:E:18:GLU:N	2:E:21:ASP:OD2	2.42	0.48
1:A:46:GLY:HA3	1:A:78:THR:OG1	2.12	0.48
1:D:930:ARG:HD2	1:D:932:ASP:OD2	2.14	0.48
1:D:799:ASP:HA	1:D:802:VAL:HG22	1.95	0.48
1:A:155:GLU:HG2	1:A:162:ASN:OD1	2.13	0.48
1:A:305:ARG:HH11	1:A:325:LEU:HD21	1.79	0.47
1:D:569:LEU:HB3	2:E:73:LEU:HD22	1.94	0.47
3:F:103:GLY:HA2	3:F:114:THR:HG21	1.96	0.47
1:A:594:GLU:OE1	1:A:861:ARG:NH1	2.41	0.47
1:A:696:PRO:HD2	1:A:699:ALA:HB2	1.97	0.47
3:C:29:PHE:CE1	3:C:125:LEU:HB3	2.50	0.47
2:E:54:ARG:NH1	8:E:101:HOH:O	2.47	0.47
1:D:179:GLU:HG3	2:E:9:THR:HB	1.96	0.47
3:F:152:ASN:HB3	3:F:155:GLN:HB2	1.96	0.47
3:F:155:GLN:O	3:F:159:ARG:HG2	2.15	0.47
1:A:514:ASN:ND2	6:A:1107:SO4:O1	2.48	0.47
1:A:228:PHE:HB3	1:A:240:ILE:HB	1.96	0.47
1:D:407:GLU:OE2	8:D:1301:HOH:O	2.21	0.47
2:B:27:ARG:HB3	2:B:38:PRO:HB3	1.97	0.46
3:C:78:ARG:NH1	3:C:91:ASP:O	2.49	0.46
3:F:21:ASP:HB3	3:F:23:LYS:N	2.31	0.46
1:A:924:TYR:CD1	1:A:1018:PRO:HG3	2.50	0.46
2:B:24:ASP:OD1	2:B:24:ASP:N	2.48	0.46
1:D:121:SER:HA	1:D:149:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:701:THR:HG22	1:A:705:GLU:O	2.15	0.45
1:A:723:TYR:CZ	1:D:139:LYS:HD3	2.51	0.45
1:A:117:VAL:HG21	1:D:723:TYR:CE2	2.51	0.45
1:D:815:LYS:HE3	1:D:817:GLU:OE2	2.17	0.45
3:C:77:PHE:H	7:C:201:EDO:H12	1.81	0.44
1:A:933:ILE:HD13	1:A:1020:ILE:HG23	1.99	0.44
1:D:444:ALA:HA	1:D:482:GLN:HG2	2.00	0.44
1:D:134:LEU:HB2	1:D:300:HIS:CG	2.53	0.44
1:D:386:LYS:HA	1:D:387:GLN:HA	1.79	0.44
1:D:530:ASP:OD1	1:D:999:SER:OG	2.36	0.44
3:C:64:MET:HE3	3:C:64:MET:HB2	1.83	0.44
1:D:1003:LEU:HB2	1:D:1020:ILE:HB	2.00	0.43
3:F:21:ASP:HB3	3:F:24:LYS:H	1.83	0.43
1:A:509:LEU:HD13	1:A:513:ILE:HD11	2.00	0.43
1:D:584:GLU:HB2	1:D:588:SER:CB	2.49	0.43
3:F:39:ILE:O	3:F:42:TRP:NE1	2.49	0.43
1:A:386:LYS:HA	1:A:387:GLN:HA	1.69	0.43
1:D:930:ARG:HG2	6:D:1204:SO4:O2	2.19	0.43
1:A:139:LYS:HD3	1:D:723:TYR:CZ	2.54	0.43
1:D:930:ARG:HD2	1:D:932:ASP:CG	2.39	0.43
3:F:26:ILE:HG22	3:F:28:SER:H	1.84	0.43
1:A:33:LYS:HE2	8:A:1411:HOH:O	2.18	0.43
1:A:178:GLY:HA3	1:A:382:PHE:HE2	1.84	0.42
1:D:986:VAL:HG11	1:D:994:ILE:HD11	2.01	0.42
1:A:437:VAL:HG11	1:A:458:LEU:HD21	2.00	0.42
2:E:6:ARG:NH1	8:E:104:HOH:O	2.51	0.42
1:A:12:GLY:HA3	1:D:36:THR:HB	2.02	0.42
1:A:1014:ASP:OD2	3:C:4:ARG:NH2	2.40	0.42
1:D:924:TYR:CD2	1:D:1018:PRO:HG3	2.55	0.42
1:A:44:LEU:HD23	1:A:44:LEU:HA	1.91	0.42
1:A:738:ARG:NH1	8:A:1234:HOH:O	2.52	0.42
1:D:1016:GLU:OE2	3:F:6:SER:HB3	2.20	0.42
1:D:470:ASP:O	1:D:517:ILE:HA	2.19	0.42
1:D:46:GLY:HA3	1:D:78:THR:OG1	2.19	0.42
1:D:33:LYS:HE2	8:D:1421:HOH:O	2.20	0.42
1:A:647:GLN:HB3	1:A:648:SER:HA	2.01	0.41
1:A:847:ILE:HA	7:A:1114:EDO:H11	2.01	0.41
1:D:228:PHE:HB3	1:D:240:ILE:HB	2.02	0.41
2:E:55:THR:OG1	2:E:58:ASP:OD1	2.32	0.41
1:A:316:ASP:OD1	1:A:353:TYR:OH	2.27	0.41
1:A:285:LYS:HB3	1:A:288:ARG:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:LEU:HB2	1:A:300:HIS:CG	2.55	0.41
7:D:1213:EDO:H11	8:D:1376:HOH:O	2.20	0.41
1:D:995:PRO:HG2	1:D:998:VAL:HG23	2.03	0.41
1:D:669:PHE:CD2	1:D:746:SER:HB2	2.55	0.41
1:D:923:LYS:HE3	1:D:923:LYS:HB2	1.83	0.41
1:D:1002:ILE:HD13	7:D:1214:EDO:H11	2.03	0.41
1:D:675:TRP:CD2	1:D:738:ARG:HD2	2.56	0.41
1:A:937:ILE:O	1:A:982:ILE:HG12	2.21	0.40
1:A:188:ASP:HA	1:A:249:TYR:CE2	2.56	0.40
3:F:88:VAL:O	3:F:142:ASN:HB2	2.22	0.40
1:A:426:LEU:HG	1:A:430:LYS:HE2	2.03	0.40
1:A:470:ASP:O	1:A:517:ILE:HA	2.22	0.40
1:A:686:HIS:HE1	8:A:1227:HOH:O	2.04	0.40
1:A:825:ASP:HB3	1:A:828:ASN:ND2	2.36	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	981/1017 (96%)	951 (97%)	29 (3%)	1 (0%)	51	45
1	D	981/1017 (96%)	948 (97%)	31 (3%)	2 (0%)	47	39
2	B	76/85 (89%)	75 (99%)	1 (1%)	0	100	100
2	E	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
3	C	166/197 (84%)	161 (97%)	5 (3%)	0	100	100
3	F	163/197 (83%)	155 (95%)	7 (4%)	1 (1%)	25	15
All	All	2442/2598 (94%)	2363 (97%)	75 (3%)	4 (0%)	47	39

