Full wwPDB X-ray Structure Validation Report (i)

Aug 20, 2023 – 03:19 AM EDT

PDB ID	:	2GMU
Title	:	Crystal structure of E coli GDP-4-keto-6-deoxy-D-mannose-3-dehydratase complexed with PLP-glutamate ketimine intermediate
Authors	:	Cook, P.D.; Thoden, J.B.; Holden, H.M.
Deposited on	:	2006-04-07
Resolution	:	1.90 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:

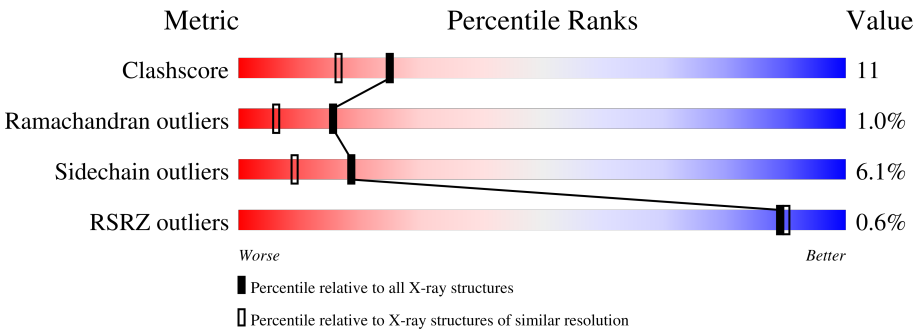
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 1.90 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))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	390	% 66% 28% 5% •
1	B	390	68% 27% 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	PDG	A	500	X	-	-	-
3	PDG	B	501	X	-	-	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6601 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 Putative pyridoxamine 5-phosphate-dependent dehydrase, WbdK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	390	3128	2005	513	595	15	0	3	0
1	B	390	3127	2005	515	592	15	0	2	0

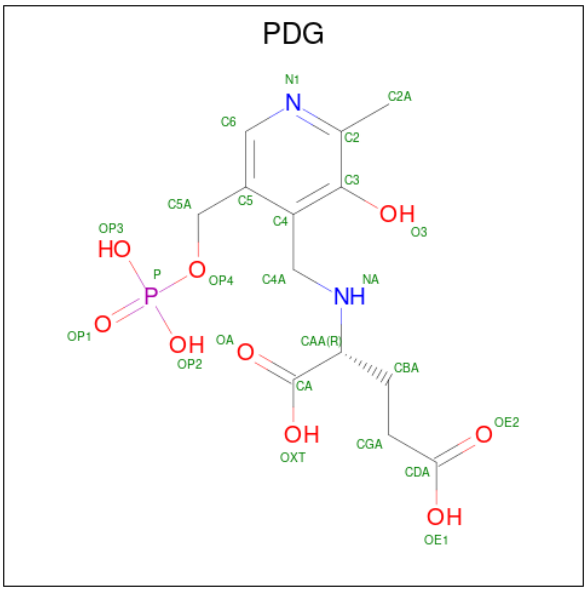
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	cloning artifact	GB 18266409
A	0	HIS	-	cloning artifact	GB 18266409
B	-1	GLY	-	cloning artifact	GB 18266409
B	0	HIS	-	cloning artifact	GB 18266409

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
2	A	1	1	1	0	0

- Molecule 3 is N-({3-HYDROXY-2-METHYL-5-[(PHOSPHONOOXY)METHYL]PYRIDIN-4-YL}METHYL)-D-GLUTAMIC ACID (three-letter code: PDG) (formula: $C_{13}H_{19}N_2O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	25	13	2	9	1	0	0
			Total	C	N	O	P		
3	B	1	25	13	2	9	1	0	0

- Molecule 4 is water.

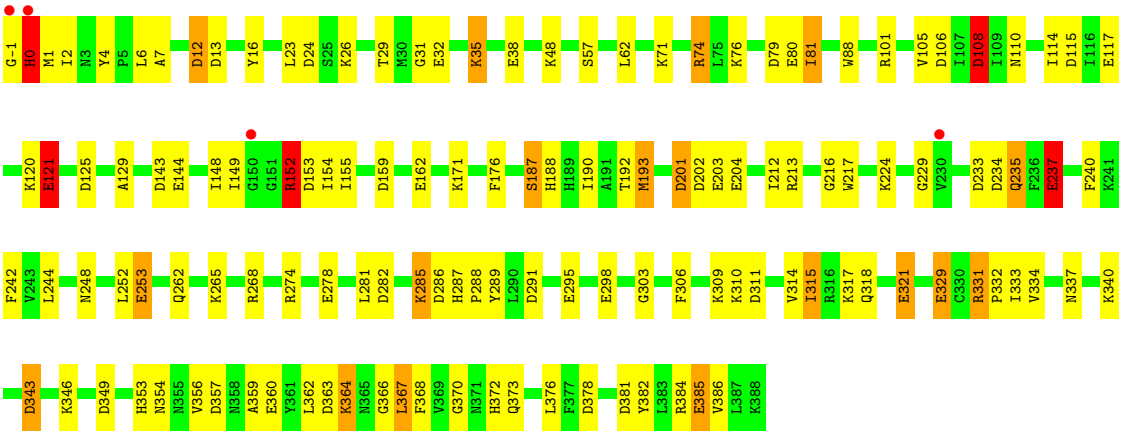
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	152	152	152	0	0
			Total	O		
4	B	143	143	143	0	0

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.

