



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 15, 2016 – 05:15 PM EST

PDB ID : 5TW7
Title : Crystal structure of a GMP synthase (glutamine-hydrolyzing) from *Neisseria gonorrhoeae*
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2016-11-11
Resolution : 2.35 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

<http://wwpdb.org/validation/2016/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 : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028320
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028320

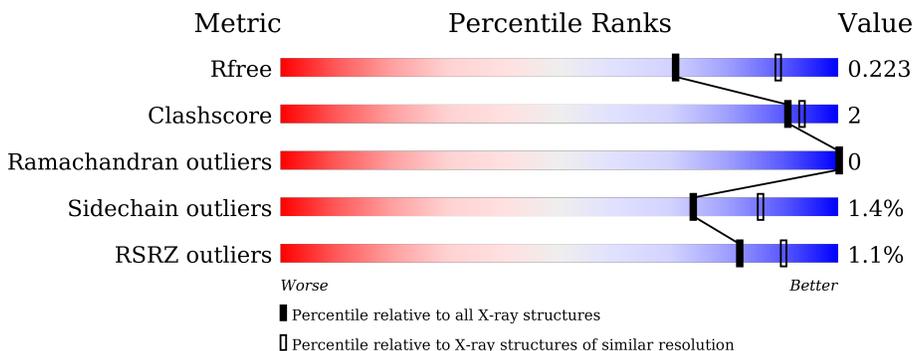
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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}	91344	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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. 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	529	<div style="display: flex; align-items: center;"> <div style="width: 10px; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 89%, grey 89%); position: relative;"> % 89% 7% </div> </div>
1	B	529	<div style="display: flex; align-items: center;"> <div style="width: 10px; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 1%, orange 1%, yellow 5%, green 87%, grey 87%); position: relative;"> % 87% 5% 7% </div> </div>
1	C	529	<div style="display: flex; align-items: center;"> <div style="width: 100%; height: 15px; background: linear-gradient(to right, green 86%, yellow 7%, grey 7%); position: relative;"> 86% 7% 7% </div> </div>
1	D	529	<div style="display: flex; align-items: center;"> <div style="width: 10px; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 1%, orange 1%, yellow 5%, green 88%, grey 88%); position: relative;"> % 88% 5% 7% </div> </div>
1	E	529	<div style="display: flex; align-items: center;"> <div style="width: 10px; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 2%, orange 2%, yellow 7%, green 85%, grey 85%); position: relative;"> 2% 85% 7% 8% </div> </div>
1	F	529	<div style="display: flex; align-items: center;"> <div style="width: 10px; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 1%, orange 1%, yellow 6%, green 86%, grey 86%); position: relative;"> % 86% 6% 7% </div> </div>

