



Full wwPDB X-ray Structure Validation Report

Jun 17, 2014 – 10:13 PM EDT

PDB ID : 4MM1
Title : GGGPS from Methanothermobacter thermautotrophicus
Authors : Rajendran, C.; Peterhoff, D.; Beer, B.; Kumpula, E.P.; Kapetaniou, E.; Guldan, H.; Wierenga, R.K.; Sterner, R.; Babinger, P.
Deposited on : 2013-09-07
Resolution : 2.80 Å(reported)

This is a full wwPDB validation 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>

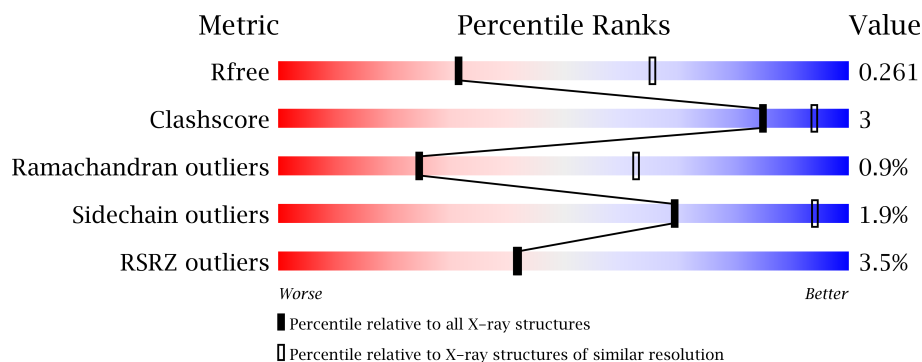
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	FAILED
Xtriage (Phenix)	:	dev-1439
EDS	:	stable23161
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)	:	stable23161

1 Overall quality at a glance

The reported resolution of this entry is 2.80 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	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)

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	250	
1	B	250	
1	C	250	
1	D	250	
1	E	250	
1	F	250	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 19944 atoms, of which 9883 are hydrogens 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.

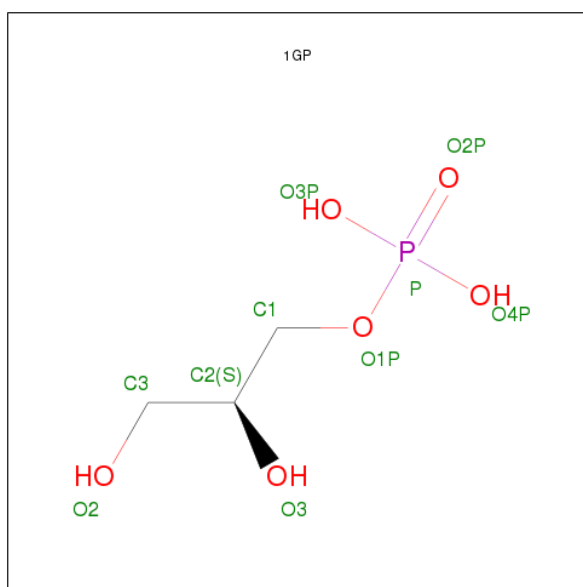
- Molecule 1 is a protein called Geranylgeranylglycerolphosphate synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	238	Total	C	H	N	O	S	0	0	0
			3482	1114	1722	298	338	10			
1	B	215	Total	C	H	N	O	S	0	0	0
			3187	1013	1588	266	312	8			
1	C	234	Total	C	H	N	O	S	0	0	0
			3386	1086	1673	292	324	11			
1	D	220	Total	C	H	N	O	S	0	0	0
			3216	1032	1592	278	305	9			
1	E	225	Total	C	H	N	O	S	0	0	0
			3330	1057	1663	282	318	10			
1	F	207	Total	C	H	N	O	S	0	0	0
			3029	967	1519	259	275	9			

There are 12 discrepancies between the modelled and reference sequences:

