



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 30, 2021 – 04:50 PM EST

PDB ID : 3FXG
Title : Crystal structure of rhamnonate dehydratase from *Gibberella zeae* complexed with Mg
Authors : Fedorov, A.A.; Fedorov, E.V.; Sauder, J.M.; Burley, S.K.; Gerlt, J.A.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2009-01-20
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	2.16
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)	:	2.16

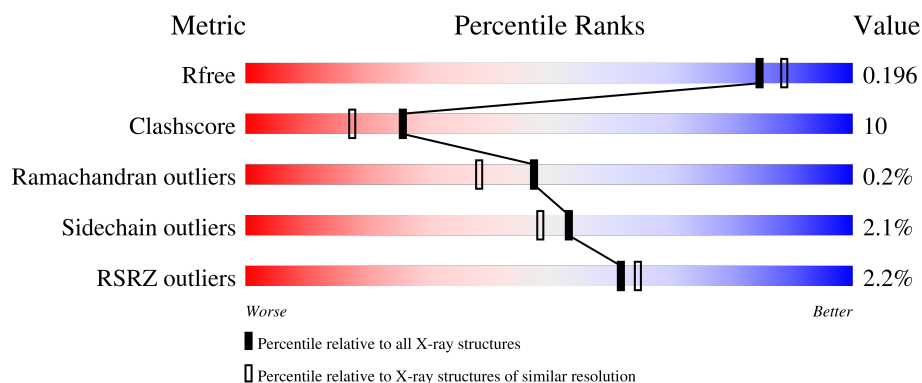
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
R_{free}	130704	6207 (1.90-1.90)
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 $\leq 5\%$. 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	455	<div> <div>2%</div> <div> <div></div> <div>73%</div> <div>15%</div> <div>•</div> <div>11%</div> </div> </div>
1	B	455	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>14%</div> <div>•</div> <div>11%</div> </div> </div>
1	C	455	<div> <div>2%</div> <div> <div></div> <div>70%</div> <div>18%</div> <div></div> <div>11%</div> </div> </div>
1	D	455	<div> <div>2%</div> <div> <div></div> <div>72%</div> <div>15%</div> <div>•</div> <div>11%</div> </div> </div>
1	E	455	<div> <div>2%</div> <div> <div></div> <div>73%</div> <div>16%</div> <div>•</div> <div>11%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	455	<div><div>%</div><div><div></div><div>73%</div><div>16%</div><div>•</div><div>11%</div></div></div>
1	G	455	<div><div>%</div><div><div></div><div>72%</div><div>16%</div><div>•</div><div>11%</div></div></div>
1	H	455	<div><div>3%</div><div><div></div><div>75%</div><div>14%</div><div></div><div>11%</div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 28853 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 Rhamnonate dehydratase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	Se	0	0	0
			3193	2071	531	579	6	6			
1	B	406	Total	C	N	O	S	Se	0	0	0
			3185	2065	530	578	6	6			
1	C	405	Total	C	N	O	S	Se	0	0	0
			3179	2062	529	576	6	6			
1	D	405	Total	C	N	O	S	Se	0	0	0
			3179	2062	529	576	6	6			
1	E	407	Total	C	N	O	S	Se	0	0	0
			3193	2071	531	579	6	6			
1	F	406	Total	C	N	O	S	Se	0	0	0
			3184	2066	530	576	6	6			
1	G	406	Total	C	N	O	S	Se	0	0	0
			3184	2066	530	576	6	6			
1	H	405	Total	C	N	O	S	Se	0	0	0
			3179	2062	529	576	6	6			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q4HYS5
A	1	LEU	-	expression tag	UNP Q4HYS5
A	448	GLU	-	expression tag	UNP Q4HYS5
A	449	GLY	-	expression tag	UNP Q4HYS5
A	450	HIS	-	expression tag	UNP Q4HYS5
A	451	HIS	-	expression tag	UNP Q4HYS5
A	452	HIS	-	expression tag	UNP Q4HYS5
A	453	HIS	-	expression tag	UNP Q4HYS5
A	454	HIS	-	expression tag	UNP Q4HYS5
B	0	SER	-	expression tag	UNP Q4HYS5
B	1	LEU	-	expression tag	UNP Q4HYS5
B	448	GLU	-	expression tag	UNP Q4HYS5
B	449	GLY	-	expression tag	UNP Q4HYS5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	450	HIS	-	expression tag	UNP Q4HYS5
B	451	HIS	-	expression tag	UNP Q4HYS5
B	452	HIS	-	expression tag	UNP Q4HYS5
B	453	HIS	-	expression tag	UNP Q4HYS5
B	454	HIS	-	expression tag	UNP Q4HYS5
C	0	SER	-	expression tag	UNP Q4HYS5
C	1	LEU	-	expression tag	UNP Q4HYS5
C	448	GLU	-	expression tag	UNP Q4HYS5
C	449	GLY	-	expression tag	UNP Q4HYS5
C	450	HIS	-	expression tag	UNP Q4HYS5
C	451	HIS	-	expression tag	UNP Q4HYS5
C	452	HIS	-	expression tag	UNP Q4HYS5
C	453	HIS	-	expression tag	UNP Q4HYS5
C	454	HIS	-	expression tag	UNP Q4HYS5
D	0	SER	-	expression tag	UNP Q4HYS5
D	1	LEU	-	expression tag	UNP Q4HYS5
D	448	GLU	-	expression tag	UNP Q4HYS5
D	449	GLY	-	expression tag	UNP Q4HYS5
D	450	HIS	-	expression tag	UNP Q4HYS5
D	451	HIS	-	expression tag	UNP Q4HYS5
D	452	HIS	-	expression tag	UNP Q4HYS5
D	453	HIS	-	expression tag	UNP Q4HYS5
D	454	HIS	-	expression tag	UNP Q4HYS5
E	0	SER	-	expression tag	UNP Q4HYS5
E	1	LEU	-	expression tag	UNP Q4HYS5
E	448	GLU	-	expression tag	UNP Q4HYS5
E	449	GLY	-	expression tag	UNP Q4HYS5
E	450	HIS	-	expression tag	UNP Q4HYS5
E	451	HIS	-	expression tag	UNP Q4HYS5
E	452	HIS	-	expression tag	UNP Q4HYS5
E	453	HIS	-	expression tag	UNP Q4HYS5
E	454	HIS	-	expression tag	UNP Q4HYS5
F	0	SER	-	expression tag	UNP Q4HYS5
F	1	LEU	-	expression tag	UNP Q4HYS5
F	448	GLU	-	expression tag	UNP Q4HYS5
F	449	GLY	-	expression tag	UNP Q4HYS5
F	450	HIS	-	expression tag	UNP Q4HYS5
F	451	HIS	-	expression tag	UNP Q4HYS5
F	452	HIS	-	expression tag	UNP Q4HYS5
F	453	HIS	-	expression tag	UNP Q4HYS5
F	454	HIS	-	expression tag	UNP Q4HYS5
G	0	SER	-	expression tag	UNP Q4HYS5