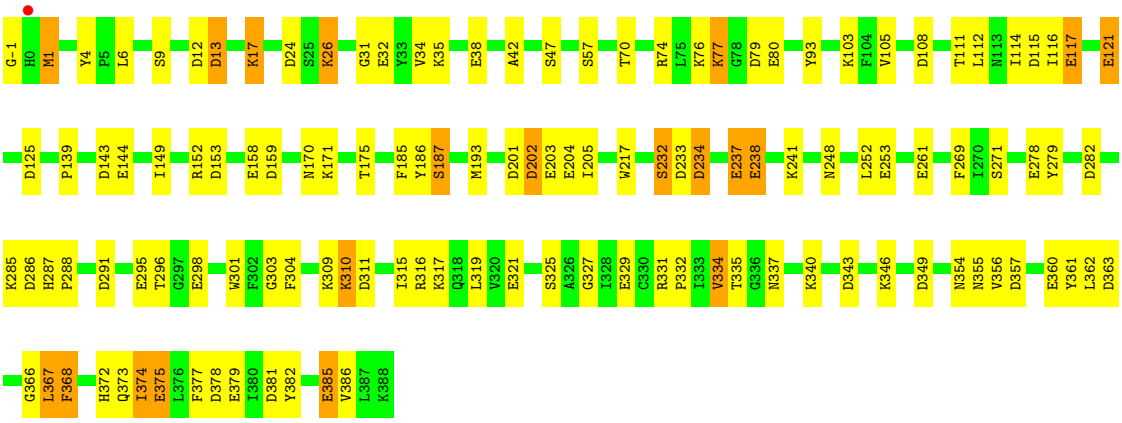
• Molecule 1: Putative pyridoxamine 5-phosphate-dependent dehydrase, WbdK

Chain A:



• Molecule 1: Putative pyridoxamine 5-phosphate-dependent dehydrase, WbdK

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	74.90Å 88.00Å 126.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.90 41.54 – 1.72	Depositor EDS
% Data completeness (in resolution range)	88.0 (30.00-1.90) 81.5 (41.54-1.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	0.73 (at 1.72Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.174 , 0.231 0.176 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	25.6	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 100.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	6601	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.77% 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: PDG, MG

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	0.82	18/3210 (0.6%)	1.19	53/4335 (1.2%)
1	B	0.81	19/3207 (0.6%)	1.18	45/4330 (1.0%)
All	All	0.82	37/6417 (0.6%)	1.19	98/8665 (1.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	1	0

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	321	GLU	CD-OE2	6.94	1.33	1.25
1	A	32	GLU	CD-OE2	6.64	1.32	1.25
1	A	121	GLU	CD-OE2	6.55	1.32	1.25
1	B	385	GLU	CD-OE2	6.48	1.32	1.25
1	B	117	GLU	CD-OE2	6.41	1.32	1.25
1	B	32	GLU	CD-OE2	6.38	1.32	1.25
1	A	385	GLU	CD-OE2	6.37	1.32	1.25
1	A	117	GLU	CD-OE2	6.33	1.32	1.25
1	B	203	GLU	CD-OE2	6.27	1.32	1.25
1	A	278	GLU	CD-OE2	6.27	1.32	1.25
1	B	321	GLU	CD-OE2	6.02	1.32	1.25
1	B	237	GLU	CD-OE2	6.02	1.32	1.25
1	B	121	GLU	CD-OE2	6.01	1.32	1.25
1	B	375	GLU	CD-OE2	5.92	1.32	1.25
1	A	360	GLU	CD-OE2	5.88	1.32	1.25
1	A	237	GLU	CD-OE2	5.83	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	144	GLU	CD-OE2	5.81	1.32	1.25
1	B	204	GLU	CD-OE2	5.75	1.31	1.25
1	A	80	GLU	CD-OE2	5.69	1.31	1.25
1	B	278	GLU	CD-OE2	5.64	1.31	1.25
1	A	298	GLU	CD-OE2	5.51	1.31	1.25
1	A	203	GLU	CD-OE2	5.50	1.31	1.25
1	A	253	GLU	CD-OE2	5.43	1.31	1.25
1	A	204	GLU	CD-OE2	5.39	1.31	1.25
1	A	295	GLU	CD-OE2	5.37	1.31	1.25
1	A	329	GLU	CD-OE2	5.37	1.31	1.25
1	A	38	GLU	CD-OE2	5.36	1.31	1.25
1	B	298	GLU	CD-OE2	5.33	1.31	1.25
1	B	379	GLU	CD-OE2	5.30	1.31	1.25
1	A	162	GLU	CD-OE2	5.27	1.31	1.25
1	B	144	GLU	CD-OE2	5.22	1.31	1.25
1	B	238	GLU	CD-OE2	5.17	1.31	1.25
1	B	295	GLU	CD-OE2	5.15	1.31	1.25
1	B	360	GLU	CD-OE2	5.15	1.31	1.25
1	B	158	GLU	CD-OE2	5.13	1.31	1.25
1	B	261	GLU	CD-OE2	5.08	1.31	1.25
1	B	80	GLU	CD-OE2	5.03	1.31	1.25