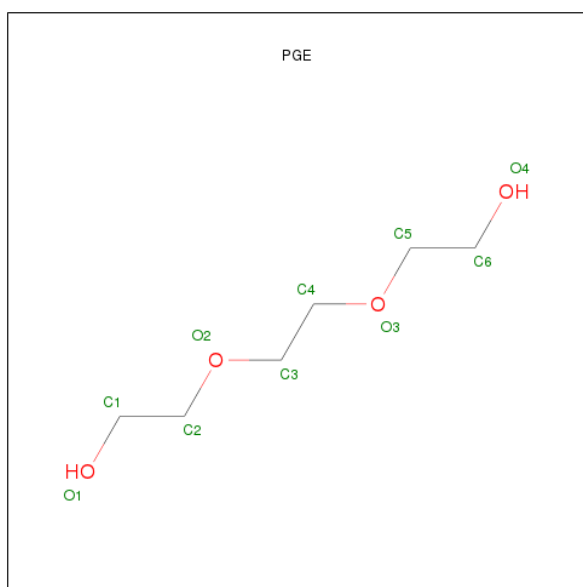
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	PHE	-	EXPRESSION TAG	UNP O26652
A	3	LYS	-	EXPRESSION TAG	UNP O26652
C	1	MET	-	EXPRESSION TAG	UNP O26652
C	2	PHE	-	EXPRESSION TAG	UNP O26652
C	3	LYS	-	EXPRESSION TAG	UNP O26652
D	2	PHE	-	EXPRESSION TAG	UNP O26652
D	3	LYS	-	EXPRESSION TAG	UNP O26652
E	1	MET	-	EXPRESSION TAG	UNP O26652
E	2	PHE	-	EXPRESSION TAG	UNP O26652
E	3	LYS	-	EXPRESSION TAG	UNP O26652
F	2	PHE	-	EXPRESSION TAG	UNP O26652
F	3	LYS	-	EXPRESSION TAG	UNP O26652

- Molecule 2 is SN-GLYCEROL-1-PHOSPHATE (three-letter code: 1GP) (formula: C₃H₉O₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	O	P	0	0
			17	3	7	6	1		
2	B	1	Total	C	H	O	P	0	0
			17	3	7	6	1		
2	C	1	Total	C	H	O	P	0	0
			17	3	7	6	1		
2	D	1	Total	C	H	O	P	0	0
			17	3	7	6	1		
2	E	1	Total	C	H	O	P	0	0
			17	3	7	6	1		
2	F	1	Total	C	H	O	P	0	0
			17	3	7	6	1		

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			24	6	14	4		
3	B	1	Total	C	H	O	0	0
			24	6	14	4		
3	C	1	Total	C	H	O	0	0
			24	6	14	4		
3	D	1	Total	C	H	O	0	0
			24	6	14	4		
3	E	1	Total	C	H	O	0	0
			24	6	14	4		
3	F	1	Total	C	H	O	0	0
			24	6	14	4		

- Molecule 4 is water.

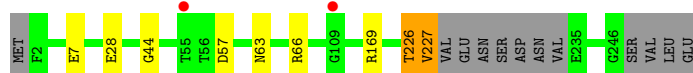
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	19	Total	O	0	0
			19	19		
4	B	10	Total	O	0	0
			10	10		
4	C	15	Total	O	0	0
			15	15		
4	D	9	Total	O	0	0
			9	9		
4	E	11	Total	O	0	0
			11	11		
4	F	4	Total	O	0	0
			4	4		

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.