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	220	ASP
1	D	220	ASP
3	F	37	SER
1	D	649	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	870/893 (97%)	861 (99%)	9 (1%)	76	75
1	D	870/893 (97%)	862 (99%)	8 (1%)	78	78
2	B	67/74 (90%)	65 (97%)	2 (3%)	41	35
2	E	67/74 (90%)	65 (97%)	2 (3%)	41	35
3	C	157/179 (88%)	153 (98%)	4 (2%)	47	41
3	F	154/179 (86%)	151 (98%)	3 (2%)	57	53
All	All	2185/2292 (95%)	2157 (99%)	28 (1%)	69	67

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LYS
1	A	79	GLN
1	A	130	ASP
1	A	286	PHE
1	A	392	ASP
1	A	456	LEU
1	A	590	ARG
1	A	918	GLU
1	A	930	ARG
2	B	24	ASP
2	B	64	GLU
3	C	41	THR
3	C	94	LEU
3	C	118	VAL
3	C	154	GLU

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Mol	Chain	Res	Type
1	D	79	GLN
1	D	369	LEU
1	D	392	ASP
1	D	645	LEU
1	D	747	ASP
1	D	930	ARG
1	D	949	ASP
1	D	993	ASP
2	E	24	ASP
2	E	29	ARG
3	F	96	ILE
3	F	118	VAL
3	F	176	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	686	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 40 ligands modelled in this entry, 2 are monoatomic - leaving 38 for Mogul analysis.