All (98) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	12	ASP	CB-CG-OD2	-7.55	111.51	118.30
1	A	234	ASP	CB-CG-OD2	-7.45	111.60	118.30
1	B	311	ASP	CB-CG-OD2	-7.31	111.72	118.30
1	A	213	ARG	NE-CZ-NH1	7.23	123.91	120.30
1	A	79	ASP	CB-CG-OD2	-7.22	111.80	118.30
1	A	378	ASP	CB-CG-OD2	-6.95	112.05	118.30
1	A	291	ASP	CB-CG-OD2	-6.87	112.11	118.30
1	A	357	ASP	CB-CG-OD2	-6.85	112.14	118.30
1	B	282	ASP	CB-CG-OD2	-6.83	112.16	118.30
1	B	108	ASP	CB-CG-OD1	6.75	124.37	118.30
1	B	12	ASP	CB-CG-OD1	6.73	124.36	118.30
1	A	153	ASP	CB-CG-OD2	-6.67	112.30	118.30
1	B	125	ASP	CB-CG-OD2	-6.66	112.31	118.30
1	B	291	ASP	CB-CG-OD2	-6.66	112.31	118.30
1	A	115	ASP	CB-CG-OD2	-6.60	112.36	118.30
1	B	357	ASP	CB-CG-OD2	-6.60	112.36	118.30
1	B	125	ASP	CB-CG-OD1	6.53	124.18	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	108	ASP	CB-CG-OD2	-6.52	112.43	118.30
1	A	115	ASP	CB-CG-OD1	6.50	124.15	118.30
1	B	13	ASP	CB-CG-OD2	-6.50	112.45	118.30
1	A	349	ASP	CB-CG-OD2	-6.46	112.49	118.30
1	A	159	ASP	CB-CG-OD2	-6.41	112.53	118.30
1	A	125	ASP	CB-CG-OD2	-6.41	112.53	118.30
1	B	187	SER	N-CA-CB	6.40	120.11	110.50
1	B	115	ASP	CB-CG-OD2	-6.40	112.54	118.30
1	A	343	ASP	CB-CG-OD2	-6.39	112.55	118.30
1	A	311	ASP	CB-CG-OD2	-6.33	112.60	118.30
1	B	143	ASP	CB-CG-OD2	-6.29	112.64	118.30
1	A	12	ASP	CB-CG-OD2	-6.29	112.64	118.30
1	A	357	ASP	CB-CG-OD1	6.29	123.96	118.30
1	A	24	ASP	CB-CG-OD1	6.24	123.91	118.30
1	B	378	ASP	CB-CG-OD2	-6.18	112.73	118.30
1	B	378	ASP	CB-CG-OD1	6.17	123.85	118.30
1	B	357	ASP	CB-CG-OD1	6.16	123.85	118.30
1	B	234	ASP	CB-CG-OD1	6.10	123.79	118.30
1	B	153	ASP	CB-CG-OD2	-6.09	112.82	118.30
1	A	234	ASP	CB-CG-OD1	6.08	123.77	118.30
1	A	349	ASP	CB-CG-OD1	6.00	123.70	118.30
1	B	13	ASP	CB-CG-OD1	6.00	123.70	118.30
1	A	108	ASP	CB-CG-OD1	5.96	123.66	118.30
1	B	24	ASP	CB-CG-OD2	-5.93	112.96	118.30
1	B	286	ASP	CB-CG-OD2	-5.92	112.97	118.30
1	A	24	ASP	CB-CG-OD2	-5.89	113.00	118.30
1	B	363	ASP	CB-CG-OD1	5.89	123.60	118.30
1	A	311	ASP	CB-CG-OD1	5.88	123.60	118.30
1	B	343	ASP	CB-CG-OD2	-5.88	113.01	118.30
1	A	108	ASP	CB-CG-OD2	-5.87	113.02	118.30
1	A	233	ASP	CB-CG-OD2	-5.85	113.04	118.30
1	A	201	ASP	CB-CG-OD2	-5.84	113.04	118.30
1	A	79	ASP	CB-CG-OD1	5.81	123.53	118.30
1	A	13	ASP	CB-CG-OD2	-5.79	113.09	118.30
1	A	282	ASP	CB-CG-OD2	-5.78	113.10	118.30
1	B	79	ASP	CB-CG-OD2	-5.75	113.12	118.30
1	A	282	ASP	CB-CG-OD1	5.74	123.47	118.30
1	B	349	ASP	CB-CG-OD2	-5.72	113.15	118.30
1	A	286[A]	ASP	CB-CG-OD2	-5.71	113.17	118.30
1	A	286[B]	ASP	CB-CG-OD2	-5.71	113.17	118.30
1	A	378	ASP	CB-CG-OD1	5.68	123.41	118.30
1	A	274	ARG	NE-CZ-NH1	5.65	123.13	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	343	ASP	CB-CG-OD1	5.62	123.36	118.30
1	A	201	ASP	CB-CG-OD1	5.62	123.36	118.30
1	B	311	ASP	CB-CG-OD1	5.61	123.35	118.30
1	B	115	ASP	CB-CG-OD1	5.60	123.34	118.30
1	A	125	ASP	CB-CG-OD1	5.59	123.33	118.30
1	A	233	ASP	CB-CG-OD1	5.58	123.32	118.30
1	B	201	ASP	CB-CG-OD2	-5.57	113.29	118.30
1	B	202	ASP	CB-CG-OD1	5.56	123.30	118.30
1	B	201	ASP	CB-CG-OD1	5.53	123.28	118.30
1	A	286[A]	ASP	CB-CG-OD1	5.52	123.27	118.30
1	A	286[B]	ASP	CB-CG-OD1	5.52	123.27	118.30
1	A	381	ASP	CB-CG-OD2	-5.52	113.33	118.30
1	A	202	ASP	CB-CG-OD2	-5.52	113.33	118.30
1	B	153	ASP	CB-CG-OD1	5.51	123.26	118.30
1	A	202	ASP	CB-CG-OD1	5.48	123.23	118.30
1	B	159	ASP	CB-CG-OD1	5.46	123.21	118.30
1	A	159	ASP	CB-CG-OD1	5.46	123.21	118.30
1	A	13	ASP	CB-CG-OD1	5.45	123.20	118.30
1	B	233	ASP	CB-CG-OD2	-5.44	113.40	118.30
1	A	143	ASP	CB-CG-OD2	-5.43	113.41	118.30
1	B	143	ASP	CB-CG-OD1	5.40	123.16	118.30
1	B	282	ASP	CB-CG-OD1	5.39	123.15	118.30
1	B	381	ASP	CB-CG-OD2	-5.39	113.45	118.30
1	B	286	ASP	CB-CG-OD1	5.38	123.14	118.30
1	B	202	ASP	CB-CG-OD2	-5.34	113.49	118.30
1	B	291	ASP	CB-CG-OD1	5.33	123.10	118.30
1	A	0	HIS	CB-CA-C	5.30	121.00	110.40
1	B	233	ASP	CB-CG-OD1	5.28	123.05	118.30
1	A	153	ASP	CB-CG-OD1	5.28	123.05	118.30
1	A	291	ASP	CB-CG-OD1	5.28	123.05	118.30
1	A	384	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	A	363	ASP	CB-CG-OD1	5.25	123.02	118.30
1	A	363	ASP	CB-CG-OD2	-5.24	113.58	118.30
1	A	143	ASP	CB-CG-OD1	5.17	122.95	118.30
1	B	79	ASP	CB-CG-OD1	5.12	122.91	118.30
1	B	159	ASP	CB-CG-OD2	-5.09	113.72	118.30
1	B	234	ASP	CB-CG-OD2	-5.08	113.73	118.30
1	B	349	ASP	CB-CG-OD1	5.07	122.86	118.30
1	A	381	ASP	CB-CG-OD1	5.01	122.81	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	187	SER	CA

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	3128	0	3096	74	0
1	B	3127	0	3092	69	0
2	A	1	0	0	0	0
3	A	25	0	13	2	0
3	B	25	0	13	3	0
4	A	152	0	0	6	0
4	B	143	0	0	5	0
All	All	6601	0	6214	135	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 11.