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1	LEU	-	expression tag	UNP Q4HYS5
G	448	GLU	-	expression tag	UNP Q4HYS5
G	449	GLY	-	expression tag	UNP Q4HYS5
G	450	HIS	-	expression tag	UNP Q4HYS5
G	451	HIS	-	expression tag	UNP Q4HYS5
G	452	HIS	-	expression tag	UNP Q4HYS5
G	453	HIS	-	expression tag	UNP Q4HYS5
G	454	HIS	-	expression tag	UNP Q4HYS5
H	0	SER	-	expression tag	UNP Q4HYS5
H	1	LEU	-	expression tag	UNP Q4HYS5
H	448	GLU	-	expression tag	UNP Q4HYS5
H	449	GLY	-	expression tag	UNP Q4HYS5
H	450	HIS	-	expression tag	UNP Q4HYS5
H	451	HIS	-	expression tag	UNP Q4HYS5
H	452	HIS	-	expression tag	UNP Q4HYS5
H	453	HIS	-	expression tag	UNP Q4HYS5
H	454	HIS	-	expression tag	UNP Q4HYS5

- 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
2	F	1	Total Mg 1 1	0	0

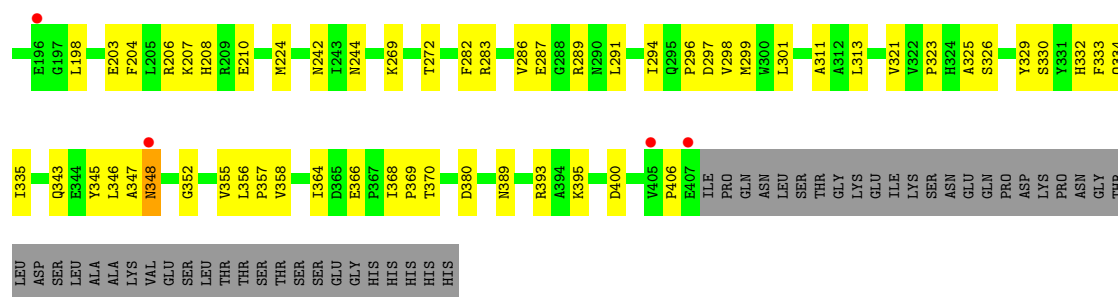
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	387	Total O 387 387	0	0