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	$\# Z > 2$
7	EDO	D	1214	-	3,3,3	0.42	0	2,2,2	0.49	0
7	EDO	A	1118	-	3,3,3	0.46	0	2,2,2	0.38	0
7	EDO	A	1113	-	3,3,3	0.43	0	2,2,2	0.32	0
7	EDO	D	1218	-	3,3,3	0.46	0	2,2,2	0.35	0
7	EDO	A	1119	-	3,3,3	0.45	0	2,2,2	0.43	0
6	SO4	D	1209	-	4,4,4	0.14	0	6,6,6	0.06	0
6	SO4	A	1104	-	4,4,4	0.14	0	6,6,6	0.04	0
6	SO4	D	1207	-	4,4,4	0.14	0	6,6,6	0.07	0
6	SO4	A	1108	-	4,4,4	0.14	0	6,6,6	0.12	0
6	SO4	A	1110	-	4,4,4	0.14	0	6,6,6	0.07	0
7	EDO	A	1116	-	3,3,3	0.41	0	2,2,2	0.35	0
7	EDO	A	1120	-	3,3,3	0.53	0	2,2,2	0.19	0
6	SO4	D	1206	-	4,4,4	0.13	0	6,6,6	0.08	0
7	EDO	A	1112	-	3,3,3	0.42	0	2,2,2	0.39	0
7	EDO	A	1111	-	3,3,3	0.40	0	2,2,2	0.47	0
6	SO4	D	1205	-	4,4,4	0.14	0	6,6,6	0.05	0
7	EDO	C	201	-	3,3,3	0.49	0	2,2,2	0.17	0
7	EDO	A	1114	-	3,3,3	0.44	0	2,2,2	0.38	0
7	EDO	A	1115	-	3,3,3	0.42	0	2,2,2	0.57	0
6	SO4	D	1208	-	4,4,4	0.14	0	6,6,6	0.09	0
6	SO4	D	1203	-	4,4,4	0.14	0	6,6,6	0.05	0
6	SO4	A	1106	-	4,4,4	0.15	0	6,6,6	0.06	0
4	ATP	A	1101	5	26,33,33	0.88	1 (3%)	31,52,52	1.37	4 (12%)
4	ATP	D	1202	5	26,33,33	0.93	1 (3%)	31,52,52	1.37	4 (12%)
7	EDO	D	1211	-	3,3,3	0.41	0	2,2,2	0.47	0
7	EDO	D	1217	-	3,3,3	0.49	0	2,2,2	0.23	0
7	EDO	D	1215	-	3,3,3	0.47	0	2,2,2	0.24	0
6	SO4	A	1103	-	4,4,4	0.14	0	6,6,6	0.06	0
7	EDO	D	1213	-	3,3,3	0.38	0	2,2,2	0.38	0
6	SO4	A	1107	-	4,4,4	0.14	0	6,6,6	0.05	0
7	EDO	D	1210	-	3,3,3	0.44	0	2,2,2	0.45	0
7	EDO	A	1117	-	3,3,3	0.47	0	2,2,2	0.19	0
6	SO4	A	1105	-	4,4,4	0.14	0	6,6,6	0.05	0
6	SO4	A	1109	-	4,4,4	0.14	0	6,6,6	0.08	0
7	EDO	D	1212	-	3,3,3	0.46	0	2,2,2	0.34	0
6	SO4	D	1204	-	4,4,4	0.16	0	6,6,6	0.05	0
7	EDO	D	1216	-	3,3,3	0.48	0	2,2,2	0.35	0
7	EDO	A	1121	-	3,3,3	0.47	0	2,2,2	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
7	EDO	D	1214	-	-	0/1/1/1	-
7	EDO	A	1118	-	-	0/1/1/1	-
7	EDO	A	1113	-	-	0/1/1/1	-
7	EDO	D	1218	-	-	0/1/1/1	-
7	EDO	A	1119	-	-	0/1/1/1	-
7	EDO	D	1215	-	-	0/1/1/1	-
7	EDO	A	1116	-	-	0/1/1/1	-
7	EDO	A	1120	-	-	0/1/1/1	-
7	EDO	A	1112	-	-	0/1/1/1	-
7	EDO	C	201	-	-	0/1/1/1	-
7	EDO	A	1114	-	-	0/1/1/1	-
7	EDO	A	1115	-	-	0/1/1/1	-
7	EDO	A	1111	-	-	0/1/1/1	-
7	EDO	D	1217	-	-	0/1/1/1	-
4	ATP	A	1101	5	-	4/18/38/38	0/3/3/3
4	ATP	D	1202	5	-	4/18/38/38	0/3/3/3
7	EDO	D	1211	-	-	0/1/1/1	-
7	EDO	D	1213	-	-	0/1/1/1	-
7	EDO	A	1121	-	-	0/1/1/1	-
7	EDO	D	1210	-	-	0/1/1/1	-
7	EDO	A	1117	-	-	0/1/1/1	-
7	EDO	D	1212	-	-	0/1/1/1	-
7	EDO	D	1216	-	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1202	ATP	C5-C4	2.46	1.47	1.40
4	A	1101	ATP	C5-C4	2.31	1.47	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1101	ATP	N3-C2-N1	-3.38	123.39	128.68
4	D	1202	ATP	N3-C2-N1	-3.15	123.75	128.68
4	D	1202	ATP	PA-O3A-PB	-2.89	122.90	132.83
4	D	1202	ATP	C4-C5-N7	-2.65	106.64	109.40
4	A	1101	ATP	PA-O3A-PB	-2.62	123.84	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1202	ATP	PB-O3B-PG	-2.51	124.23	132.83
4	A	1101	ATP	C4-C5-N7	-2.35	106.95	109.40
4	A	1101	ATP	PB-O3B-PG	-2.23	125.16	132.83

