



wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 01:13 PM GMT

PDB ID : 4H2H
Title : Crystal structure of an enolase (mandalate racemase subgroup, target EFI-502101) from *Pelagibaca bermudensis* htcc2601, with bound mg and l-4-hydroxyproline betaine (betonidine)
Authors : Vetting, M.W.; Morisco, L.L.; Wasserman, S.R.; Sojitra, S.; Imker, H.J.; Gerlt, J.A.; Almo, S.C.; Enzyme Function Initiative (EFI)
Deposited on : 2012-09-12
Resolution : 1.70 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

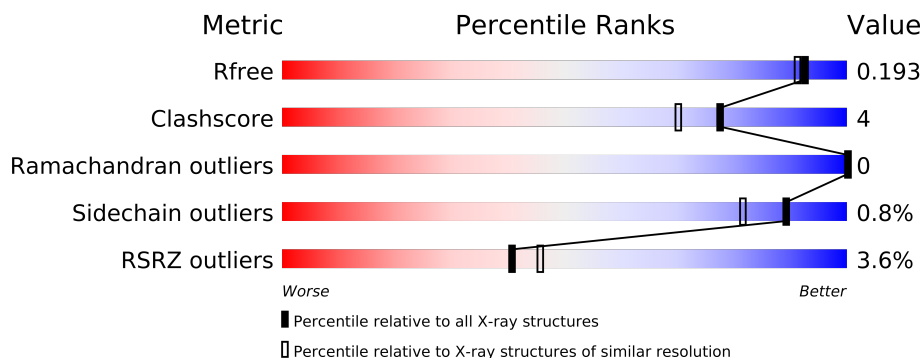
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.70 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}	66092	2456 (1.70-1.70)
Clashscore	79885	2929 (1.70-1.70)
Ramachandran outliers	78287	2878 (1.70-1.70)
Sidechain outliers	78261	2878 (1.70-1.70)
RSRZ outliers	66119	2456 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	376	
1	B	376	
1	C	376	
1	D	376	
1	E	376	
1	F	376	
1	G	376	
1	H	376	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	0XW	C	402	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	0XW	G	402	-	X
4	0XW	H	402	-	X
5	IOD	A	409	-	X
5	IOD	E	408	-	X
5	IOD	G	408	-	X
5	IOD	H	407	-	X
6	MPD	C	403	-	X
6	MPD	D	403	-	X
6	MPD	E	403	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 24627 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Mandelate racemase/muconate lactonizing enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	0	5	0
			2829	1785	498	530	16			
1	B	367	Total	C	N	O	S	0	5	0
			2828	1783	500	530	15			
1	C	367	Total	C	N	O	S	0	2	0
			2800	1766	494	525	15			
1	D	367	Total	C	N	O	S	0	4	0
			2809	1771	494	529	15			
1	E	355	Total	C	N	O	S	0	4	0
			2713	1707	478	512	16			
1	F	367	Total	C	N	O	S	0	1	0
			2792	1762	492	523	15			
1	G	367	Total	C	N	O	S	0	2	0
			2800	1768	493	524	15			
1	H	367	Total	C	N	O	S	0	2	0
			2803	1768	496	524	15			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	EXPRESSION TAG	UNP Q0FPQ4
A	-7	ALA	-	EXPRESSION TAG	UNP Q0FPQ4
A	-6	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
A	-5	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
A	-4	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
A	-3	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
A	-2	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
A	-1	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
A	0	SER	-	EXPRESSION TAG	UNP Q0FPQ4
A	1	LEU	-	EXPRESSION TAG	UNP Q0FPQ4
B	-8	MET	-	EXPRESSION TAG	UNP Q0FPQ4
B	-7	ALA	-	EXPRESSION TAG	UNP Q0FPQ4
B	-6	HIS	-	EXPRESSION TAG	UNP Q0FPQ4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
B	-4	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
B	-3	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
B	-2	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
B	-1	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
B	0	SER	-	EXPRESSION TAG	UNP Q0FPQ4
B	1	LEU	-	EXPRESSION TAG	UNP Q0FPQ4
C	-8	MET	-	EXPRESSION TAG	UNP Q0FPQ4
C	-7	ALA	-	EXPRESSION TAG	UNP Q0FPQ4
C	-6	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
C	-5	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
C	-4	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
C	-3	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
C	-2	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
C	-1	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
C	0	SER	-	EXPRESSION TAG	UNP Q0FPQ4
C	1	LEU	-	EXPRESSION TAG	UNP Q0FPQ4
D	-8	MET	-	EXPRESSION TAG	UNP Q0FPQ4
D	-7	ALA	-	EXPRESSION TAG	UNP Q0FPQ4
D	-6	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
D	-5	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
D	-4	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
D	-3	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
D	-2	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
D	-1	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
D	0	SER	-	EXPRESSION TAG	UNP Q0FPQ4
D	1	LEU	-	EXPRESSION TAG	UNP Q0FPQ4
E	-8	MET	-	EXPRESSION TAG	UNP Q0FPQ4
E	-7	ALA	-	EXPRESSION TAG	UNP Q0FPQ4
E	-6	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
E	-5	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
E	-4	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
E	-3	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
E	-2	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
E	-1	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
E	0	SER	-	EXPRESSION TAG	UNP Q0FPQ4
E	1	LEU	-	EXPRESSION TAG	UNP Q0FPQ4
F	-8	MET	-	EXPRESSION TAG	UNP Q0FPQ4
F	-7	ALA	-	EXPRESSION TAG	UNP Q0FPQ4
F	-6	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
F	-5	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
F	-4	HIS	-	EXPRESSION TAG	UNP Q0FPQ4