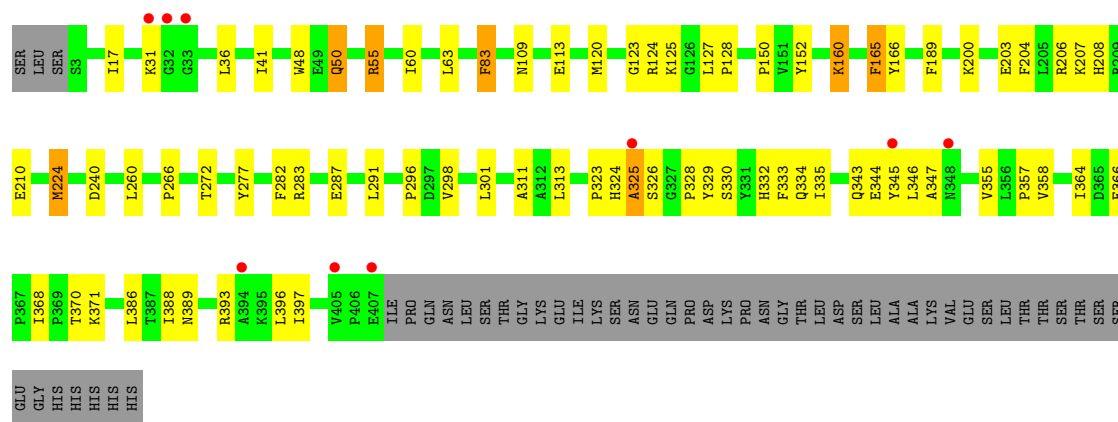
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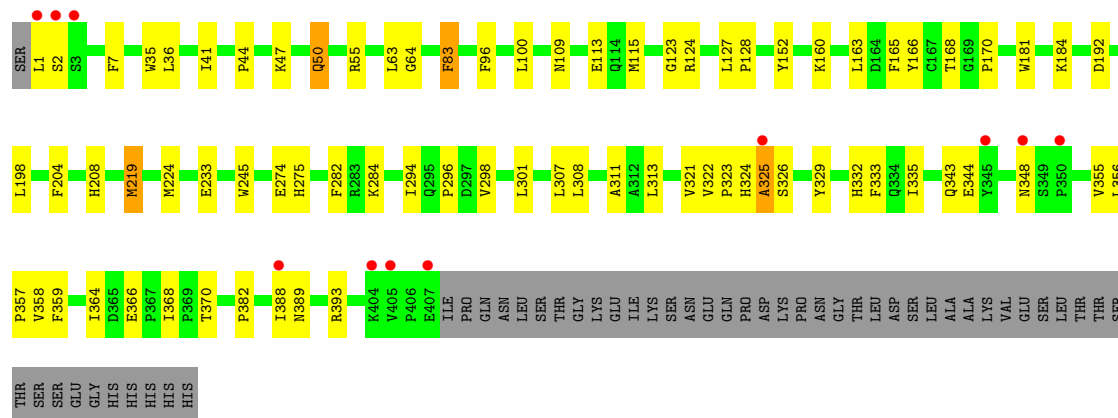
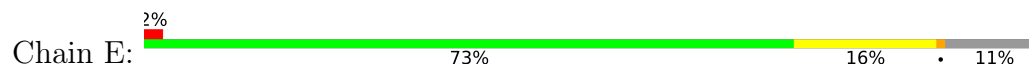
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	416	Total 416	O 416	0	0
3	C	451	Total 451	O 451	0	0
3	D	410	Total 410	O 410	0	0
3	E	412	Total 412	O 412	0	0
3	F	416	Total 416	O 416	0	0
3	G	444	Total 444	O 444	0	0
3	H	433	Total 433	O 433	0	0