There are no chirality outliers.

All (8) torsion outliers are listed below:

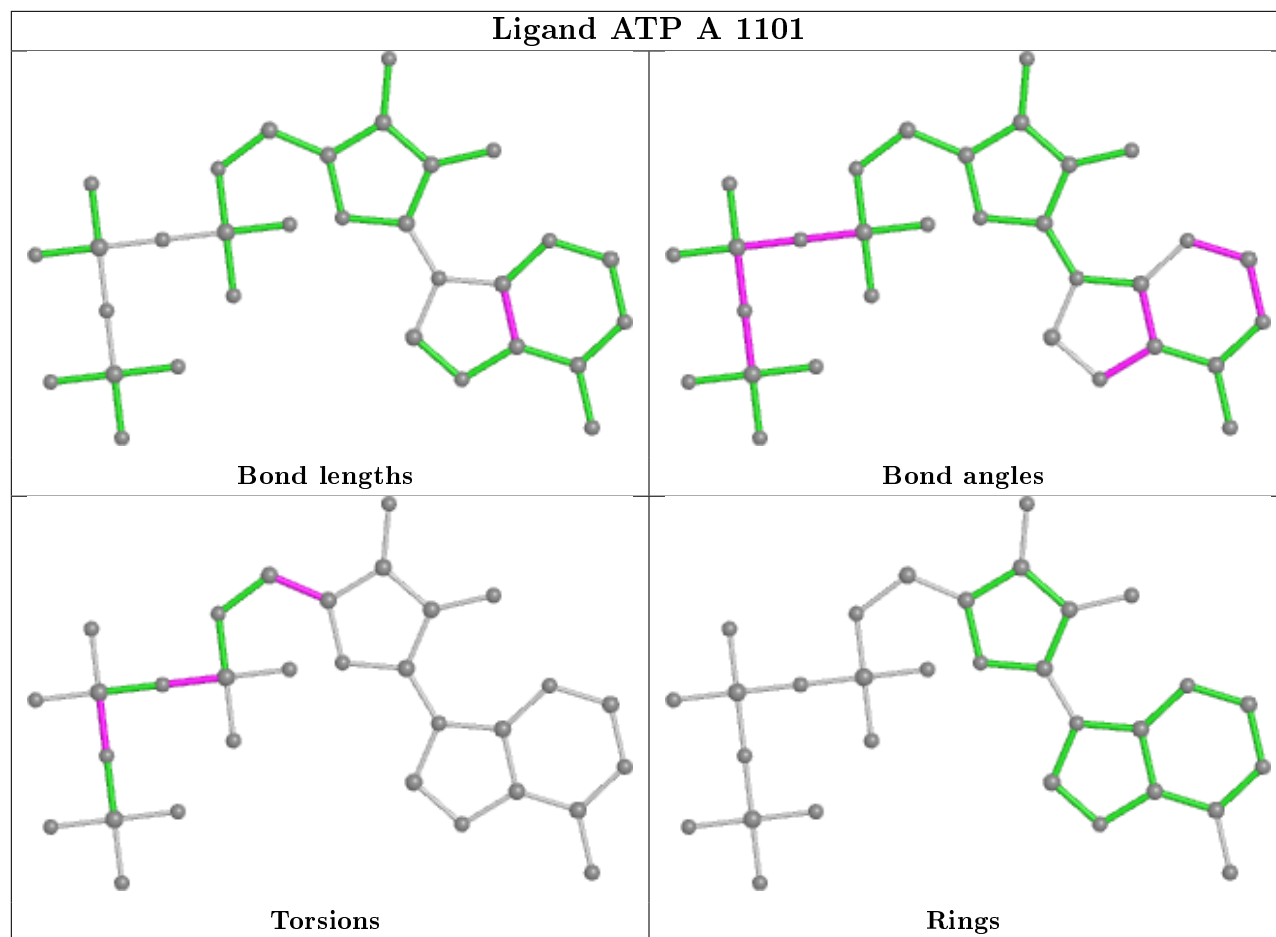
Mol	Chain	Res	Type	Atoms
4	D	1202	ATP	O4'-C4'-C5'-O5'
4	A	1101	ATP	O4'-C4'-C5'-O5'
4	D	1202	ATP	C3'-C4'-C5'-O5'
4	A	1101	ATP	C3'-C4'-C5'-O5'
4	D	1202	ATP	PB-O3A-PA-O2A
4	A	1101	ATP	PB-O3A-PA-O2A
4	A	1101	ATP	PG-O3B-PB-O1B
4	D	1202	ATP	PB-O3A-PA-O1A

