WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 10, 2023 – 08:58 AM EDT

PDB ID	:	4HN8
Title	:	Crystal structure of a putative D-glucarate dehydratase from Pseudomonas mendocina ymp
Authors	:	Hegde, R.P.; Toro, R.; Burley, S.K.; Almo, S.C.; Ramagopal, U.A.; New York Structural Genomics Research Consortium (NYSGRC)
Deposited on	:	2012-10-19
Resolution	:	2.20 Å(reported)

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	:	2.35.1
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

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 2.20 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.
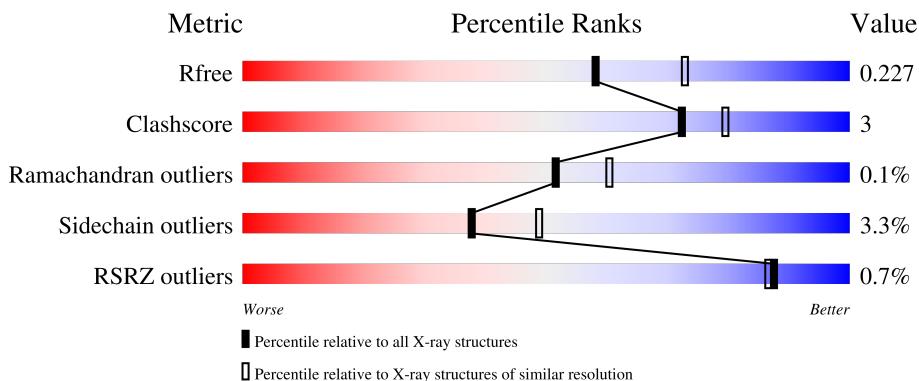
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	473	84% — 6% — 10%
1	B	473	83% — 6% · 10%
1	C	473	83% — 7% — 10%
1	D	473	83% — 7% — 10%
1	E	473	81% — 8% · 10%

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Mol	Chain	Length	Quality of chain
1	F	473	84% 6% 10%
1	G	473	.% 79% 10% 10%
1	H	473	.% 82% 7% · 10%

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
2	GOL	G	501	-	-	X	-

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 27164 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 D-glucarate dehydratase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	Se	0	4	0
			3328	2089	617	602	6	14			
1	B	426	Total	C	N	O	S	Se	0	1	0
			3301	2071	611	599	6	14			
1	C	427	Total	C	N	O	S	Se	0	7	0
			3348	2102	620	606	6	14			
1	D	427	Total	C	N	O	S	Se	0	6	0
			3333	2095	612	606	6	14			
1	E	426	Total	C	N	O	S	Se	0	3	0
			3312	2079	614	599	6	14			
1	F	426	Total	C	N	O	S	Se	0	3	0
			3319	2082	619	598	6	14			
1	G	426	Total	C	N	O	S	Se	0	3	0
			3314	2079	615	600	6	14			
1	H	427	Total	C	N	O	S	Se	0	2	0
			3313	2081	612	600	6	14			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	expression tag	UNP A4XRL3
A	0	SER	-	expression tag	UNP A4XRL3
A	1	LEU	-	expression tag	UNP A4XRL3
A	464	GLU	-	expression tag	UNP A4XRL3
A	465	GLY	-	expression tag	UNP A4XRL3
A	466	HIS	-	expression tag	UNP A4XRL3
A	467	HIS	-	expression tag	UNP A4XRL3
A	468	HIS	-	expression tag	UNP A4XRL3
A	469	HIS	-	expression tag	UNP A4XRL3
A	470	HIS	-	expression tag	UNP A4XRL3
A	471	HIS	-	expression tag	UNP A4XRL3
B	-1	MSE	-	expression tag	UNP A4XRL3
B	0	SER	-	expression tag	UNP A4XRL3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1	LEU	-	expression tag	UNP A4XRL3
B	464	GLU	-	expression tag	UNP A4XRL3
B	465	GLY	-	expression tag	UNP A4XRL3
B	466	HIS	-	expression tag	UNP A4XRL3
B	467	HIS	-	expression tag	UNP A4XRL3
B	468	HIS	-	expression tag	UNP A4XRL3
B	469	HIS	-	expression tag	UNP A4XRL3
B	470	HIS	-	expression tag	UNP A4XRL3
B	471	HIS	-	expression tag	UNP A4XRL3
C	-1	MSE	-	expression tag	UNP A4XRL3
C	0	SER	-	expression tag	UNP A4XRL3
C	1	LEU	-	expression tag	UNP A4XRL3
C	464	GLU	-	expression tag	UNP A4XRL3
C	465	GLY	-	expression tag	UNP A4XRL3
C	466	HIS	-	expression tag	UNP A4XRL3
C	467	HIS	-	expression tag	UNP A4XRL3
C	468	HIS	-	expression tag	UNP A4XRL3
C	469	HIS	-	expression tag	UNP A4XRL3
C	470	HIS	-	expression tag	UNP A4XRL3
C	471	HIS	-	expression tag	UNP A4XRL3
D	-1	MSE	-	expression tag	UNP A4XRL3
D	0	SER	-	expression tag	UNP A4XRL3
D	1	LEU	-	expression tag	UNP A4XRL3
D	464	GLU	-	expression tag	UNP A4XRL3
D	465	GLY	-	expression tag	UNP A4XRL3
D	466	HIS	-	expression tag	UNP A4XRL3
D	467	HIS	-	expression tag	UNP A4XRL3
D	468	HIS	-	expression tag	UNP A4XRL3
D	469	HIS	-	expression tag	UNP A4XRL3
D	470	HIS	-	expression tag	UNP A4XRL3
D	471	HIS	-	expression tag	UNP A4XRL3
E	-1	MSE	-	expression tag	UNP A4XRL3
E	0	SER	-	expression tag	UNP A4XRL3
E	1	LEU	-	expression tag	UNP A4XRL3
E	464	GLU	-	expression tag	UNP A4XRL3
E	465	GLY	-	expression tag	UNP A4XRL3
E	466	HIS	-	expression tag	UNP A4XRL3
E	467	HIS	-	expression tag	UNP A4XRL3
E	468	HIS	-	expression tag	UNP A4XRL3
E	469	HIS	-	expression tag	UNP A4XRL3
E	470	HIS	-	expression tag	UNP A4XRL3
E	471	HIS	-	expression tag	UNP A4XRL3