All (135) 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:A:306:PHE:HB2	1:A:367:LEU:CD1	2.00	0.91
1:A:306:PHE:HB2	1:A:367:LEU:HD11	1.63	0.79
1:B:6:LEU:HG	1:B:329:GLU:HG2	1.65	0.78
1:A:0:HIS:ND1	1:A:1:MET:N	2.31	0.78
1:A:287:HIS:CG	1:A:288:PRO:HD2	2.19	0.77
1:A:331:ARG:HD2	1:A:332:PRO:O	1.85	0.76
1:A:317:LYS:O	1:A:321:GLU:HG3	1.85	0.76
1:A:23:LEU:O	1:A:26:LYS:HD3	1.86	0.73
1:A:149:ILE:O	1:A:152:ARG:HG3	1.89	0.73
1:B:382:TYR:O	1:B:386:VAL:HG23	1.90	0.71
1:B:-1:GLY:HA3	1:B:325:SER:HA	1.70	0.71
1:B:1:MET:O	1:B:327:GLY:HA2	1.91	0.70
1:A:62:LEU:HD22	1:A:212:ILE:HD12	1.73	0.70
1:B:232:SER:HB3	1:B:238:GLU:OE1	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:310:LYS:HD3	1:B:361:TYR:CE1	2.27	0.69
1:B:331:ARG:NH2	1:B:334:VAL:HA	2.11	0.66
1:B:149:ILE:O	1:B:152:ARG:HD3	1.97	0.65
1:A:318:GLN:NE2	4:A:681:HOH:O	2.29	0.65
1:A:314:VAL:C	1:A:315:ILE:HD13	2.16	0.65
1:A:315:ILE:HD13	1:A:315:ILE:N	2.10	0.64
1:A:171:LYS:HB3	1:A:176:PHE:CZ	2.33	0.64
1:B:287:HIS:CG	1:B:288:PRO:HD2	2.33	0.63
1:B:287:HIS:O	1:B:309:LYS:NZ	2.31	0.63
1:A:-1:GLY:O	1:A:0:HIS:HB3	1.98	0.63
1:B:70:THR:HG21	1:B:74:ARG:HE	1.64	0.63
1:B:234:ASP:OD2	1:B:237:GLU:HG2	2.00	0.61
1:B:103:LYS:NZ	4:B:536:HOH:O	2.34	0.61
1:B:13:ASP:O	1:B:17:LYS:HG3	2.01	0.59
1:A:303:GLY:HA3	1:A:368:PHE:CE1	2.38	0.59
3:B:501:PDG:HGA1	3:B:501:PDG:OXT	2.04	0.58
1:A:57:SER:HB2	1:B:248:ASN:HB3	1.86	0.58
1:B:105:VAL:HB	1:B:114:ILE:HD11	1.86	0.58
1:A:242:PHE:HE1	1:B:335:THR:HG1	1.51	0.57
1:B:74:ARG:HD3	4:B:628:HOH:O	2.04	0.57
1:A:88:TRP:CZ2	3:A:500:PDG:HBA2	2.41	0.55
1:A:252:LEU:HD12	1:B:252:LEU:HD12	1.87	0.55
1:B:337:ASN:O	1:B:340:LYS:HG2	2.06	0.55
1:A:240:PHE:CZ	1:B:332:PRO:HD2	2.42	0.54
1:A:29:THR:HG21	1:B:185:PHE:CE1	2.41	0.54
1:A:309:LYS:NZ	4:A:679:HOH:O	2.29	0.54
1:B:331:ARG:HH21	1:B:334:VAL:HA	1.72	0.54
1:B:366:GLY:C	1:B:367:LEU:HD23	2.27	0.54
1:A:121:GLU:OE1	1:A:353:HIS:HE1	1.91	0.54
1:B:31:GLY:N	1:B:253:GLU:OE1	2.34	0.53
1:B:372:HIS:C	1:B:374:ILE:H	2.10	0.53
1:B:76:LYS:HG2	1:B:77:LYS:N	2.24	0.53
1:B:303:GLY:HA3	1:B:368:PHE:CE1	2.44	0.53
1:A:340:LYS:HE3	4:A:696:HOH:O	2.07	0.53
1:A:120:LYS:HG2	1:A:148:ILE:HG12	1.91	0.53
1:B:238:GLU:HA	1:B:241:LYS:HE3	1.91	0.53
1:B:367:LEU:HD23	1:B:367:LEU:N	2.23	0.52
3:B:501:PDG:OA	3:B:501:PDG:H4A1	2.09	0.52
1:A:287:HIS:ND1	1:A:288:PRO:HD2	2.24	0.52
1:A:81:ILE:HD12	1:A:129:ALA:HB3	1.91	0.52
1:A:306:PHE:HB2	1:A:367:LEU:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:LYS:HD2	4:A:694:HOH:O	2.10	0.51
1:A:6:LEU:O	1:A:372:HIS:HE1	1.93	0.51
1:B:34:VAL:O	1:B:38:GLU:HG3	2.10	0.51
1:B:331:ARG:HB2	1:B:332:PRO:HD2	1.91	0.51
3:B:501:PDG:OA	3:B:501:PDG:OP1	2.30	0.50
1:A:337:ASN:O	1:A:340:LYS:HG2	2.11	0.50
1:A:190:ILE:HB	1:A:262:GLN:HB3	1.94	0.50
1:B:375:GLU:HG2	4:B:613:HOH:O	2.11	0.50
1:A:331:ARG:HB2	1:A:332:PRO:HD2	1.94	0.50
1:B:362:LEU:HD23	1:B:362:LEU:C	2.32	0.50
1:A:6:LEU:HG	1:A:329:GLU:HB3	1.94	0.49