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 23028 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 GMP synthase [glutamine-hydrolyzing].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	490	3791	2423	647	704	17	0	3	0
1	B	490	3807	2431	647	712	17	0	5	0
1	C	492	3804	2427	646	713	18	0	1	0
1	D	491	3759	2399	640	703	17	0	1	0
1	E	489	3757	2398	636	706	17	0	0	0
1	F	490	3772	2409	639	706	18	0	2	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP B4RJH7
A	-6	ALA	-	expression tag	UNP B4RJH7
A	-5	HIS	-	expression tag	UNP B4RJH7
A	-4	HIS	-	expression tag	UNP B4RJH7
A	-3	HIS	-	expression tag	UNP B4RJH7
A	-2	HIS	-	expression tag	UNP B4RJH7
A	-1	HIS	-	expression tag	UNP B4RJH7
A	0	HIS	-	expression tag	UNP B4RJH7
B	-7	MET	-	expression tag	UNP B4RJH7
B	-6	ALA	-	expression tag	UNP B4RJH7
B	-5	HIS	-	expression tag	UNP B4RJH7
B	-4	HIS	-	expression tag	UNP B4RJH7
B	-3	HIS	-	expression tag	UNP B4RJH7
B	-2	HIS	-	expression tag	UNP B4RJH7
B	-1	HIS	-	expression tag	UNP B4RJH7
B	0	HIS	-	expression tag	UNP B4RJH7
C	-7	MET	-	expression tag	UNP B4RJH7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	ALA	-	expression tag	UNP B4RJH7
C	-5	HIS	-	expression tag	UNP B4RJH7
C	-4	HIS	-	expression tag	UNP B4RJH7
C	-3	HIS	-	expression tag	UNP B4RJH7
C	-2	HIS	-	expression tag	UNP B4RJH7
C	-1	HIS	-	expression tag	UNP B4RJH7
C	0	HIS	-	expression tag	UNP B4RJH7
D	-7	MET	-	expression tag	UNP B4RJH7
D	-6	ALA	-	expression tag	UNP B4RJH7
D	-5	HIS	-	expression tag	UNP B4RJH7
D	-4	HIS	-	expression tag	UNP B4RJH7
D	-3	HIS	-	expression tag	UNP B4RJH7
D	-2	HIS	-	expression tag	UNP B4RJH7
D	-1	HIS	-	expression tag	UNP B4RJH7
D	0	HIS	-	expression tag	UNP B4RJH7
E	-7	MET	-	expression tag	UNP B4RJH7
E	-6	ALA	-	expression tag	UNP B4RJH7
E	-5	HIS	-	expression tag	UNP B4RJH7
E	-4	HIS	-	expression tag	UNP B4RJH7
E	-3	HIS	-	expression tag	UNP B4RJH7
E	-2	HIS	-	expression tag	UNP B4RJH7
E	-1	HIS	-	expression tag	UNP B4RJH7
E	0	HIS	-	expression tag	UNP B4RJH7
F	-7	MET	-	expression tag	UNP B4RJH7
F	-6	ALA	-	expression tag	UNP B4RJH7
F	-5	HIS	-	expression tag	UNP B4RJH7
F	-4	HIS	-	expression tag	UNP B4RJH7
F	-3	HIS	-	expression tag	UNP B4RJH7
F	-2	HIS	-	expression tag	UNP B4RJH7
F	-1	HIS	-	expression tag	UNP B4RJH7
F	0	HIS	-	expression tag	UNP B4RJH7

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

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

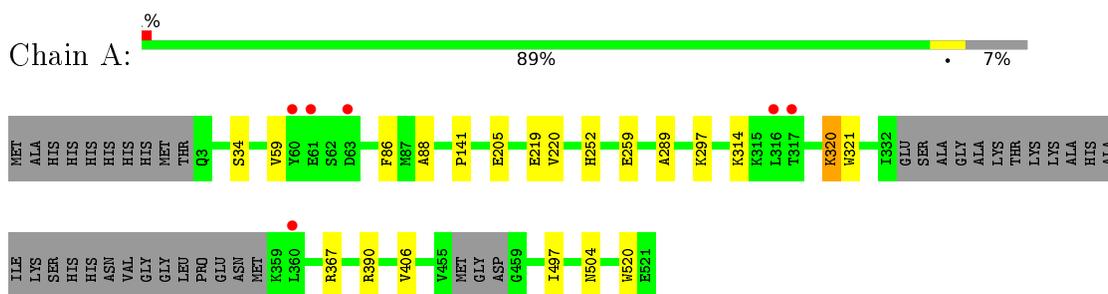
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total O 2 2	0	0
3	D	1	Total O 1 1	0	0
3	E	147	Total O 147 147	0	0
3	F	186	Total O 186 186	0	0

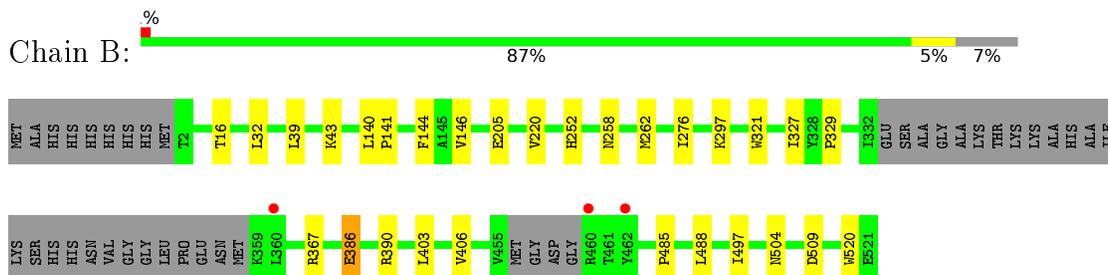
3 Residue-property plots

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.