• Molecule 1: Rhamnonate dehydratase

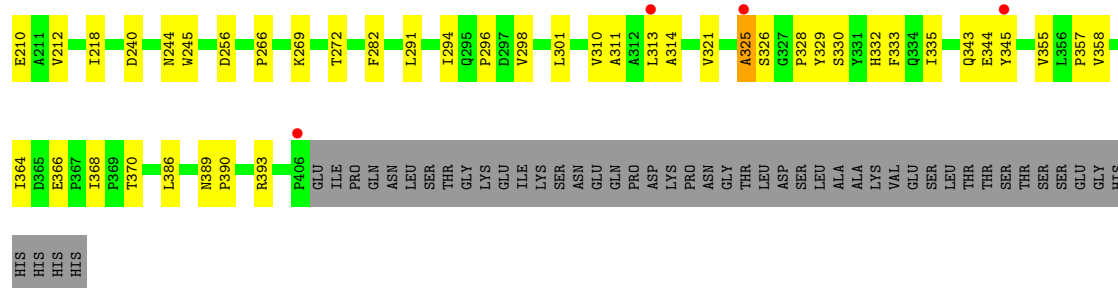


• Molecule 1: Rhamnonate dehydratase

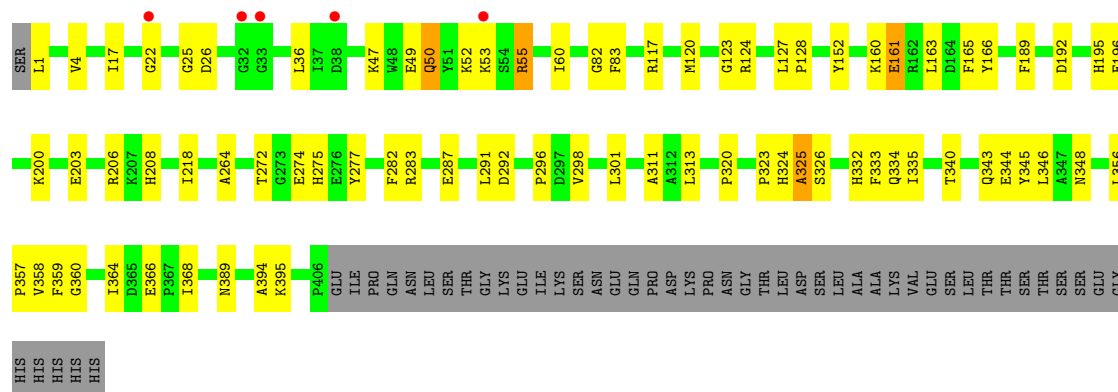


• Molecule 1: Rhamnonate dehydratase

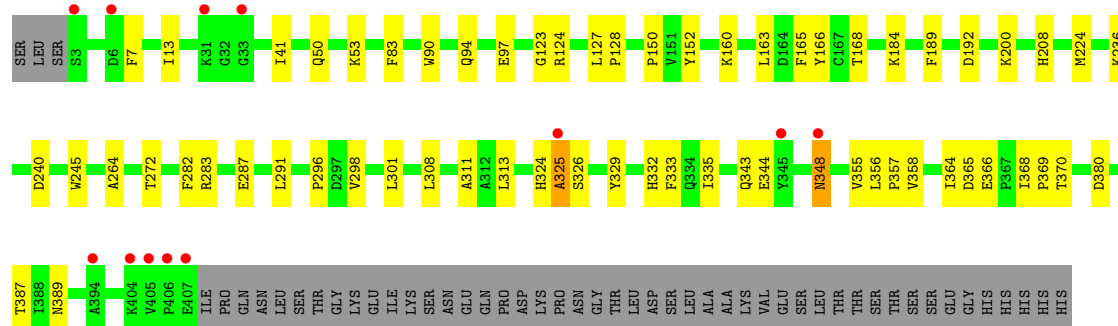
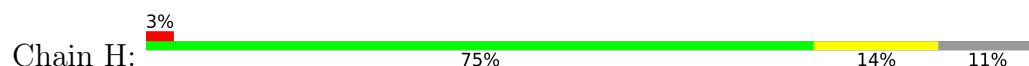




• Molecule 1: Rhamnonate dehydratase



• Molecule 1: Rhamnonate dehydratase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	200.90Å 201.09Å 82.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.94 – 1.90 39.43 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.2 (24.94-1.90) 99.4 (39.43-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.45 (at 1.91Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.163 , 0.196 0.163 , 0.196	Depositor DCC
R_{free} test set	12999 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	16.5	Xtriage
Anisotropy	0.434	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 60.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.011 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	28853	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.64% 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

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	0.31	0/3283	0.58	0/4457
1	B	0.32	0/3275	0.59	0/4446
1	C	0.32	0/3269	0.59	0/4438
1	D	0.32	0/3269	0.59	0/4438
1	E	0.31	0/3283	0.59	0/4457
1	F	0.31	0/3274	0.59	0/4445
1	G	0.31	0/3274	0.59	0/4445
1	H	0.31	0/3269	0.59	0/4438
All	All	0.31	0/26196	0.59	0/35564

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3193	0	3147	62	0
1	B	3185	0	3133	71	0
1	C	3179	0	3128	77	0
1	D	3179	0	3128	80	0
1	E	3193	0	3147	74	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3184	0	3141	66	0
1	G	3184	0	3141	61	0
1	H	3179	0	3128	59	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	387	0	0	11	0
3	B	416	0	0	12	0
3	C	451	0	0	15	0
3	D	410	0	0	17	0
3	E	412	0	0	16	0
3	F	416	0	0	11	0
3	G	444	0	0	12	0
3	H	433	0	0	12	0
All	All	28853	0	25093	530	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 10.