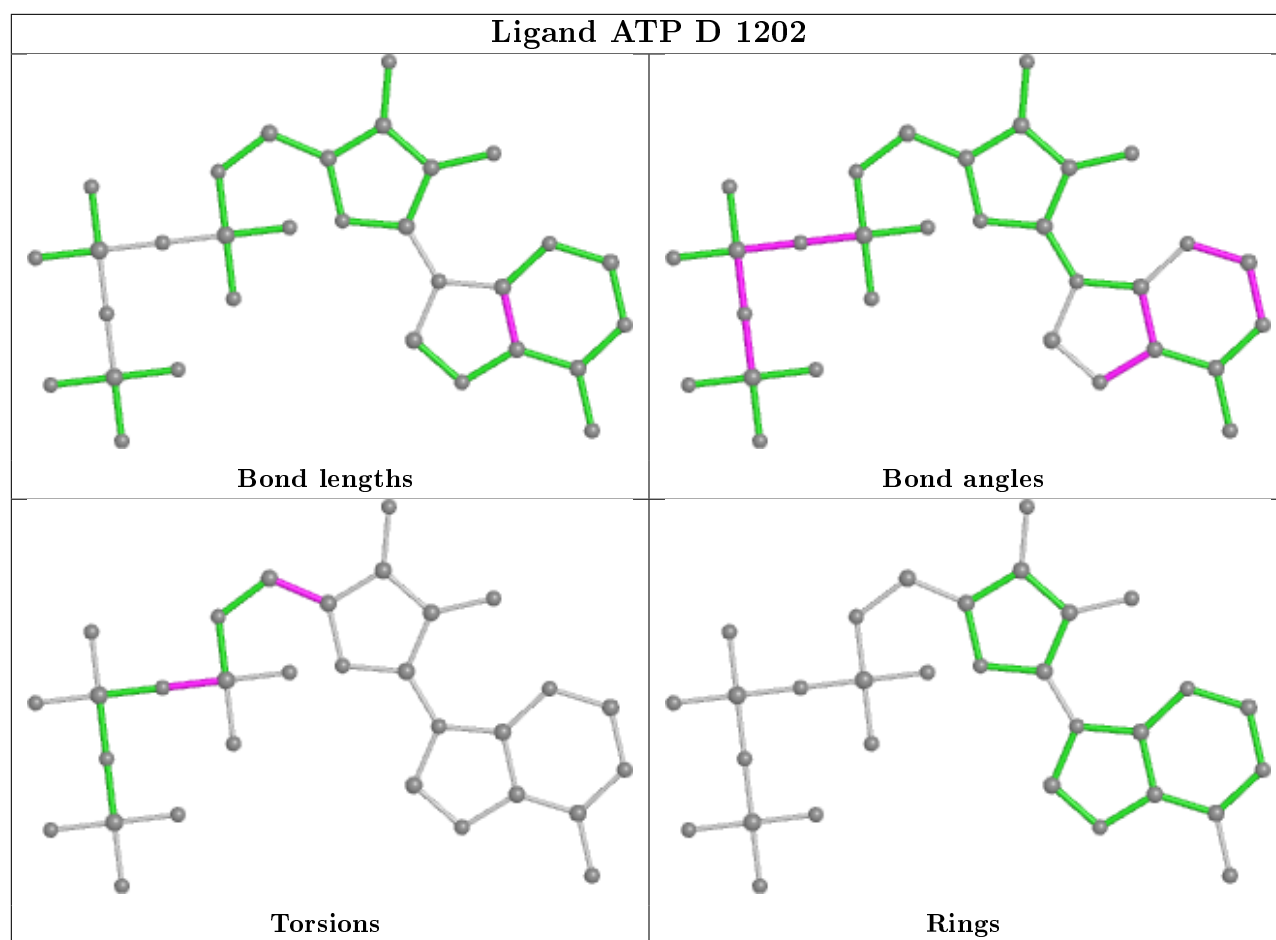
There are no ring outliers.