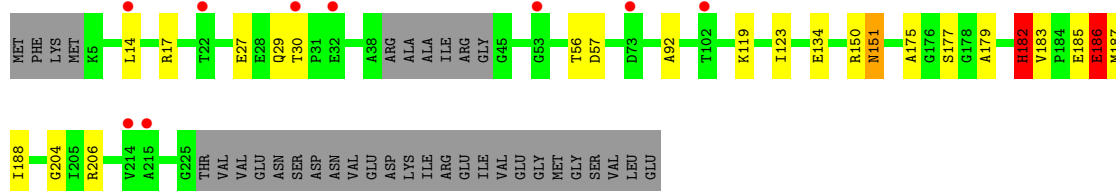
- Molecule 1: Geranylgeranylglycerolphosphate synthase

Chain A: 



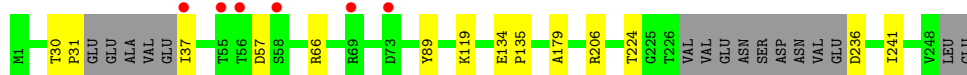
- Molecule 1: Geranylgeranylglycerolphosphate synthase

Chain B: 



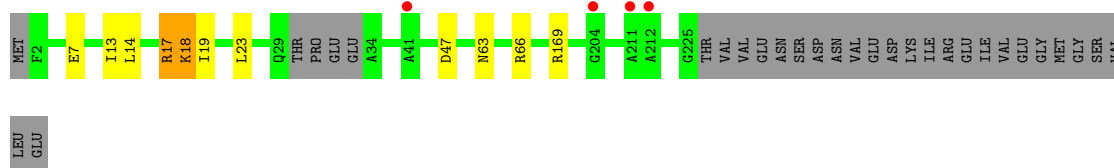
- Molecule 1: Geranylgeranylglycerolphosphate synthase

Chain C: 



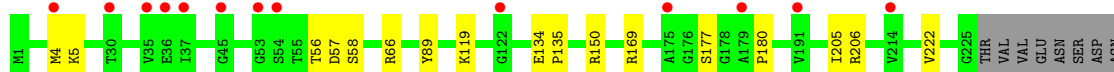
- Molecule 1: Geranylgeranylglycerolphosphate synthase

Chain D: 



- Molecule 1: Geranylgeranylglycerolphosphate synthase

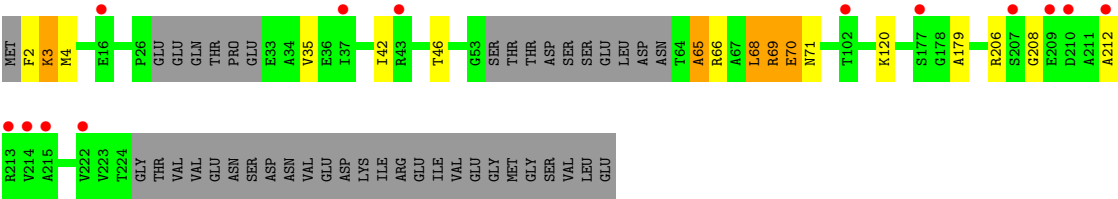
Chain E: 



VAL
GLU
ASP
LYS
ILE
ARG
GLU
ILE
VAL
GLU
GLY
MET
GLY
SER
VAL
LEU
GLU

● Molecule 1: Geranylgeranylglycerolphosphate synthase

Chain F:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.68Å 148.76Å 91.50Å 90.00° 109.50° 90.00°	Depositor
Resolution (Å)	46.56 – 2.80 48.86 – 2.80	Depositor EDS
% Data completeness (in resolution range)	95.0 (46.56-2.80) 95.1 (48.86-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 2.81Å)	Xtriage
Refinement program	Phenix (phenix.refine: dev_1417)	Depositor
R, R_{free}	0.200 , 0.271 0.220 , 0.261	Depositor DCC
R_{free} test set	2118 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	42.2	Xtriage
Anisotropy	0.363	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 17.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 42401 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	19944	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% of the height of the origin peak. No significant pseudotranslation is detected.*