1:A:248:ASN:HB3	1:B:57:SER:HB2	1.93	0.49
1:B:202:ASP:CG	1:B:205:ILE:HD12	2.32	0.49
1:A:108:ASP:OD1	1:A:110:ASN:N	2.46	0.48
1:A:216:GLY:HA3	1:A:244:LEU:O	2.14	0.48
1:A:367:LEU:HD12	1:A:367:LEU:N	2.27	0.48
1:A:242:PHE:HE1	1:B:335:THR:OG1	1.97	0.48
1:A:287:HIS:HE1	1:A:289:TYR:CE2	2.32	0.48
1:A:6:LEU:HD23	1:A:370:GLY:N	2.29	0.47
1:B:6:LEU:HG	1:B:329:GLU:CG	2.42	0.47
1:A:74:ARG:HB3	1:A:155:ILE:HD11	1.95	0.47
1:A:224:LYS:HA	1:A:229:GLY:O	2.15	0.47
1:A:192:THR:O	1:A:193:MET:HB2	2.15	0.47
1:A:373:GLN:H	1:A:373:GLN:CD	2.17	0.47
1:B:269:PHE:CD2	1:B:373:GLN:HG3	2.50	0.47
1:A:333:ILE:HD12	1:A:366:GLY:HA3	1.96	0.47
1:B:356:VAL:O	1:B:356:VAL:HG23	2.14	0.47
1:A:0:HIS:CE1	1:A:2:ILE:H	2.32	0.47
3:A:500:PDG:OP1	3:A:500:PDG:OXT	2.33	0.46
1:B:355:ASN:HB2	4:B:624:HOH:O	2.14	0.46
1:A:7:ALA:HB1	1:A:187:SER:OG	2.15	0.46
1:A:29:THR:HG21	1:B:185:PHE:CZ	2.51	0.46
1:B:171:LYS:HE3	1:B:175:THR:OG1	2.15	0.46
1:A:29:THR:CG2	1:B:185:PHE:CE1	2.99	0.45
1:A:242:PHE:HB3	1:B:93:TYR:OH	2.15	0.45
1:A:343:ASP:HB2	4:B:640:HOH:O	2.15	0.45
1:A:287:HIS:O	1:A:309:LYS:NZ	2.50	0.45
1:A:105:VAL:HB	1:A:114:ILE:HD11	1.98	0.45
1:A:152:ARG:HB2	1:A:154:ILE:HD12	1.99	0.45
1:B:234:ASP:O	1:B:238:GLU:N	2.35	0.45
1:A:35:LYS:HB3	1:A:35:LYS:HE3	1.74	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:ILE:HA	1:B:116:ILE:HD13	1.73	0.44
1:B:354:ASN:HB3	1:B:355:ASN:H	1.59	0.44
1:A:287:HIS:HE1	1:A:289:TYR:CD2	2.36	0.44
1:B:319:LEU:HD23	1:B:319:LEU:HA	1.72	0.44
1:B:139:PRO:HD2	1:B:296:THR:O	2.17	0.43
1:B:269:PHE:CE2	1:B:373:GLN:HG3	2.53	0.43
1:A:48:LYS:HB2	1:A:201:ASP:HA	1.99	0.43
1:A:71:LYS:HA	1:A:71:LYS:HD3	1.74	0.43
1:B:6:LEU:O	1:B:372:HIS:HE1	2.02	0.43
1:A:106:ASP:CG	1:A:356:VAL:HA	2.39	0.43
1:B:6:LEU:CG	1:B:329:GLU:HG2	2.40	0.43
1:B:42:ALA:HB1	1:B:47:SER:O	2.18	0.43
1:A:188:HIS:HB3	4:A:663:HOH:O	2.19	0.42
1:A:372:HIS:HD2	1:A:376:LEU:HD21	1.85	0.42
1:A:121:GLU:HB2	1:A:353:HIS:HE2	1.84	0.42
1:B:373:GLN:O	1:B:373:GLN:HG2	2.19	0.42
1:A:16:TYR:OH	1:B:26:LYS:HG2	2.19	0.42
1:B:185:PHE:CG	1:B:186:TYR:N	2.86	0.42
1:A:364:LYS:HG2	4:A:747:HOH:O	2.20	0.42
1:A:281:LEU:O	1:A:285:LYS:HB2	2.20	0.41
1:B:346:LYS:HB2	1:B:346:LYS:HE2	1.63	0.41
1:A:362:LEU:C	1:A:362:LEU:HD23	2.41	0.41
1:B:382:TYR:O	1:B:385:GLU:HB2	2.20	0.41
1:A:382:TYR:O	1:A:386:VAL:HG23	2.20	0.41
1:B:279:TYR:HB2	1:B:377:PHE:CE2	2.56	0.41
1:A:57:SER:CB	1:B:248:ASN:HB3	2.50	0.41
1:A:356:VAL:HB	1:A:359:ALA:HB3	2.02	0.41
1:A:62:LEU:HD22	1:A:212:ILE:CD1	2.47	0.40
1:B:111:THR:O	1:B:112:LEU:HB2	2.20	0.40
1:A:31:GLY:N	1:A:253:GLU:OE1	2.49	0.40
1:A:235:GLN:C	1:A:237:GLU:H	2.24	0.40
1:B:304:PHE:O	1:B:368:PHE:HA	2.22	0.40
1:A:12:ASP:CG	1:A:265:LYS:HZ1	2.23	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	391/390 (100%)	367 (94%)	19 (5%)	5 (1%)	12 4
1	B	390/390 (100%)	370 (95%)	17 (4%)	3 (1%)	19 9
All	All	781/780 (100%)	737 (94%)	36 (5%)	8 (1%)	15 6