8 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	1214	EDO	1	0
7	A	1112	EDO	1	0
7	C	201	EDO	1	0
7	A	1114	EDO	1	0
7	D	1213	EDO	1	0
6	A	1107	SO4	1	0
7	D	1212	EDO	1	0
6	D	1204	SO4	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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	987/1017 (97%)	-0.22	22 (2%) 62 64	19, 33, 77, 152	0
1	D	987/1017 (97%)	0.03	51 (5%) 27 27	19, 39, 100, 137	0
2	B	78/85 (91%)	0.02	0 100 100	23, 53, 81, 95	0
2	E	77/85 (90%)	0.30	4 (5%) 27 27	24, 59, 95, 106	0
3	C	170/197 (86%)	0.68	20 (11%) 4 4	43, 66, 104, 139	0
3	F	167/197 (84%)	1.03	24 (14%) 2 2	52, 79, 111, 156	0
All	All	2466/2598 (94%)	0.05	121 (4%) 29 30	19, 40, 98, 156	0

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	143	VAL	7.7
1	A	648	SER	6.0
1	D	200	ASP	5.7
1	A	664	SER	5.4
3	F	173	LYS	5.2
1	D	746	SER	5.2
1	D	698	ASP	5.2
3	F	151	LYS	5.1
1	D	701	THR	4.9
1	A	647	GLN	4.9
1	D	801	LEU	4.7
1	D	647	GLN	4.7
1	D	980	LEU	4.7
3	C	141	ALA	4.7
1	D	639	ASN	4.6
3	F	103	GLY	4.6
3	F	89	TYR	4.3
1	A	646	LYS	4.0
1	D	969	PHE	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	649	GLY	3.8
1	D	649	GLY	3.8
3	F	105	PRO	3.7
3	F	102	SER	3.6
3	F	142	ASN	3.5
1	D	934	LYS	3.5
1	D	1005	ILE	3.5
1	A	642	GLU	3.5
1	D	930	ARG	3.5
1	D	970	PRO	3.4
1	D	975	LYS	3.4
1	D	965	TYR	3.4
1	A	639	ASN	3.4
1	A	655	LEU	3.4
1	A	702	SER	3.3
3	F	104	ASP	3.3
1	D	966	ALA	3.3
1	A	644	THR	3.2
1	A	651	VAL	3.2
1	A	645	LEU	3.2
1	D	978	LEU	3.2
3	F	143	VAL	3.1
1	D	982	ILE	3.1
3	F	174	GLY	3.1
1	D	937	ILE	3.0
1	D	968	PHE	3.0
1	A	698	ASP	3.0
1	D	799	ASP	3.0
3	F	79	PHE	2.9
1	D	944	GLU	2.9
1	A	746	SER	2.9
3	F	95	CYS	2.9
3	F	23	LYS	2.9
2	E	56	LEU	2.9
1	D	645	LEU	2.9
3	F	66	PHE	2.8
3	C	156	TYR	2.8
1	D	803	SER	2.8
1	D	754	ASN	2.8
1	D	648	SER	2.7
1	D	979	ASN	2.7
1	D	933	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
3	C	179	THR	2.7
1	D	948	LYS	2.6
3	C	162	MET	2.6
3	C	142	ASN	2.6
1	D	702	SER	2.6
1	D	940	SER	2.6
3	C	161	LYS	2.6
1	A	800	GLN	2.6
3	C	112	ALA	2.5
3	C	5	LYS	2.5
1	A	200	ASP	2.5
1	D	1020	ILE	2.5
1	D	640	PHE	2.5
3	F	24	LYS	2.5
1	D	990	THR	2.4
3	C	147	VAL	2.4
1	D	941	ASP	2.4
3	C	176	ILE	2.4
1	D	804	SER	2.4
1	D	992	LYS	2.4
3	C	3	SER	2.4
3	C	174	GLY	2.4
1	D	984	GLN	2.4
1	A	701	THR	2.4
3	F	64	MET	2.3
3	F	144	ASP	2.3
3	C	181	GLU	2.3
3	F	83	ILE	2.3
1	D	919	TYR	2.3
1	D	643	GLN	2.3
1	D	973	LYS	2.3
1	D	953	GLU	2.3
3	F	94	LEU	2.2
3	C	25	ALA	2.2
3	F	159	ARG	2.2
3	F	5	LYS	2.2
1	D	989	VAL	2.2
2	E	16	GLU	2.2
3	F	36	ASP	2.2
1	A	803	SER	2.2
3	C	180	SER	2.2
1	A	807	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
3	C	6	SER	2.1
3	F	31	ILE	2.1
1	A	975	LYS	2.1
1	D	972	LYS	2.1
1	D	1014	ASP	2.1
1	D	981	PRO	2.1
1	D	923	LYS	2.1
1	A	804	SER	2.1
2	E	25	ASN	2.1
2	E	17	VAL	2.1
3	C	151	LYS	2.1
3	C	90	ARG	2.0
1	D	971	PRO	2.0
1	D	932	ASP	2.0
1	D	798	ILE	2.0
1	A	636	THR	2.0
3	C	150	ARG	2.0
3	F	161	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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(\AA^2)	Q<0.9
6	SO4	D	1203	5/5	0.59	0.38	126,127,129,130	0
7	EDO	A	1121	4/4	0.63	0.19	64,66,68,69	0
6	SO4	A	1104	5/5	0.66	0.43	137,138,139,140	0
6	SO4	A	1105	5/5	0.69	0.29	138,140,140,140	0
7	EDO	A	1112	4/4	0.81	0.25	42,47,49,57	0