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: PGE, 1GP

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	0.24	0/1790	0.52	1/2430 (0.0%)
1	B	0.24	0/1628	0.54	1/2213 (0.0%)
1	C	0.26	0/1742	0.51	0/2364
1	D	0.24	0/1653	0.48	0/2243
1	E	0.25	0/1698	0.47	0/2307
1	F	0.24	0/1538	0.51	0/2088
All	All	0.25	0/10049	0.50	2/13645 (0.0%)

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	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	GLY	N-CA-C	-6.45	96.97	113.10
1	B	186	GLU	N-CA-C	-5.20	96.96	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	182	HIS	Peptide

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	1760	1722	25	5	0
1	B	1599	1588	0	11	0
1	C	1713	1673	25	4	0
1	D	1624	1592	35	12	0
1	E	1667	1663	0	12	0
1	F	1510	1519	0	12	0
2	A	10	7	0	0	0
2	B	10	7	0	0	0
2	C	10	7	0	0	0
2	D	10	7	0	0	0
2	E	10	7	0	1	0
2	F	10	7	0	0	0
3	A	10	14	0	0	0
3	B	10	14	0	0	0
3	C	10	14	0	0	0
3	D	10	14	0	0	0
3	E	10	14	0	0	0
3	F	10	14	0	0	0
4	A	19	0	0	0	0
4	B	10	0	0	0	0
4	C	15	0	0	0	0
4	D	9	0	0	0	0
4	E	11	0	0	2	0
4	F	4	0	0	0	0
All	All	10061	9883	85	56	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 3.

All (56) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:13:ILE:HG23	1:D:17:ARG:HE	1.08	1.09
1:D:14:LEU:HG	1:D:19:ILE:HD11	1.34	1.04
1:D:13:ILE:HG23	1:D:17:ARG:NE	1.81	0.96