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	152	ARG
1	A	193	MET
1	B	193	MET
1	B	334	VAL
1	A	334	VAL
1	B	301	TRP
1	A	354	ASN

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	348/345 (101%)	326 (94%)	22 (6%)	18 8
1	B	347/345 (101%)	327 (94%)	20 (6%)	20 10
All	All	695/690 (101%)	653 (94%)	42 (6%)	18 9

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	4	TYR
1	A	35	LYS
1	A	74	ARG
1	A	76	LYS
1	A	81	ILE
1	A	101	ARG
1	A	108	ASP
1	A	121	GLU
1	A	152	ARG
1	A	187	SER
1	A	217	TRP
1	A	235	GLN
1	A	237	GLU
1	A	268	ARG
1	A	285	LYS
1	A	310	LYS
1	A	315	ILE
1	A	331	ARG
1	A	364	LYS
1	A	367	LEU
1	A	385	GLU
1	B	1	MET
1	B	4	TYR
1	B	9	SER
1	B	17	LYS
1	B	26	LYS
1	B	35	LYS
1	B	77	LYS
1	B	117	GLU
1	B	121	GLU
1	B	170	ASN
1	B	187	SER
1	B	217	TRP
1	B	232	SER
1	B	271	SER
1	B	285	LYS
1	B	310	LYS
1	B	317	LYS
1	B	367	LEU
1	B	368	PHE
1	B	374	ILE

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

sidechains are listed below:

Mol	Chain	Res	Type
1	A	235	GLN
1	A	322	ASN
1	A	324	ASN
1	A	372	HIS
1	B	40	GLN
1	B	294	GLN
1	B	322	ASN
1	B	324	ASN
1	B	372	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\#\|Z\| > 2$
3	PDG	B	501	-	25,25,25	1.84	6 (24%)	31,35,35	3.25	9 (29%)
3	PDG	A	500	-	25,25,25	1.73	8 (32%)	31,35,35	2.91	11 (35%)

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	PDG	B	501	-	1/1/4/5	8/20/20/20	0/1/1/1
3	PDG	A	500	-	1/1/4/5	7/20/20/20	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	PDG	CAA-NA	-5.61	1.33	1.46
3	A	500	PDG	C5A-C5	-4.45	1.38	1.50
3	B	501	PDG	C5A-C5	-3.59	1.41	1.50
3	A	500	PDG	CAA-NA	-3.36	1.38	1.46
3	A	500	PDG	C4A-C4	2.55	1.55	1.51
3	A	500	PDG	OP4-C5A	-2.45	1.35	1.45
3	A	500	PDG	C3-C2	-2.39	1.38	1.40
3	B	501	PDG	OP4-C5A	-2.39	1.36	1.45
3	A	500	PDG	OA-CA	2.32	1.29	1.22
3	B	501	PDG	OA-CA	2.20	1.28	1.22
3	B	501	PDG	C3-C2	-2.14	1.38	1.40
3	A	500	PDG	P-OP3	2.05	1.62	1.54
3	B	501	PDG	OE2-CDA	2.04	1.28	1.22
3	A	500	PDG	CGA-CDA	2.01	1.55	1.50

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	501	PDG	OP4-C5A-C5	14.93	137.80	109.35
3	A	500	PDG	OP4-C5A-C5	12.66	133.47	109.35
3	B	501	PDG	CBA-CAA-CA	4.40	120.96	110.35
3	B	501	PDG	C5A-C5-C6	4.24	126.34	119.37
3	A	500	PDG	C5A-C5-C6	3.98	125.92	119.37
3	A	500	PDG	C6-C5-C4	-3.72	115.48	118.12
3	A	500	PDG	CBA-CAA-CA	3.39	118.53	110.35
3	A	500	PDG	C3-C4-C5	2.97	121.57	118.72
3	B	501	PDG	C3-C4-C5	2.87	121.47	118.72
3	B	501	PDG	C4A-NA-CAA	2.81	119.24	113.92
3	A	500	PDG	C4A-NA-CAA	2.69	119.01	113.92
3	A	500	PDG	CGA-CBA-CAA	-2.67	108.17	113.16
3	B	501	PDG	C6-C5-C4	-2.41	116.41	118.12
3	A	500	PDG	OE1-CDA-CGA	2.28	121.35	114.03
3	B	501	PDG	O3-C3-C2	2.23	122.36	117.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	500	PDG	OP3-P-OP4	2.14	112.43	106.73
3	A	500	PDG	O3-C3-C2	2.13	122.14	117.49
3	B	501	PDG	C4A-C4-C3	-2.12	117.77	120.04
3	B	501	PDG	OE1-CDA-CGA	2.04	120.58	114.03
3	A	500	PDG	C4A-C4-C3	-2.02	117.89	120.04

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	500	PDG	CAA
3	B	501	PDG	CAA

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	500	PDG	CA-CAA-NA-C4A
3	B	501	PDG	CA-CAA-NA-C4A
3	A	500	PDG	CA-CAA-CBA-CGA
3	B	501	PDG	CA-CAA-CBA-CGA
3	A	500	PDG	OA-CA-CAA-NA
3	A	500	PDG	OXT-CA-CAA-NA
3	A	500	PDG	C6-C5-C5A-OP4
3	B	501	PDG	C4-C5-C5A-OP4
3	B	501	PDG	OXT-CA-CAA-NA
3	B	501	PDG	CAA-CBA-CGA-CDA
3	B	501	PDG	OA-CA-CAA-NA
3	B	501	PDG	OE2-CDA-CGA-CBA
3	A	500	PDG	CAA-CBA-CGA-CDA
3	B	501	PDG	OE1-CDA-CGA-CBA
3	A	500	PDG	OE2-CDA-CGA-CBA

There are no ring outliers.