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	MSE	-	expression tag	UNP A4XRL3
F	0	SER	-	expression tag	UNP A4XRL3
F	1	LEU	-	expression tag	UNP A4XRL3
F	464	GLU	-	expression tag	UNP A4XRL3
F	465	GLY	-	expression tag	UNP A4XRL3
F	466	HIS	-	expression tag	UNP A4XRL3
F	467	HIS	-	expression tag	UNP A4XRL3
F	468	HIS	-	expression tag	UNP A4XRL3
F	469	HIS	-	expression tag	UNP A4XRL3
F	470	HIS	-	expression tag	UNP A4XRL3
F	471	HIS	-	expression tag	UNP A4XRL3
G	-1	MSE	-	expression tag	UNP A4XRL3
G	0	SER	-	expression tag	UNP A4XRL3
G	1	LEU	-	expression tag	UNP A4XRL3
G	464	GLU	-	expression tag	UNP A4XRL3
G	465	GLY	-	expression tag	UNP A4XRL3
G	466	HIS	-	expression tag	UNP A4XRL3
G	467	HIS	-	expression tag	UNP A4XRL3
G	468	HIS	-	expression tag	UNP A4XRL3
G	469	HIS	-	expression tag	UNP A4XRL3
G	470	HIS	-	expression tag	UNP A4XRL3
G	471	HIS	-	expression tag	UNP A4XRL3
H	-1	MSE	-	expression tag	UNP A4XRL3
H	0	SER	-	expression tag	UNP A4XRL3
H	1	LEU	-	expression tag	UNP A4XRL3
H	464	GLU	-	expression tag	UNP A4XRL3
H	465	GLY	-	expression tag	UNP A4XRL3
H	466	HIS	-	expression tag	UNP A4XRL3
H	467	HIS	-	expression tag	UNP A4XRL3
H	468	HIS	-	expression tag	UNP A4XRL3
H	469	HIS	-	expression tag	UNP A4XRL3
H	470	HIS	-	expression tag	UNP A4XRL3
H	471	HIS	-	expression tag	UNP A4XRL3