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:186:GLU:O	1:B:188:ILE:N	2.05	0.90
1:D:14:LEU:HG	1:D:19:ILE:CD1	2.08	0.81
1:D:13:ILE:CG2	1:D:17:ARG:HE	1.95	0.76
1:D:13:ILE:CG2	1:D:17:ARG:NE	2.49	0.75
1:E:66:ARG:NH1	1:E:89:TYR:OH	2.23	0.71
1:B:150:ARG:NH1	1:B:182:HIS:O	2.28	0.67
1:A:226:THR:O	1:A:227:VAL:HG13	1.98	0.64
1:B:151:ASN:OD1	1:B:151:ASN:N	2.33	0.61
1:A:7:GLU:OE1	1:A:169:ARG:NH1	2.34	0.61
1:C:179:ALA:O	1:C:206:ARG:NH2	2.34	0.60
1:E:169:ARG:NH2	4:E:404:HOH:O	2.36	0.57
1:A:63:ASN:OD1	1:A:66:ARG:NH2	2.38	0.56
1:E:206:ARG:NH1	4:E:402:HOH:O	2.41	0.54
1:F:69:ARG:HA	1:F:71:ASN:N	2.22	0.53
1:D:14:LEU:CG	1:D:19:ILE:CD1	2.84	0.53
1:C:30:THR:O	1:C:31:PRO:C	2.46	0.53
1:B:179:ALA:O	1:B:206:ARG:NH2	2.42	0.52
1:E:4:MET:HG2	1:E:5:LYS:H	1.76	0.51
1:F:65:ALA:CA	1:F:66:ARG:HB3	2.42	0.50
1:F:65:ALA:HA	1:F:66:ARG:HB3	1.92	0.50
1:D:17:ARG:NH2	1:D:47:ASP:OD1	2.41	0.49
1:D:63:ASN:OD1	1:D:66:ARG:NH2	2.46	0.49
1:B:27:GLU:HB2	1:B:56:THR:HG21	1.93	0.48
1:E:180:PRO:O	1:E:206:ARG:NH2	2.41	0.48
1:B:134:GLU:HB3	1:B:150:ARG:HG3	1.96	0.48
1:F:69:ARG:HA	1:F:71:ASN:H	1.78	0.47
1:F:42:ILE:HA	1:F:46:THR:HG22	1.97	0.47
1:A:226:THR:O	1:A:227:VAL:HG22	2.15	0.47
1:B:56:THR:HG22	1:B:57:ASP:N	2.30	0.47
1:E:56:THR:HG22	1:E:57:ASP:N	2.30	0.47
1:B:14:LEU:HA	1:B:17:ARG:O	2.15	0.46
1:B:185:GLU:O	1:B:186:GLU:CB	2.63	0.46
1:E:134:GLU:HG2	1:E:135:PRO:HA	1.98	0.46
1:F:179:ALA:O	1:F:206:ARG:NH2	2.44	0.46
1:D:7:GLU:OE1	1:D:169:ARG:NH1	2.49	0.45
1:E:4:MET:HG2	1:E:5:LYS:N	2.32	0.45
1:D:14:LEU:HD21	1:D:19:ILE:HD12	1.99	0.45
1:B:175:ALA:HB2	1:B:183:VAL:HG21	2.00	0.43
1:F:68:LEU:O	1:F:69:ARG:HB2	2.18	0.43
1:E:4:MET:CG	1:E:5:LYS:H	2.31	0.43
1:E:134:GLU:HB3	1:E:150:ARG:HG3	1.99	0.43
1:E:205:ILE:HD13	1:E:222:VAL:HG13	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:66:ARG:NH1	1:C:89:TYR:OH	2.52	0.42
1:B:92:ALA:CA	1:B:123:ILE:HD11	2.49	0.42
1:F:35:VAL:CG2	1:F:68:LEU:HB1	2.49	0.42
1:A:226:THR:C	1:A:227:VAL:HG22	2.39	0.42
1:D:18:LYS:HA	1:D:18:LYS:HD3	1.76	0.42
1:F:3:LYS:HA	1:F:4:MET:HA	1.84	0.42
1:E:177:SER:HA	2:E:301:1GP:H11	2.02	0.41
1:C:224:THR:HG21	1:C:241:ILE:HD13	2.03	0.41
1:F:208:GLY:O	1:F:212:ALA:N	2.52	0.41
1:F:69:ARG:N	1:F:70:GLU:CB	2.84	0.40
1:F:65:ALA:N	1:F:66:ARG:HB3	2.36	0.40

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	234/250 (94%)	226 (97%)	7 (3%)	1 (0%)	43	80
1	B	211/250 (84%)	201 (95%)	6 (3%)	4 (2%)	12	37
1	C	228/250 (91%)	217 (95%)	9 (4%)	2 (1%)	25	63
1	D	216/250 (86%)	209 (97%)	6 (3%)	1 (0%)	38	76
1	E	223/250 (89%)	216 (97%)	7 (3%)	0	100	100
1	F	201/250 (80%)	193 (96%)	4 (2%)	4 (2%)	11	35
All	All	1313/1500 (88%)	1262 (96%)	39 (3%)	12 (1%)	25	63

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	182	HIS
1	B	186	GLU
1	B	187	MET
1	C	135	PRO

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Mol	Chain	Res	Type
1	F	65	ALA
1	F	69	ARG
1	D	18	LYS
1	F	68	LEU
1	A	226	THR
1	B	204	GLY
1	F	70	GLU
1	C	134	GLU

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	178/196 (91%)	175 (98%)	3 (2%)	73	95
1	B	165/196 (84%)	160 (97%)	5 (3%)	53	87
1	C	171/196 (87%)	167 (98%)	4 (2%)	63	92
1	D	162/196 (83%)	160 (99%)	2 (1%)	82	97
1	E	169/196 (86%)	167 (99%)	2 (1%)	82	97
1	F	146/196 (74%)	143 (98%)	3 (2%)	66	93
All	All	991/1176 (84%)	972 (98%)	19 (2%)	69	94