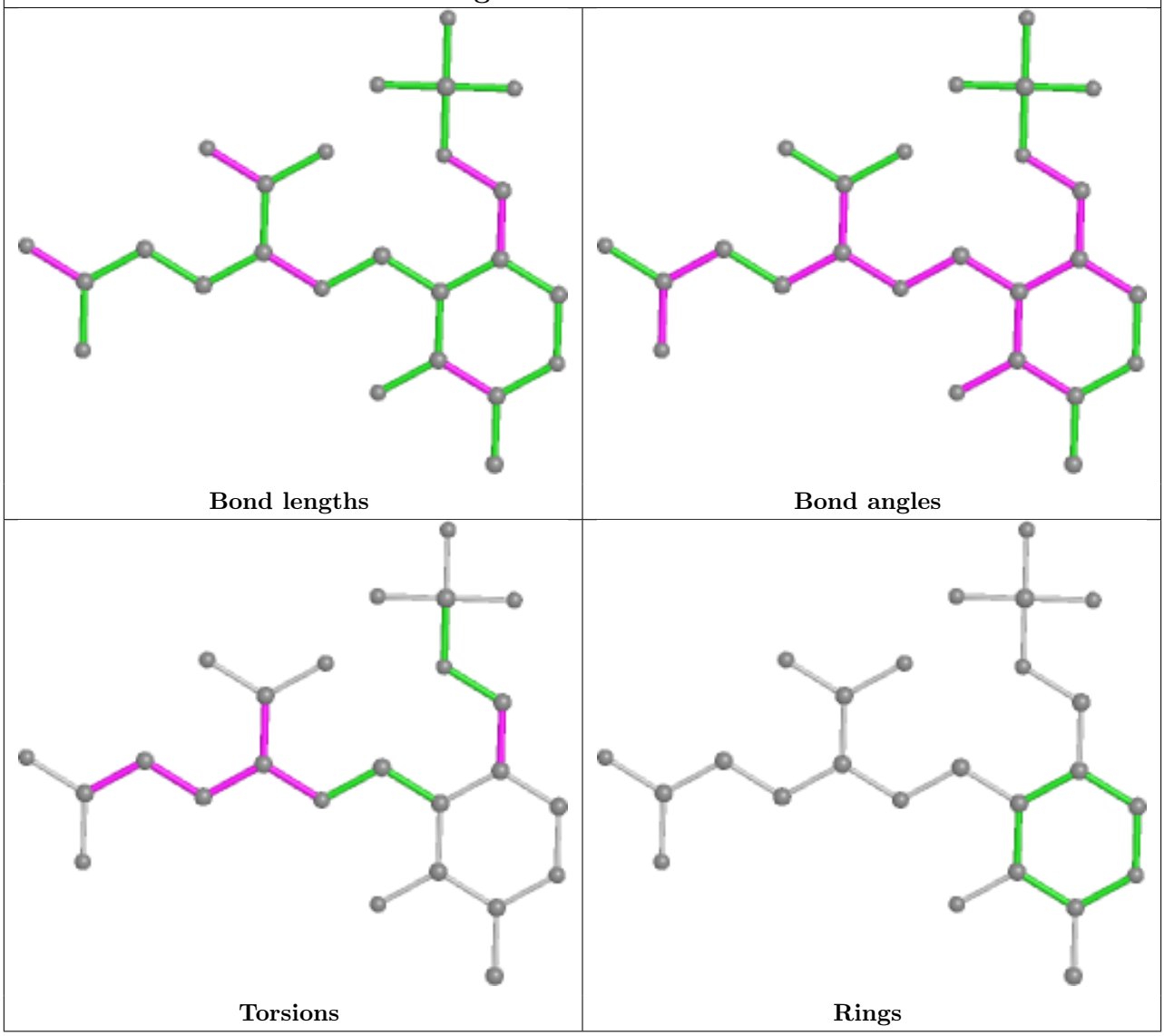
2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	PDG	3	0
3	A	500	PDG	2	0

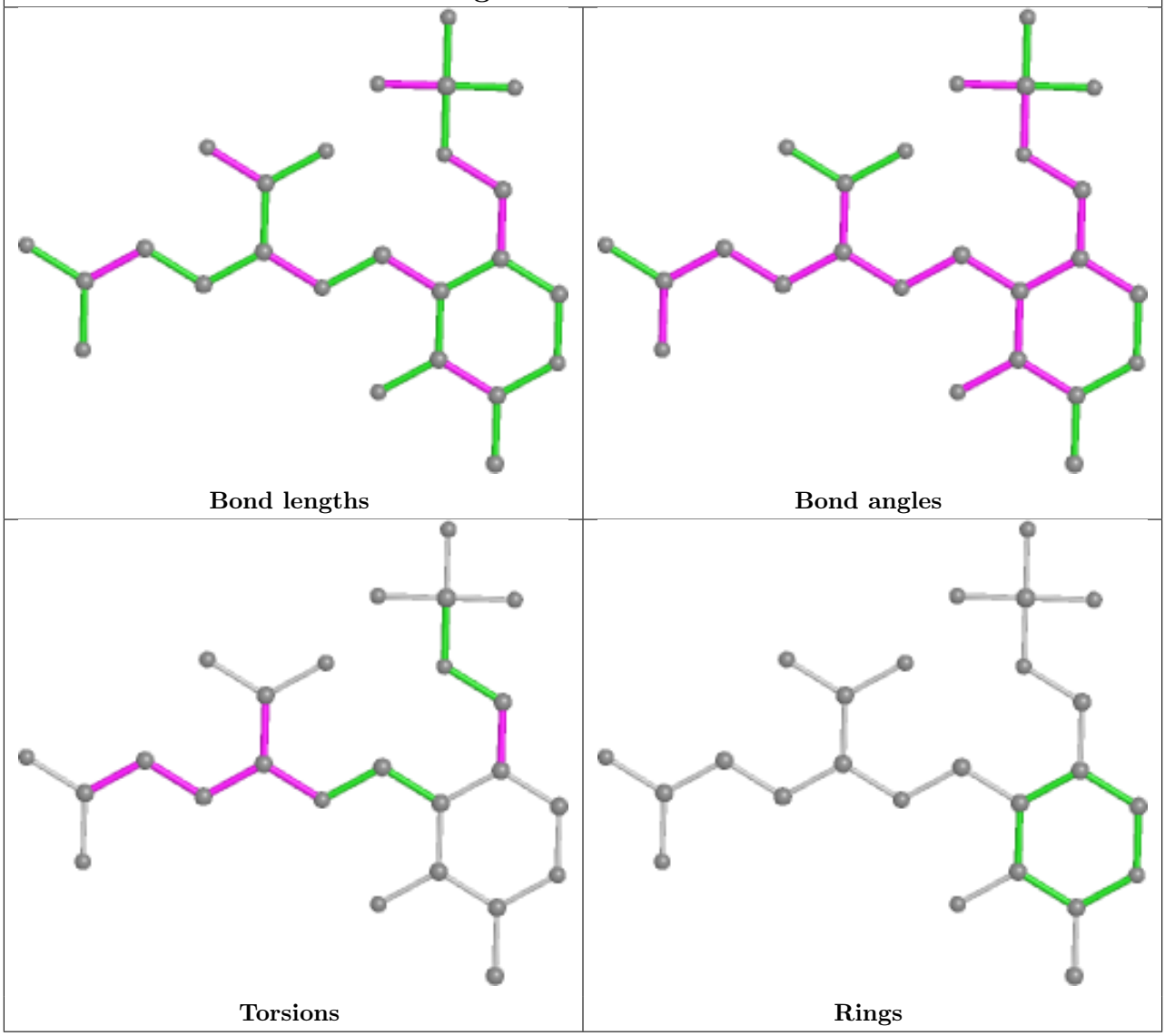
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 PDG B 501