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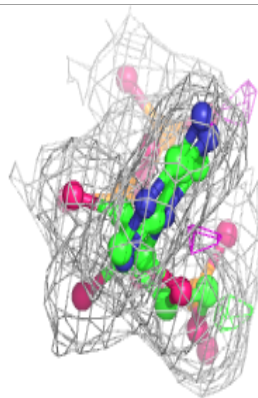
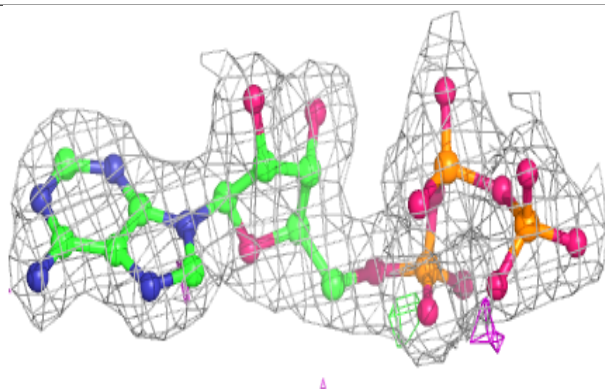
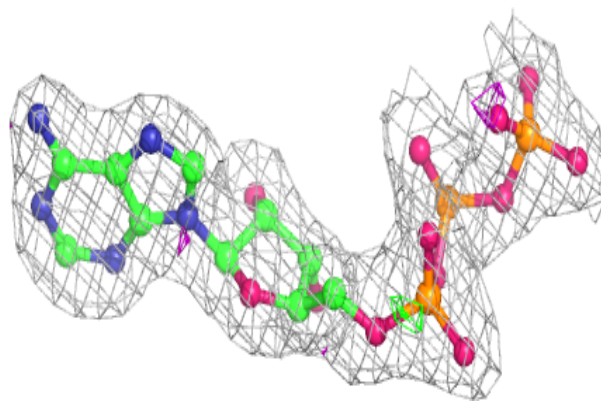
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	SO4	A	1107	5/5	0.81	0.33	122,124,125,127	0
7	EDO	A	1119	4/4	0.86	0.12	51,51,56,60	0
7	EDO	D	1212	4/4	0.86	0.20	51,54,57,61	0
6	SO4	D	1208	5/5	0.86	0.14	68,72,76,76	0
7	EDO	D	1218	4/4	0.87	0.15	57,59,60,60	0
6	SO4	A	1106	5/5	0.87	0.33	110,111,111,113	0
7	EDO	A	1117	4/4	0.88	0.16	53,56,56,60	0
7	EDO	A	1115	4/4	0.88	0.15	46,51,51,52	0
7	EDO	D	1215	4/4	0.89	0.14	52,56,63,68	0
6	SO4	D	1209	5/5	0.89	0.17	99,101,102,103	0
6	SO4	D	1205	5/5	0.90	0.19	105,105,106,107	0
7	EDO	D	1210	4/4	0.90	0.15	36,37,40,43	0
7	EDO	D	1217	4/4	0.90	0.12	47,51,52,52	0
7	EDO	A	1116	4/4	0.90	0.18	47,48,49,55	0
6	SO4	A	1103	5/5	0.90	0.15	105,106,107,108	0
6	SO4	D	1204	5/5	0.90	0.26	120,121,121,122	0
7	EDO	D	1213	4/4	0.90	0.23	42,45,51,51	0
7	EDO	D	1211	4/4	0.91	0.16	49,49,52,57	0
7	EDO	D	1214	4/4	0.91	0.23	58,58,61,65	0
7	EDO	D	1216	4/4	0.91	0.12	30,39,42,43	0
7	EDO	A	1120	4/4	0.91	0.10	34,42,43,45	0
6	SO4	D	1207	5/5	0.92	0.12	82,85,86,87	0
7	EDO	A	1118	4/4	0.92	0.14	33,38,49,60	0
7	EDO	A	1111	4/4	0.93	0.14	27,28,34,36	0
6	SO4	A	1109	5/5	0.93	0.21	86,88,92,93	0
7	EDO	A	1113	4/4	0.93	0.15	32,38,42,45	0
6	SO4	D	1206	5/5	0.94	0.16	91,93,96,98	0
7	EDO	A	1114	4/4	0.94	0.16	46,47,48,55	0
6	SO4	A	1108	5/5	0.94	0.14	61,72,78,78	0
6	SO4	A	1110	5/5	0.94	0.18	82,85,86,89	0
7	EDO	C	201	4/4	0.97	0.09	44,44,44,45	0
5	MG	A	1102	1/1	0.97	0.06	24,24,24,24	0
4	ATP	A	1101	31/31	0.98	0.11	18,24,28,31	0
4	ATP	D	1202	31/31	0.98	0.10	18,28,36,38	0
5	MG	D	1201	1/1	0.98	0.06	31,31,31,31	0