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	GLU
1	A	57	ASP
1	A	227	VAL
1	B	29	GLN
1	B	30	THR
1	B	119	LYS
1	B	151	ASN
1	B	177	SER
1	C	37	ILE
1	C	57	ASP
1	C	119	LYS

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Mol	Chain	Res	Type
1	C	236	ASP
1	D	17	ARG
1	D	23	LEU
1	E	58	SER
1	E	119	LYS
1	F	2	PHE
1	F	3	LYS
1	F	120	LYS

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 ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

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	238/250 (95%)	0.06	2 (0%) 83 83	16, 29, 56, 130	0
1	B	215/250 (86%)	0.39	9 (4%) 35 35	20, 47, 90, 120	0
1	C	234/250 (93%)	0.11	6 (2%) 53 54	17, 30, 73, 128	0
1	D	220/250 (88%)	0.15	4 (1%) 65 66	17, 32, 63, 96	0
1	E	225/250 (90%)	0.51	13 (5%) 22 22	18, 43, 81, 138	0
1	F	207/250 (82%)	0.26	13 (6%) 19 18	22, 44, 79, 128	0
All	All	1339/1500 (89%)	0.24	47 (3%) 42 42	16, 36, 79, 138	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	54	SER	4.0
1	B	53	GLY	3.7
1	E	45	GLY	3.6
1	E	53	GLY	3.6
1	A	55	THR	3.5
1	F	207	SER	3.3
1	E	37	ILE	3.3
1	C	55	THR	3.3
1	F	43	ARG	3.2
1	D	211	ALA	2.9
1	E	179	ALA	2.9
1	B	32	GLU	2.8
1	C	37	ILE	2.6
1	C	73	ASP	2.6
1	F	210	ASP	2.6
1	F	177	SER	2.6
1	F	213	ARG	2.5
1	B	73	ASP	2.5
1	F	37	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	F	222	VAL	2.4
1	E	4	MET	2.4
1	B	14	LEU	2.4
1	A	109	GLY	2.4
1	E	191	VAL	2.3
1	B	22	THR	2.3
1	F	214	VAL	2.3
1	E	36	GLU	2.3
1	E	175	ALA	2.3
1	C	58	SER	2.3
1	D	41	ALA	2.3
1	F	215	ALA	2.3
1	E	214	VAL	2.2
1	F	16	GLU	2.2
1	F	209	GLU	2.2
1	C	56	THR	2.2
1	C	69	ARG	2.2
1	B	102	THR	2.2
1	B	214	VAL	2.1
1	E	30	THR	2.1
1	B	30	THR	2.1
1	B	215	ALA	2.1
1	F	102	THR	2.0
1	D	204	GLY	2.0
1	E	35	VAL	2.0
1	F	212	ALA	2.0
1	D	212	ALA	2.0
1	E	122	GLY	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
3	PGE	C	302	10/10	0.24	1.69	42,57,70,77	0
3	PGE	D	302	10/10	0.21	0.58	29,43,64,81	0
2	1GP	F	301	10/10	0.21	0.02	31,53,66,74	0
3	PGE	F	302	10/10	0.18	-0.02	42,53,63,67	0
3	PGE	A	302	10/10	0.18	-0.41	35,47,58,58	0
3	PGE	B	302	10/10	0.17	-0.51	36,45,52,56	0
3	PGE	E	302	10/10	0.17	-0.70	30,48,60,63	0
2	1GP	E	301	10/10	0.18	-0.91	29,40,55,62	0
2	1GP	C	301	10/10	0.13	-0.97	16,28,34,40	0
2	1GP	B	301	10/10	0.13	-1.10	41,49,61,71	0
2	1GP	A	301	10/10	0.13	-1.25	11,18,30,36	0
2	1GP	D	301	10/10	0.12	-1.45	23,33,43,46	0

6.5 Other polymers ⓘ

There are no such residues in this entry.