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

GOL

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 6	C 3	O 3	0	0
2	A	1	Total 6	C 3	O 3	0	0
2	B	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	D	1	Total 6	C 3	O 3	0	0
2	E	1	Total 6	C 3	O 3	0	0
2	F	1	Total 6	C 3	O 3	0	0
2	G	1	Total 6	C 3	O 3	0	0
2	H	1	Total 6	C 3	O 3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	103	Total 103	O 103	0	0
3	B	84	Total 84	O 84	0	0
3	C	71	Total 71	O 71	0	0

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| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	64	Total 64	O 64	0	0
3	E	61	Total 61	O 61	0	0
3	F	32	Total 32	O 32	0	0
3	G	53	Total 53	O 53	0	0
3	H	74	Total 74	O 74	0	0

3 Residue-property plots ⓘ

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.
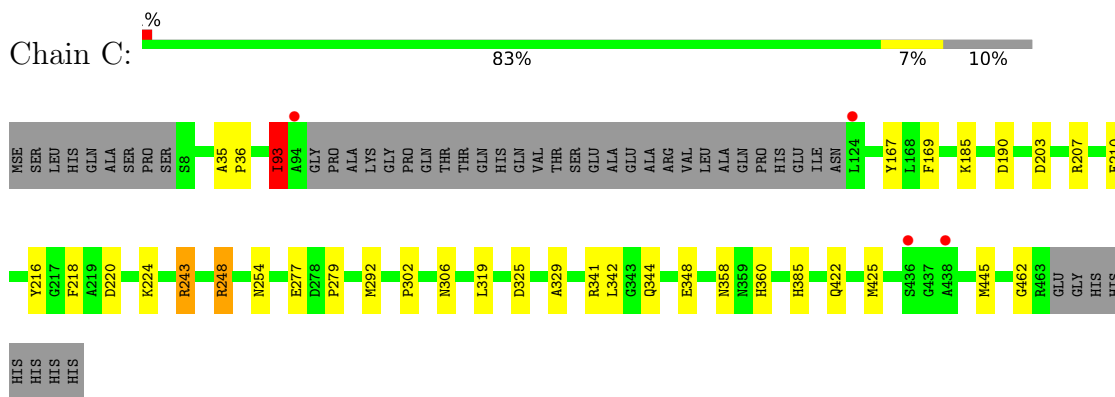
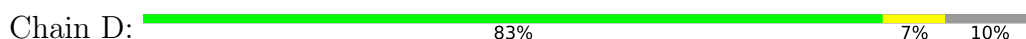- Molecule 1: D-glucarate dehydratase
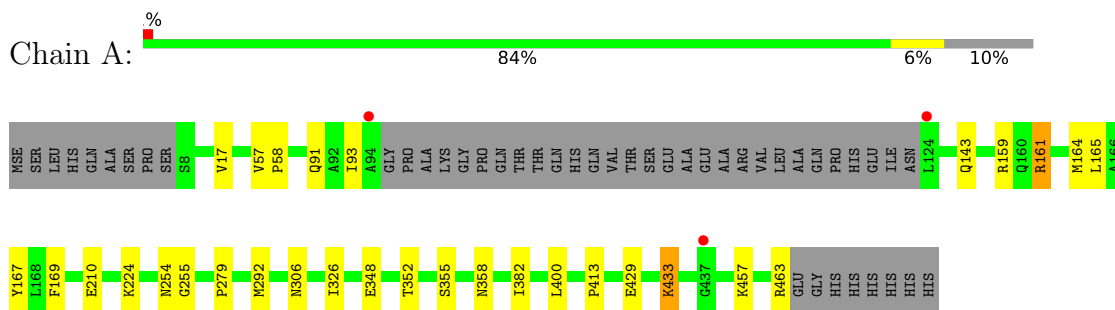
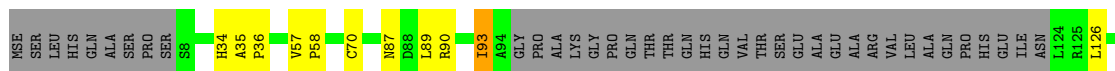Chain A:

- Molecule 1: D-glucarate dehydratase

Chain B:

- Molecule 1: D-glucarate dehydratase

Chain C:

- Molecule 1: D-glucarate dehydratase

Chain D:
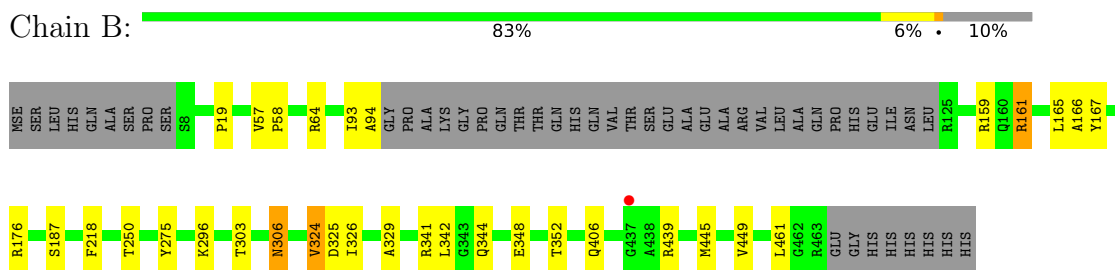
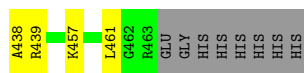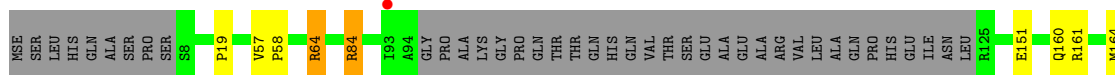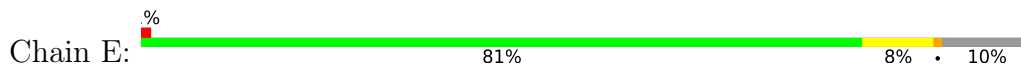• Molecule 1: D-glucarate dehydratase

Chain E:

• Molecule 1: D-glucarate dehydratase

Chain F:

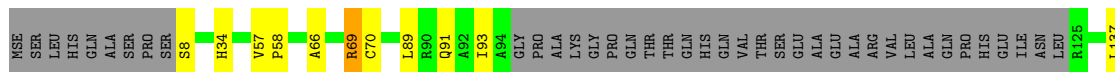
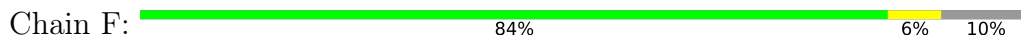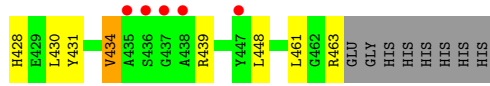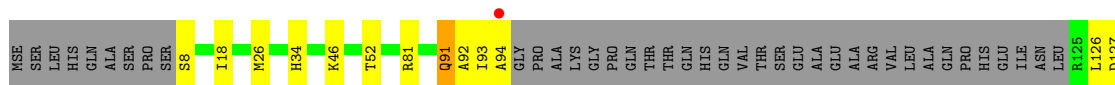• Molecule 1: D-glucarate dehydratase

Chain G:

• Molecule 1: D-glucarate dehydratase

Chain H:
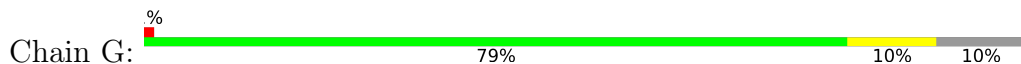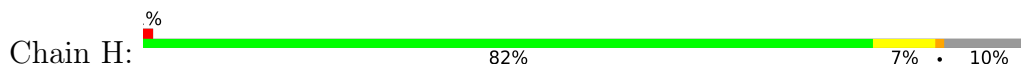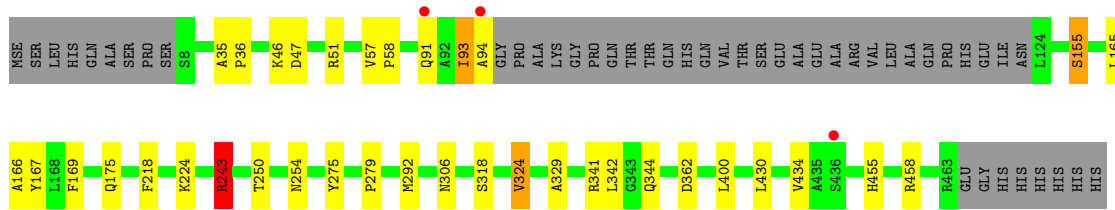
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	126.36Å 148.84Å 198.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.18 – 2.20 46.18 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.18-2.20) 99.7 (46.18-2.20)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	0.11	Depositor
$< I/\sigma(I) >$ [1]	2.68 (at 2.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.176 , 0.222 0.185 , 0.227	Depositor DCC
R_{free} test set	9478 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	24.4	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 30.9	EDS
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	27164	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.18% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