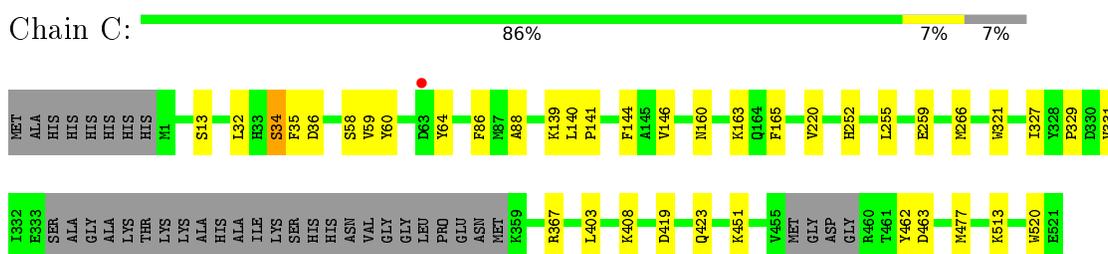
- Molecule 1: GMP synthase [glutamine-hydrolyzing]



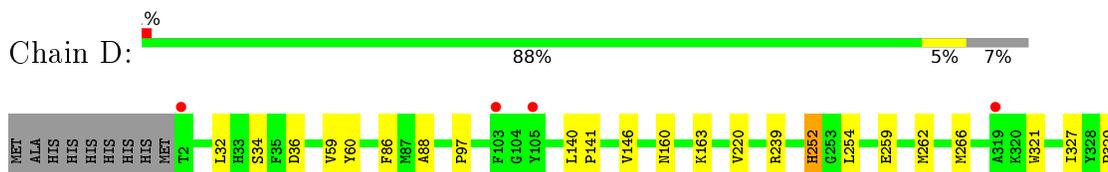
- Molecule 1: GMP synthase [glutamine-hydrolyzing]



- Molecule 1: GMP synthase [glutamine-hydrolyzing]

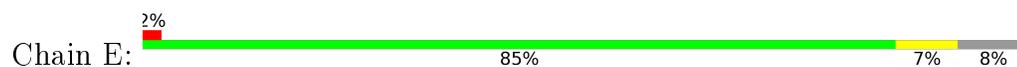


- Molecule 1: GMP synthase [glutamine-hydrolyzing]

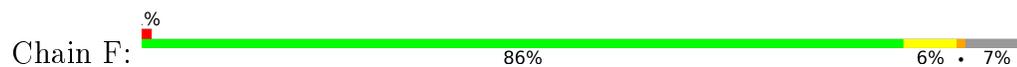




- Molecule 1: GMP synthase [glutamine-hydrolyzing]



- Molecule 1: GMP synthase [glutamine-hydrolyzing]



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	108.39Å 109.35Å 109.91Å 115.33° 100.00° 108.06°	Depositor
Resolution (Å)	46.12 – 2.35 49.39 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.3 (46.12-2.35) 79.4 (49.39-2.35)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 2.34Å)	Xtrriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.186 , 0.223 0.185 , 0.223	Depositor DCC
R_{free} test set	7932 reflections (4.78%)	DCC
Wilson B-factor (Å ²)	34.4	Xtrriage
Anisotropy	0.298	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	23028	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% 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	0.42	0/3877	0.59	0/5259
1	B	0.47	0/3902	0.61	0/5295
1	C	0.43	0/3887	0.57	0/5273
1	D	0.39	0/3842	0.56	0/5221
1	E	0.37	0/3837	0.56	0/5213
1	F	0.38	0/3858	0.55	0/5239
All	All	0.41	0/23203	0.57	0/31500

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	3791	0	3731	10	0
1	B	3807	0	3735	15	0
1	C	3804	0	3728	20	0
1	D	3759	0	3651	13	0
1	E	3757	0	3656	22	0
1	F	3772	0	3686	21	0
2	E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1	0	0	0	0
3	B	2	0	0	0	0
3	D	1	0	0	0	0
3	E	147	0	0	1	0
3	F	186	0	0	2	0
All	All	23028	0	22187	97	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 2.