Ligand PDG A 500



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	390/390 (100%)	-0.50	4 (1%)	82	84	23, 34, 68, 99	0
1	B	390/390 (100%)	-0.52	1 (0%)	94	94	24, 36, 69, 98	0
All	All	780/780 (100%)	-0.51	5 (0%)	89	90	23, 35, 69, 99	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	0	HIS	6.1
1	A	0	HIS	4.8
1	A	-1	GLY	3.1
1	A	150	GLY	2.0
1	A	230	VAL	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)

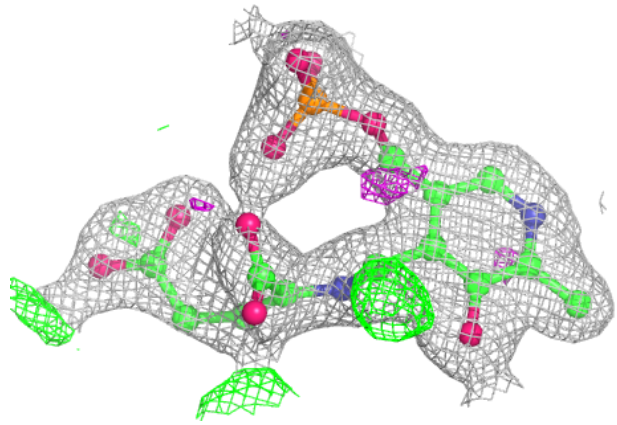
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

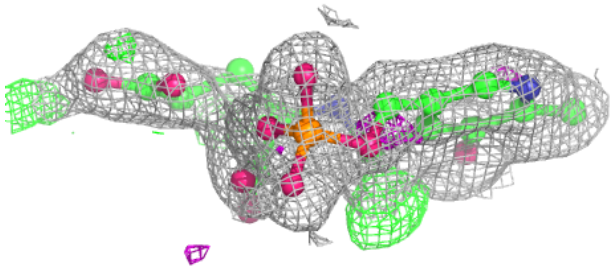
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	PDG	A	500	25/25	0.97	0.15	22,33,100,100	0
3	PDG	B	501	25/25	0.97	0.16	21,33,100,100	0
2	MG	A	601	1/1	0.99	0.07	47,47,47,47	0

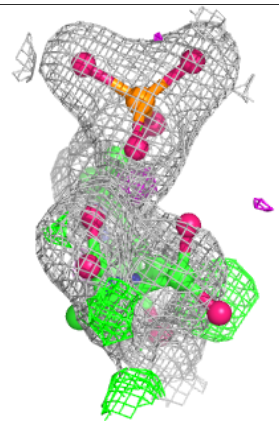
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PDG A 500:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

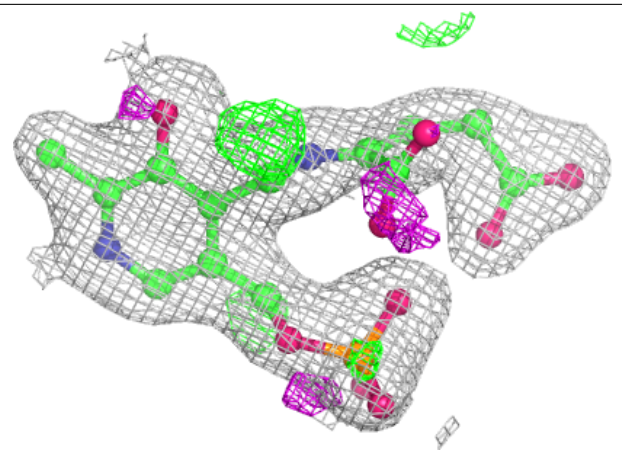


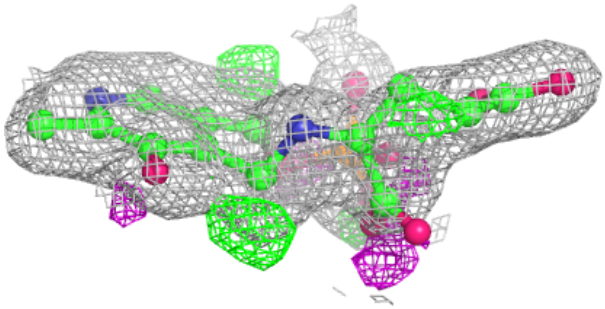


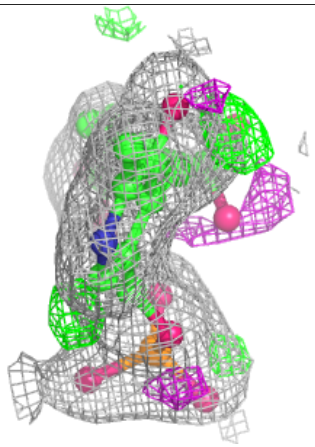


Electron density around PDG B 501:

$2mF_o$-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.