5.1   Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL

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	0.59	0/3394	0.69	0/4574
1	B	0.59	0/3361	0.68	0/4530
1	C	0.57	0/3423	0.69	0/4613
1	D	0.57	0/3409	0.70	0/4597
1	E	0.54	0/3379	0.69	0/4555
1	F	0.53	0/3386	0.66	0/4563
1	G	0.53	0/3377	0.69	1/4551 (0.0%)
1	H	0.56	0/3377	0.69	1/4553 (0.0%)
All	All	0.56	0/27106	0.69	2/36536 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	243	ARG	NE-CZ-NH1	7.08	123.84	120.30
1	G	139	ASP	CB-CG-OD1	5.49	123.24	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2   Too-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 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	3328	0	3295	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3301	0	3262	32	0
1	C	3348	0	3320	15	0
1	D	3333	0	3299	21	0
1	E	3312	0	3279	32	0
1	F	3319	0	3293	16	0
1	G	3314	0	3276	28	0
1	H	3313	0	3279	21	0
2	A	12	0	16	3	0
2	B	6	0	8	3	0
2	C	6	0	8	1	0
2	D	6	0	8	3	0
2	E	6	0	8	1	0
2	F	6	0	8	2	0
2	G	6	0	8	4	0
2	H	6	0	8	0	0
3	A	103	0	0	2	0
3	B	84	0	0	1	0
3	C	71	0	0	0	0
3	D	64	0	0	0	0
3	E	61	0	0	3	0
3	F	32	0	0	0	0
3	G	53	0	0	1	0
3	H	74	0	0	1	0
All	All	27164	0	26375	181	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.

The worst 5 of 181 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:E:213[A]:ARG:HG2	1:E:213[A]:ARG:HH11	1.08	1.15
1:B:161:ARG:HH11	1:B:161:ARG:HG3	1.27	1.00
1:D:445:MSE:HE1	1:D:461:LEU:CD1	1.94	0.97
1:E:84:ARG:HH11	1:E:84:ARG:HG3	1.26	0.96
1:B:445:MSE:HE1	1:B:461:LEU:HD11	1.46	0.96

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	427/473 (90%)	417 (98%)	10 (2%)	0	100	100
1	B	423/473 (89%)	414 (98%)	9 (2%)	0	100	100
1	C	430/473 (91%)	420 (98%)	8 (2%)	2 (0%)	29	31
1	D	429/473 (91%)	419 (98%)	10 (2%)	0	100	100
1	E	425/473 (90%)	414 (97%)	10 (2%)	1 (0%)	47	55
1	F	425/473 (90%)	408 (96%)	14 (3%)	3 (1%)	22	22
1	G	425/473 (90%)	415 (98%)	10 (2%)	0	100	100
1	H	425/473 (90%)	419 (99%)	6 (1%)	0	100	100
All	All	3409/3784 (90%)	3326 (98%)	77 (2%)	6 (0%)	51	55

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	462	GLY
1	E	438	ALA
1	F	187	SER
1	C	93	ILE
1	F	69[A]	ARG

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	335/356 (94%)	326 (97%)	9 (3%)	44	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	332/356 (93%)	325 (98%)	7 (2%)	53	67
1	C	338/356 (95%)	323 (96%)	15 (4%)	28	35
1	D	336/356 (94%)	327 (97%)	9 (3%)	44	57
1	E	333/356 (94%)	321 (96%)	12 (4%)	35	45
1	F	334/356 (94%)	323 (97%)	11 (3%)	38	49
1	G	333/356 (94%)	317 (95%)	16 (5%)	25	32
1	H	333/356 (94%)	322 (97%)	11 (3%)	38	49
All	All	2674/2848 (94%)	2584 (97%)	90 (3%)	38	47