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-3	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
F	-2	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
F	-1	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
F	0	SER	-	EXPRESSION TAG	UNP Q0FPQ4
F	1	LEU	-	EXPRESSION TAG	UNP Q0FPQ4
G	-8	MET	-	EXPRESSION TAG	UNP Q0FPQ4
G	-7	ALA	-	EXPRESSION TAG	UNP Q0FPQ4
G	-6	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
G	-5	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
G	-4	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
G	-3	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
G	-2	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
G	-1	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
G	0	SER	-	EXPRESSION TAG	UNP Q0FPQ4
G	1	LEU	-	EXPRESSION TAG	UNP Q0FPQ4
H	-8	MET	-	EXPRESSION TAG	UNP Q0FPQ4
H	-7	ALA	-	EXPRESSION TAG	UNP Q0FPQ4
H	-6	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
H	-5	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
H	-4	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
H	-3	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
H	-2	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
H	-1	HIS	-	EXPRESSION TAG	UNP Q0FPQ4
H	0	SER	-	EXPRESSION TAG	UNP Q0FPQ4
H	1	LEU	-	EXPRESSION TAG	UNP Q0FPQ4

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	E	1	Total Mg 1 1	0	0
2	H	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	A	1	Total Mg 1 1	0	0

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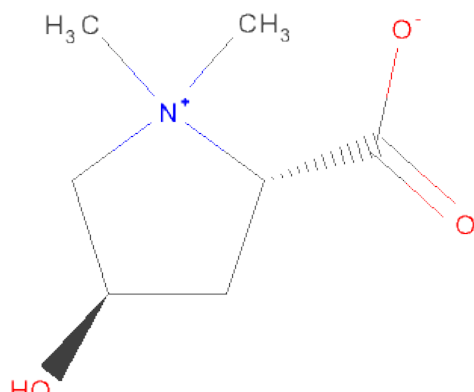
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	F	1	Total	Mg	0	0
			1	1		

- Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Ni	0	0
			1	1		
3	A	1	Total	Ni	0	0
			1	1		

- Molecule 4 is (2S,4R)-4-HYDROXY-1,1-DIMETHYLPYRROLIDINIUM-2-CARBOXYLATE (three-letter code: OXW) (formula: C₇H₁₃NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			11	7	1	3		
4	B	1	Total	C	N	O	0	0
			11	7	1	3		
4	C	1	Total	C	N	O	0	0
			11	7	1	3		
4	D	1	Total	C	N	O	0	0
			11	7	1	3		
4	E	1	Total	C	N	O	0	0
			11	7	1	3		
4	F	1	Total	C	N	O	0	0
			11	7	1	3		