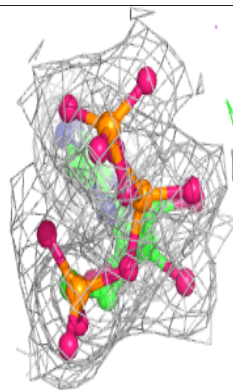
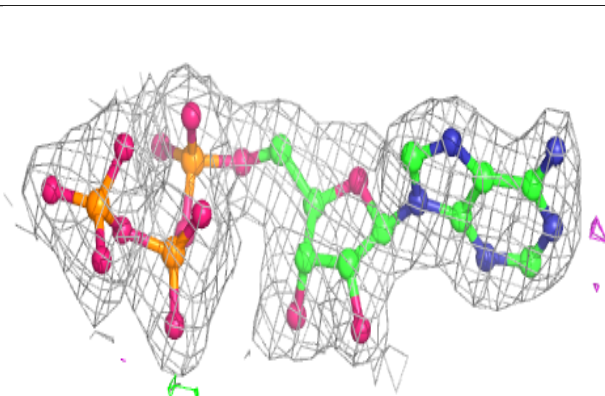
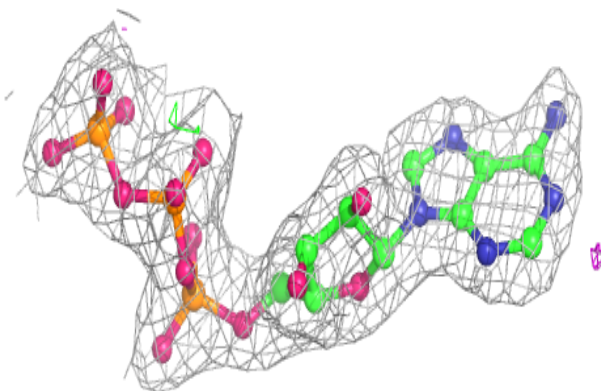
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ATP A 1101:

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

**Electron density around ATP D 1202:**

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



6.5 Other polymers

There are no such residues in this entry.