All (97) 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:59:VAL:HG21	1:A:86:PHE:HA	1.76	0.66
1:D:59:VAL:HG21	1:D:86:PHE:HA	1.77	0.66
1:E:220:VAL:HG22	1:E:321:TRP:HB2	1.79	0.65
1:D:88:ALA:HA	1:D:141:PRO:HG3	1.80	0.64
1:F:220:VAL:HG22	1:F:321:TRP:HB2	1.84	0.60
1:A:219:GLU:H	1:A:320:LYS:NZ	1.99	0.60
1:E:327:ILE:HG13	1:E:329:PRO:HD2	1.85	0.58
1:E:238:HIS:ND1	3:E:702:HOH:O	2.32	0.58
1:F:59:VAL:HG21	1:F:86:PHE:HA	1.85	0.58
1:A:88:ALA:HA	1:A:141:PRO:HG3	1.86	0.57
1:C:220:VAL:HG22	1:C:321:TRP:HB2	1.86	0.56
1:E:60:TYR:CE2	1:E:95:VAL:HB	2.40	0.56
1:F:283:GLN:O	1:F:287:LYS:HG2	2.05	0.56
1:F:117:ARG:NH1	3:F:706:HOH:O	2.38	0.55
1:E:88:ALA:HA	1:E:141:PRO:HG3	1.88	0.55
1:C:331:VAL:HG21	1:C:367:ARG:HB2	1.87	0.55
1:C:59:VAL:HG21	1:C:86:PHE:HA	1.87	0.55
1:A:520:TRP:O	1:D:453:VAL:HG12	2.06	0.55
1:F:259[B]:GLU:HG3	1:F:390:ARG:HH22	1.72	0.55
1:B:297:LYS:HE3	1:B:406:VAL:HG23	1.90	0.54
1:C:403:LEU:HD11	1:C:520:TRP:HE3	1.71	0.54
1:F:269:ARG:HG3	1:F:270:ASN:N	2.23	0.53
1:F:160:ASN:ND2	1:F:163:LYS:HD2	2.24	0.53
1:F:432:ASN:ND2	3:F:709:HOH:O	2.42	0.52
1:C:403:LEU:HD11	1:C:520:TRP:CE3	2.45	0.52
1:D:259:GLU:HA	1:D:262:MET:HE2	1.92	0.51
1:F:283:GLN:NE2	1:F:304:GLU:OE1	2.36	0.51
1:D:327:ILE:HG13	1:D:329:PRO:HD2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:327:ILE:HG13	1:C:329:PRO:HD2	1.93	0.50
1:E:297:LYS:HE3	1:E:406:VAL:HG23	1.93	0.50
1:E:419:ASP:OD2	1:E:423:GLN:NE2	2.42	0.50
1:E:297:LYS:NZ	1:E:521:GLU:OE1	2.41	0.50
1:F:141:PRO:HG2	1:F:144:PHE:CD1	2.47	0.49
1:E:228:VAL:HG21	1:E:375:ARG:NH2	2.27	0.49
1:F:252:HIS:CE1	1:F:254:LEU:HB2	2.47	0.49
1:B:485:PRO:HD2	1:B:488[A]:LEU:HD23	1.94	0.49
1:D:60:TYR:OH	1:D:97:PRO:HB3	2.13	0.48
1:F:163:LYS:HD3	1:F:165:PHE:CE2	2.48	0.48
1:B:220:VAL:HG22	1:B:321:TRP:HB2	1.96	0.47
1:F:297:LYS:HE3	1:F:406:VAL:HG23	1.95	0.47
1:A:259:GLU:CG	1:A:390:ARG:HH22	2.27	0.47
1:C:34:SER:OG	1:C:36:ASP:OD1	2.33	0.47
1:F:88:ALA:HA	1:F:141:PRO:HG3	1.95	0.47
1:F:327:ILE:HG13	1:F:329:PRO:HD2	1.97	0.47
1:C:451:LYS:HA	1:C:463:ASP:O	2.14	0.47
1:C:451:LYS:HB2	1:C:462:TYR:CZ	2.49	0.47
1:D:34:SER:OG	1:D:36:ASP:OD1	2.31	0.47
1:C:419:ASP:OD2	1:C:423:GLN:NE2	2.46	0.47
1:C:141:PRO:HG2	1:C:144:PHE:CD1	2.50	0.47
1:E:59:VAL:HG21	1:E:86:PHE:HA	1.95	0.47
1:F:34:SER:OG	1:F:36:ASP:OD1	2.31	0.47
1:B:497:ILE:HG23	1:B:504:ASN:HA	1.97	0.46
1:F:255:LEU:HD13	1:F:259[A]:GLU:HG2	1.97	0.45
1:B:16:THR:HG22	1:B:32:LEU:HD11	1.98	0.45