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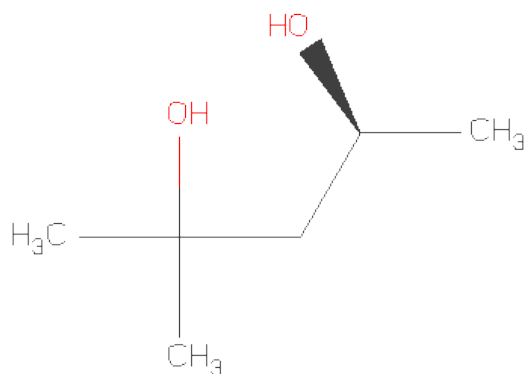
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	G	1	Total	C	N	O	0	0
			11	7	1	3		
4	H	1	Total	C	N	O	0	0
			11	7	1	3		

- Molecule 5 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	G	8	Total	I	0	0
			8	8		
5	D	8	Total	I	0	0
			8	8		
5	E	7	Total	I	0	0
			7	7		
5	H	6	Total	I	0	0
			6	6		
5	B	6	Total	I	0	0
			6	6		
5	C	10	Total	I	0	0
			10	10		
5	A	8	Total	I	0	0
			8	8		
5	F	8	Total	I	0	0
			8	8		

- Molecule 6 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	1	Total C O 8 6 2	0	0
6	D	1	Total C O 8 6 2	0	0
6	E	1	Total C O 8 6 2	0	0

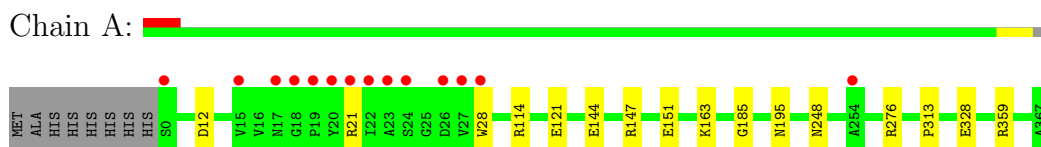
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	275	Total O 275 275	0	0
7	B	293	Total O 294 294	0	1
7	C	272	Total O 273 273	0	1
7	D	251	Total O 251 251	0	0
7	E	250	Total O 251 251	0	1
7	F	266	Total O 266 266	0	0
7	G	227	Total O 228 228	0	1
7	H	232	Total O 232 232	0	0

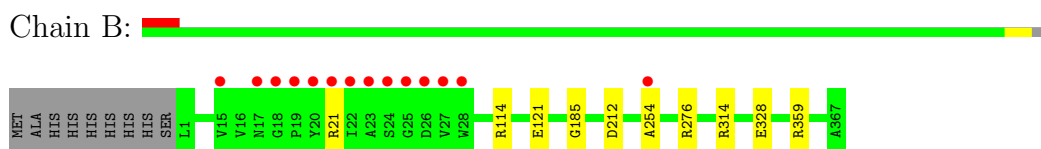
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

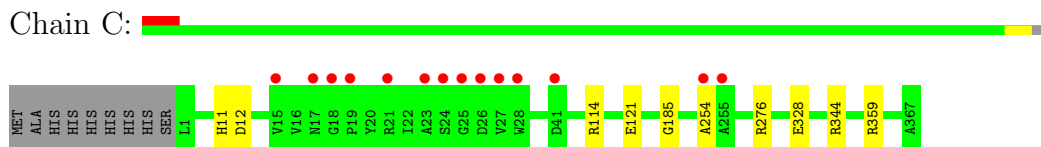
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme



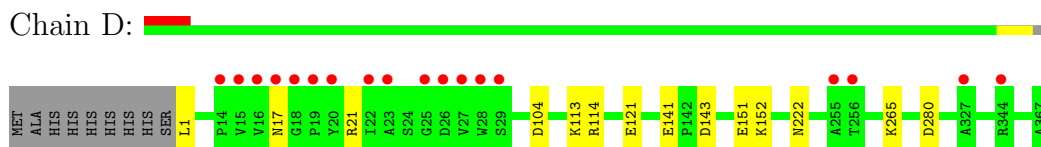
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme



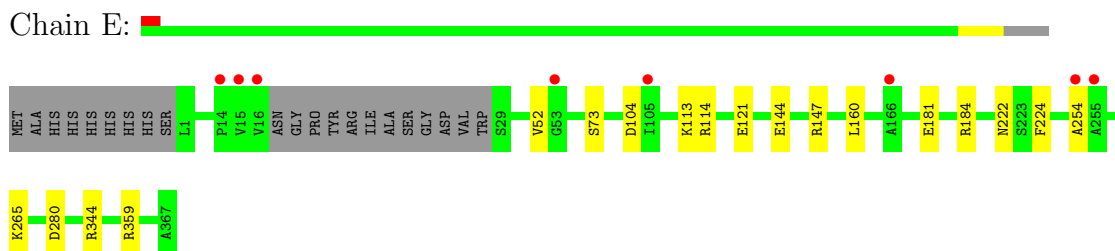
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme



- Molecule 1: Mandelate racemase/muconate lactonizing enzyme

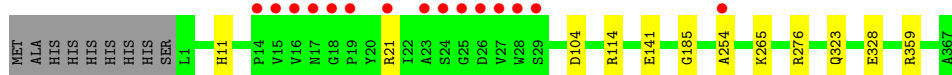


- Molecule 1: Mandelate racemase/muconate lactonizing enzyme



- Molecule 1: Mandelate racemase/muconate lactonizing enzyme





- Molecule 1: Mandelate racemase/muconate lactonizing enzyme

Chain G:



- Molecule 1: Mandelate racemase/muconate lactonizing enzyme

Chain H:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.03Å 152.82Å 113.03Å 90.00° 105.20° 90.00°	Depositor
Resolution (Å)	25.68 – 1.70 25.68 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (25.68-1.70) 99.9 (25.68-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 1.70Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8-1069)	Depositor
R, R_{free}	0.159 , 0.192 0.159 , 0.193	Depositor DCC
R_{free} test set	16414 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	18.0	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 44.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	5 of 325892 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	24627	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 68.87 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.0650e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NI, MG, IOD, OXW, MPD

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	0.36	0/2894	0.56	0/3936
1	B	0.37	0/2893	0.56	1/3936 (0.0%)
1	C	0.35	0/2865	0.55	0/3899
1	D	0.35	0/2879	0.54	0/3918
1	E	0.34	0/2772	0.55	0/3770
1	F	0.35	0/2857	0.54	0/3888
1	G	0.34	0/2865	0.53	0/3899
1	H	0.32	0/2868	0.51	0/3902
All	All	0.35	0/22893	0.54	1/31148 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	212	ASP	CB-CG-OD1	5.27	123.04	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2829	0	18	12	0
1	B	2828	0	13	8	0
1	C	2800	0	13	7	0
1	D	2809	0	13	11	0
1	E	2713	0	13	14	0
1	F	2792	0	13	7	0
1	G	2800	0	13	11	0
1	H	2803	0	13	8	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	11	0	13	0	0
4	B	11	0	13	0	0
4	C	11	0	13	0	0
4	D	11	0	13	0	0
4	E	11	0	13	0	0
4	F	11	0	13	0	0
4	G	11	0	13	1	0
4	H	11	0	13	2	0
5	A	8	0	0	4	0
5	B	6	0	0	2	0
5	C	10	0	0	2	0
5	D	8	0	0	5	0
5	E	7	0	0	4	0
5	F	8	0	0	3	0
5	G	8	0	0	5	0
5	H	6	0	0	4	0
6	C	8	0	14	0	0
6	D	8	0	14	0	0
6	E	8	0	14	2	0
7	A	275	0	0	6	0
7	B	294	0	0	4	0
7	C	273	0	0	6	0
7	D	251	0	0	4	0
7	E	251	0	0	8	0
7	F	266	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	228	0	0	5	0
7	H	232	0	0	4	0
All	All	24627	0	255	85	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

The worst 5 of 85 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:406:IOD:I	7:E:693:HOH:O	2.33	1.16
5:A:407:IOD:I	7:A:663:HOH:O	2.39	1.08
5:D:406:IOD:I	7:D:638:HOH:O	2.44	1.06
5:G:404:IOD:I	7:G:614:HOH:O	2.49	1.00
5:C:405:IOD:I	7:C:709[B]:HOH:O	2.52	0.95