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	241	LYS
1	G	243	ARG
1	F	267	LYS
1	G	127	ASP
1	G	400	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	344	GLN
1	G	344	GLN
1	H	344	GLN
1	H	65	GLN
1	C	344	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

9 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
2	GOL	E	501	-	5,5,5	0.60	0	5,5,5	1.38	1 (20%)
2	GOL	H	501	-	5,5,5	0.92	0	5,5,5	1.30	1 (20%)
2	GOL	C	501	-	5,5,5	0.65	0	5,5,5	0.66	0
2	GOL	A	501	-	5,5,5	0.22	0	5,5,5	0.30	0
2	GOL	F	501	-	5,5,5	0.60	0	5,5,5	0.82	0
2	GOL	G	501	-	5,5,5	0.65	0	5,5,5	0.76	0
2	GOL	D	501	-	5,5,5	0.62	0	5,5,5	1.15	0
2	GOL	B	501	-	5,5,5	0.76	0	5,5,5	0.85	0
2	GOL	A	502	-	5,5,5	0.69	0	5,5,5	1.27	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
2	GOL	E	501	-	-	4/4/4/4	-
2	GOL	H	501	-	-	0/4/4/4	-
2	GOL	C	501	-	-	2/4/4/4	-
2	GOL	A	501	-	-	2/4/4/4	-
2	GOL	F	501	-	-	4/4/4/4	-
2	GOL	G	501	-	-	4/4/4/4	-
2	GOL	D	501	-	-	4/4/4/4	-
2	GOL	B	501	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	502	-	-	3/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	501	GOL	O2-C2-C1	-2.34	98.80	109.12
2	H	501	GOL	O2-C2-C1	-2.02	100.21	109.12

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	O1-C1-C2-O2
2	A	501	GOL	O1-C1-C2-C3
2	A	502	GOL	O1-C1-C2-O2
2	A	502	GOL	O1-C1-C2-C3
2	C	501	GOL	C1-C2-C3-O3

There are no ring outliers.

8 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	501	GOL	1	0
2	C	501	GOL	1	0
2	A	501	GOL	1	0
2	F	501	GOL	2	0
2	G	501	GOL	4	0
2	D	501	GOL	3	0
2	B	501	GOL	3	0
2	A	502	GOL	2	0

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(Å²)	Q<0.9
1	A	413/473 (87%)	-0.48	3 (0%)	87	86	11, 18, 39, 70	0
1	B	412/473 (87%)	-0.58	1 (0%)	95	94	10, 20, 41, 66	0
1	C	413/473 (87%)	-0.49	4 (0%)	82	81	11, 21, 45, 88	0
1	D	413/473 (87%)	-0.41	1 (0%)	95	94	10, 23, 47, 82	0
1	E	412/473 (87%)	-0.44	3 (0%)	87	86	14, 25, 46, 74	0
1	F	412/473 (87%)	-0.39	1 (0%)	95	94	14, 28, 50, 77	0
1	G	412/473 (87%)	-0.44	7 (1%)	70	68	14, 24, 47, 72	0
1	H	413/473 (87%)	-0.47	3 (0%)	87	86	11, 22, 48, 91	0
All	All	3300/3784 (87%)	-0.46	23 (0%)	87	86	10, 23, 46, 91	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	94	ALA	4.6
1	H	436	SER	4.1
1	C	94	ALA	4.0
1	D	436	SER	3.8
1	A	124	LEU	3.7

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 monosaccharides 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(Å^2)	Q<0.9
2	GOL	F	501	6/6	0.80	0.27	29,37,45,46	0
2	GOL	G	501	6/6	0.86	0.19	23,32,37,52	0
2	GOL	D	501	6/6	0.89	0.23	29,32,41,42	0
2	GOL	C	501	6/6	0.90	0.19	24,32,34,43	0
2	GOL	H	501	6/6	0.91	0.19	21,26,32,37	0
2	GOL	A	501	6/6	0.92	0.12	35,36,44,45	0
2	GOL	A	502	6/6	0.93	0.16	20,26,28,37	0
2	GOL	E	501	6/6	0.94	0.17	30,32,38,44	0
2	GOL	B	501	6/6	0.94	0.14	21,27,28,36	0

6.5 Other polymers ⓘ

There are no such residues in this entry.