The worst 5 of 530 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:96:PHE:HB3	1:E:115:MSE:HE2	1.35	1.08
1:D:323:PRO:HG2	3:D:3242:HOH:O	1.68	0.94
1:E:50:GLN:NE2	1:E:50:GLN:H	1.68	0.92
1:B:50:GLN:NE2	1:B:50:GLN:H	1.68	0.92
1:D:313:LEU:HD13	1:G:313:LEU:HG	1.52	0.92

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	405/455 (89%)	393 (97%)	12 (3%)	0	100	100
1	B	404/455 (89%)	391 (97%)	13 (3%)	0	100	100
1	C	403/455 (89%)	391 (97%)	12 (3%)	0	100	100
1	D	403/455 (89%)	393 (98%)	9 (2%)	1 (0%)	47	38
1	E	405/455 (89%)	393 (97%)	11 (3%)	1 (0%)	47	38
1	F	404/455 (89%)	393 (97%)	10 (2%)	1 (0%)	47	38
1	G	404/455 (89%)	392 (97%)	11 (3%)	1 (0%)	47	38
1	H	403/455 (89%)	391 (97%)	11 (3%)	1 (0%)	47	38
All	All	3231/3640 (89%)	3137 (97%)	89 (3%)	5 (0%)	47	38

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	325	ALA
1	E	325	ALA
1	F	325	ALA
1	G	325	ALA
1	H	325	ALA

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	340/377 (90%)	331 (97%)	9 (3%)	46	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	339/377 (90%)	332 (98%)	7 (2%)	53	48
1	C	338/377 (90%)	332 (98%)	6 (2%)	59	55
1	D	338/377 (90%)	331 (98%)	7 (2%)	53	48
1	E	340/377 (90%)	333 (98%)	7 (2%)	53	48
1	F	339/377 (90%)	334 (98%)	5 (2%)	65	62
1	G	339/377 (90%)	332 (98%)	7 (2%)	53	48
1	H	338/377 (90%)	330 (98%)	8 (2%)	49	43
All	All	2711/3016 (90%)	2655 (98%)	56 (2%)	53	48

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	160	LYS
1	E	83	PHE
1	H	192	ASP
1	D	165	PHE
1	D	301	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	195	HIS
1	E	148	ASN
1	H	244	ASN
1	D	208	HIS
1	D	337	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](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	401/455 (88%)	-0.08	11 (2%) 54 57	9, 16, 31, 49	0
1	B	400/455 (87%)	-0.22	10 (2%) 57 60	9, 15, 28, 51	0
1	C	399/455 (87%)	-0.19	7 (1%) 68 71	9, 15, 27, 53	0
1	D	399/455 (87%)	-0.13	9 (2%) 60 63	8, 15, 28, 47	0
1	E	401/455 (88%)	-0.07	11 (2%) 54 57	9, 16, 30, 55	0
1	F	400/455 (87%)	-0.27	4 (1%) 82 84	8, 15, 27, 42	0
1	G	400/455 (87%)	-0.24	5 (1%) 77 79	8, 14, 29, 42	0
1	H	399/455 (87%)	-0.14	12 (3%) 50 53	9, 15, 27, 48	0
All	All	3199/3640 (87%)	-0.17	69 (2%) 62 64	8, 15, 29, 55	0

The worst 5 of 69 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	1	LEU	10.1
1	E	407	GLU	5.2
1	C	407	GLU	4.7
1	H	407	GLU	4.5
1	H	345	TYR	4.0

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
2	MG	G	501	1/1	0.94	0.11	16,16,16,16	0
2	MG	H	501	1/1	0.97	0.07	20,20,20,20	0
2	MG	D	501	1/1	0.97	0.07	20,20,20,20	0
2	MG	F	501	1/1	0.98	0.15	18,18,18,18	0
2	MG	E	501	1/1	0.98	0.05	20,20,20,20	0
2	MG	A	501	1/1	0.98	0.07	20,20,20,20	0
2	MG	B	501	1/1	0.99	0.07	18,18,18,18	0
2	MG	C	501	1/1	0.99	0.15	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.