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	371/376 (99%)	367 (99%)	4 (1%)	0	100	100
1	B	370/376 (98%)	365 (99%)	5 (1%)	0	100	100
1	C	367/376 (98%)	362 (99%)	5 (1%)	0	100	100
1	D	369/376 (98%)	364 (99%)	5 (1%)	0	100	100
1	E	355/376 (94%)	351 (99%)	4 (1%)	0	100	100
1	F	366/376 (97%)	360 (98%)	6 (2%)	0	100	100
1	G	367/376 (98%)	362 (99%)	5 (1%)	0	100	100
1	H	367/376 (98%)	363 (99%)	4 (1%)	0	100	100
All	All	2932/3008 (98%)	2894 (99%)	38 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	292/294 (99%)	289 (99%)	3 (1%)	85	76
1	B	291/294 (99%)	290 (100%)	1 (0%)	96	93
1	C	288/294 (98%)	286 (99%)	2 (1%)	91	85
1	D	290/294 (99%)	289 (100%)	1 (0%)	96	93
1	E	281/294 (96%)	278 (99%)	3 (1%)	84	72
1	F	287/294 (98%)	283 (99%)	4 (1%)	78	62
1	G	288/294 (98%)	284 (99%)	4 (1%)	78	62
1	H	288/294 (98%)	288 (100%)	0	100	100
All	All	2305/2352 (98%)	2287 (99%)	18 (1%)	89	81

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	104	ASP
1	E	160	LEU
1	G	88	ARG
1	D	104	ASP
1	E	52	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 82 ligands modelled in this entry, 71 are monoatomic - leaving 11 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$
4	0XW	A	403	2	8,11,11	2.85	4 (50%)	14,17,17	2.29	5 (35%)
4	0XW	B	403	2	8,11,11	2.74	4 (50%)	14,17,17	2.56	7 (50%)
4	0XW	C	402	2	8,11,11	2.78	4 (50%)	14,17,17	2.35	5 (35%)
6	MPD	C	403	-	7,7,7	0.25	0	10,10,10	0.62	0
4	0XW	D	402	2	8,11,11	2.95	4 (50%)	14,17,17	2.49	5 (35%)
6	MPD	D	403	-	7,7,7	0.25	0	10,10,10	0.49	0
4	0XW	E	402	2	8,11,11	2.78	4 (50%)	14,17,17	2.74	5 (35%)
6	MPD	E	403	-	7,7,7	0.28	0	10,10,10	0.48	0
4	0XW	F	402	2	8,11,11	2.75	5 (62%)	14,17,17	2.51	6 (42%)
4	0XW	G	402	2	8,11,11	2.82	4 (50%)	14,17,17	2.35	7 (50%)
4	0XW	H	402	2	8,11,11	2.80	4 (50%)	14,17,17	2.41	6 (42%)

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	0XW	A	403	2	-	0/0/19/19	0/1/1/1
4	0XW	B	403	2	-	0/0/19/19	0/1/1/1
4	0XW	C	402	2	-	0/0/19/19	0/1/1/1
6	MPD	C	403	-	-	0/5/5/5	0/0/0/0
4	0XW	D	402	2	-	0/0/19/19	0/1/1/1
6	MPD	D	403	-	-	0/5/5/5	0/0/0/0
4	0XW	E	402	2	-	0/0/19/19	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MPD	E	403	-	-	0/5/5/5	0/0/0/0
4	0XW	F	402	2	-	0/0/19/19	0/1/1/1
4	0XW	G	402	2	-	0/0/19/19	0/1/1/1
4	0XW	H	402	2	-	0/0/19/19	0/1/1/1

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	402	0XW	C08-N02	-5.15	1.45	1.53
4	A	403	0XW	C08-N02	-4.72	1.45	1.53
4	E	402	0XW	C08-N02	-4.65	1.46	1.53
4	G	402	0XW	C08-N02	-4.56	1.46	1.53
4	H	402	0XW	C08-N02	-4.55	1.46	1.53

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	402	0XW	C07-C08-N02	-5.72	99.19	103.30
4	H	402	0XW	O06-C05-C07	5.70	125.60	110.16
4	C	402	0XW	O06-C05-C07	5.58	125.28	110.16
4	G	402	0XW	O06-C05-C07	5.57	125.24	110.16
4	E	402	0XW	O06-C05-C07	5.50	125.07	110.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	368/376 (97%)	-0.18	14 (3%) 38 43	9, 17, 39, 78	0
1	B	367/376 (97%)	-0.17	14 (3%) 38 43	9, 17, 42, 73	0
1	C	367/376 (97%)	-0.20	14 (3%) 38 43	10, 19, 39, 74	0
1	D	367/376 (97%)	-0.15	18 (4%) 28 33	9, 19, 41, 68	0
1	E	355/376 (94%)	-0.23	8 (2%) 57 63	10, 20, 39, 47	0
1	F	367/376 (97%)	-0.13	15 (4%) 35 40	9, 19, 44, 86	0
1	G	367/376 (97%)	-0.00	15 (4%) 35 40	12, 25, 46, 72	0
1	H	367/376 (97%)	-0.09	10 (2%) 52 57	11, 23, 44, 73	0
All	All	2925/3008 (97%)	-0.15	108 (3%) 41 44	9, 20, 42, 86	0

The worst 5 of 108 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	28	TRP	8.5
1	D	28	TRP	8.5
1	C	28	TRP	8.1
1	B	28	TRP	7.1
1	C	17	ASN	6.4

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	IOD	A	409	1/1	0.12	8.70	57,57,57,57	1
6	MPD	D	403	8/8	0.16	7.19	43,48,49,50	0
6	MPD	E	403	8/8	0.14	6.47	32,45,48,50	0
5	IOD	E	408	1/1	0.15	4.92	65,65,65,65	1
6	MPD	C	403	8/8	0.14	3.50	32,35,39,40	0
4	0XW	C	402	11/11	0.14	2.62	23,38,45,47	0
4	0XW	G	402	11/11	0.14	2.42	23,36,41,42	0
5	IOD	G	408	1/1	0.19	2.25	76,76,76,76	1
5	IOD	H	407	1/1	0.15	2.20	73,73,73,73	1
4	0XW	H	402	11/11	0.13	2.16	27,39,45,48	0
5	IOD	C	412	1/1	0.19	1.82	65,65,65,65	1
5	IOD	F	410	1/1	0.20	1.80	49,49,49,49	1
5	IOD	C	411	1/1	0.12	1.77	62,62,62,62	1
5	IOD	D	408	1/1	0.10	1.61	49,49,49,49	1
4	0XW	D	402	11/11	0.15	1.35	24,38,43,45	0
4	0XW	E	402	11/11	0.12	1.20	39,40,45,49	0
5	IOD	A	408	1/1	0.09	1.19	52,52,52,52	1
5	IOD	C	413	1/1	0.17	0.55	79,79,79,79	1
5	IOD	B	409	1/1	0.14	0.43	83,83,83,83	1
4	0XW	F	402	11/11	0.11	0.30	29,35,40,40	0
5	IOD	G	407	1/1	0.14	-0.04	47,47,47,47	1
5	IOD	C	404	1/1	0.06	-0.13	34,34,34,34	1
5	IOD	E	407	1/1	0.07	-0.14	50,50,50,50	1
4	0XW	A	403	11/11	0.10	-0.16	25,29,31,32	0
5	IOD	H	406	1/1	0.13	-0.17	64,64,64,64	1
5	IOD	G	410	1/1	0.14	-0.18	66,66,66,66	1
4	0XW	B	403	11/11	0.10	-0.20	24,28,31,32	0
5	IOD	A	410	1/1	0.08	-0.28	69,69,69,69	1
5	IOD	D	410	1/1	0.27	-0.52	91,91,91,91	1
5	IOD	D	409	1/1	0.11	-0.57	77,77,77,77	1
5	IOD	F	404	1/1	0.05	-0.58	35,35,35,35	1
5	IOD	A	404	1/1	0.07	-0.71	44,44,44,44	1
5	IOD	G	406	1/1	0.09	-1.08	64,64,64,64	1
5	IOD	E	406	1/1	0.06	-1.11	29,29,29,29	1
5	IOD	G	405	1/1	0.04	-1.32	34,34,34,34	1

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	IOD	D	404	1/1	0.04	-1.37	46,46,46,46	1
5	IOD	E	404	1/1	0.04	-1.50	45,45,45,45	1
5	IOD	B	407	1/1	0.06	-1.53	53,53,53,53	1
5	IOD	H	405	1/1	0.05	-1.54	35,35,35,35	1
2	MG	E	401	1/1	0.04	-1.59	18,18,18,18	0
5	IOD	A	405	1/1	0.03	-1.60	30,30,30,30	1
5	IOD	F	408	1/1	0.05	-1.67	19,19,19,19	1
5	IOD	D	407	1/1	0.04	-1.72	28,28,28,28	1
5	IOD	C	406	1/1	0.03	-1.72	29,29,29,29	1
5	IOD	B	404	1/1	0.05	-1.74	46,46,46,46	1
5	IOD	H	408	1/1	0.03	-1.78	45,45,45,45	1
5	IOD	E	410	1/1	0.04	-2.00	47,47,47,47	1
5	IOD	D	411	1/1	0.04	-2.06	39,39,39,39	1
5	IOD	G	409	1/1	0.04	-2.06	52,52,52,52	1
5	IOD	E	409	1/1	0.04	-2.08	40,40,40,40	1
5	IOD	C	410	1/1	0.03	-2.08	34,34,34,34	1
5	IOD	D	406	1/1	0.05	-2.16	18,18,18,18	1
2	MG	B	401	1/1	0.04	-2.18	15,15,15,15	0
2	MG	A	401	1/1	0.03	-2.24	14,14,14,14	0
5	IOD	D	405	1/1	0.03	-2.24	41,41,41,41	1
5	IOD	C	408	1/1	0.04	-2.26	40,40,40,40	1
5	IOD	H	403	1/1	0.02	-2.33	27,27,27,27	1
2	MG	G	401	1/1	0.03	-2.39	17,17,17,17	0
5	IOD	H	404	1/1	0.03	-2.40	22,22,22,22	1
5	IOD	F	406	1/1	0.04	-2.69	31,31,31,31	1
5	IOD	B	405	1/1	0.03	-2.69	23,23,23,23	1
5	IOD	F	407	1/1	0.02	-2.71	27,27,27,27	1
5	IOD	C	409	1/1	0.04	-2.73	23,23,23,23	1
2	MG	D	401	1/1	0.03	-2.74	17,17,17,17	0
5	IOD	A	407	1/1	0.03	-2.86	20,20,20,20	1
5	IOD	B	406	1/1	0.03	-2.89	25,25,25,25	1
2	MG	F	401	1/1	0.03	-3.01	15,15,15,15	0
2	MG	C	401	1/1	0.03	-3.04	14,14,14,14	0
5	IOD	B	408	1/1	0.03	-3.15	22,22,22,22	1
5	IOD	F	409	1/1	0.03	-3.25	24,24,24,24	1
5	IOD	A	411	1/1	0.03	-3.57	31,31,31,31	1
5	IOD	E	405	1/1	0.03	-3.62	29,29,29,29	1
2	MG	H	401	1/1	0.03	-3.81	16,16,16,16	0
5	IOD	A	406	1/1	0.03	-3.89	23,23,23,23	1
5	IOD	G	403	1/1	0.03	-4.41	30,30,30,30	1
5	IOD	C	405	1/1	0.03	-5.16	23,23,23,23	1
5	IOD	F	403	1/1	0.03	-5.75	27,27,27,27	1

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	IOD	C	407	1/1	0.03	-5.88	23,23,23,23	1
5	IOD	G	404	1/1	0.02	-6.23	23,23,23,23	1
5	IOD	F	405	1/1	0.04	-7.14	41,41,41,41	1
3	NI	B	402	1/1	0.02	-8.49	12,12,12,12	1
3	NI	A	402	1/1	0.02	-11.33	12,12,12,12	1

6.5 Other polymers ⓘ

There are no such residues in this entry.