1:E:291:VAL:HG12	1:E:297:LYS:HG3	1.98	0.45
1:E:221:ILE:HA	1:E:246:THR:O	2.16	0.45
1:B:520:TRP:O	1:E:453:VAL:HG12	2.16	0.45
1:A:297:LYS:HE3	1:A:406:VAL:HG23	1.98	0.45
1:D:140:LEU:HD11	1:D:146:VAL:HG23	1.99	0.45
1:C:255:LEU:HD13	1:C:259:GLU:HG2	1.98	0.45
1:B:140:LEU:HD11	1:B:146:VAL:HG23	1.99	0.45
1:F:441:SER:CB	1:F:473:THR:HG23	2.47	0.45
1:D:160:ASN:ND2	1:D:163:LYS:HD2	2.32	0.44
1:E:259:GLU:HA	1:E:262:MET:HE2	1.99	0.44
1:A:220:VAL:HG22	1:A:321:TRP:HB2	2.00	0.44
1:C:35:PHE:CE2	1:C:64:TYR:HA	2.52	0.44
1:B:327:ILE:HG13	1:B:329:PRO:HD2	2.00	0.44
1:F:403:LEU:HD11	1:F:520:TRP:CE3	2.53	0.44
1:A:289:ALA:HB1	1:B:276:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:160:ASN:ND2	1:C:163:LYS:HD2	2.33	0.43
1:D:220:VAL:HG22	1:D:321:TRP:HB2	2.00	0.43
1:B:403:LEU:HD11	1:B:520:TRP:CE3	2.53	0.43
1:E:441:SER:CB	1:E:473:THR:HG23	2.48	0.43
1:F:403:LEU:HD11	1:F:520:TRP:HE3	1.84	0.43
1:E:253:GLY:HA3	1:E:281:GLU:HG3	2.01	0.42
1:C:58:SER:HB3	1:C:60:TYR:CZ	2.54	0.42
1:B:258:ASN:O	1:B:262:MET:HG3	2.19	0.42
1:A:497:ILE:HG23	1:A:504:ASN:HA	2.02	0.42
1:D:403:LEU:HD11	1:D:520:TRP:CE3	2.55	0.42
1:B:141:PRO:HG2	1:B:144:PHE:CD1	2.54	0.42
1:A:314:LYS:HB3	1:A:314:LYS:HE2	1.87	0.41
1:C:140:LEU:HD11	1:C:146:VAL:HG23	2.02	0.41
1:B:39:LEU:HG	1:B:43:LYS:HE3	2.01	0.41
1:C:477:MET:O	1:C:513:LYS:HE2	2.20	0.41
1:E:271:LEU:HA	1:E:271:LEU:HD23	1.80	0.41
1:B:386:GLU:O	1:B:390:ARG:HG3	2.20	0.41
1:E:441:SER:HB2	1:E:473:THR:HG23	2.02	0.41
1:D:252:HIS:CE1	1:D:254:LEU:HB2	2.55	0.41
1:E:96:GLN:HA	1:E:97:PRO:HD3	1.95	0.41
1:D:403:LEU:HD11	1:D:520:TRP:HE3	1.86	0.41
1:C:139:LYS:HE3	1:C:139:LYS:HB2	1.83	0.41
1:C:88:ALA:HA	1:C:141:PRO:HG3	2.02	0.41
1:C:163:LYS:HD3	1:C:165:PHE:CE2	2.56	0.41
1:E:252:HIS:CE1	1:E:254:LEU:HB2	2.55	0.41
1:B:509:ASP:HA	1:E:507:VAL:HG12	2.02	0.40
1:F:222:LEU:HB2	1:F:323:ALA:HB3	2.03	0.40
1:E:403:LEU:HB2	1:E:449:PRO:HD3	2.04	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	487/529 (92%)	479 (98%)	8 (2%)	0	100	100
1	B	489/529 (92%)	482 (99%)	7 (1%)	0	100	100
1	C	487/529 (92%)	481 (99%)	6 (1%)	0	100	100
1	D	486/529 (92%)	479 (99%)	7 (1%)	0	100	100
1	E	483/529 (91%)	476 (99%)	7 (1%)	0	100	100
1	F	486/529 (92%)	479 (99%)	7 (1%)	0	100	100
All	All	2918/3174 (92%)	2876 (99%)	42 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	397/440 (90%)	392 (99%)	5 (1%)	76	87
1	B	400/440 (91%)	396 (99%)	4 (1%)	82	91
1	C	399/440 (91%)	393 (98%)	6 (2%)	72	85
1	D	389/440 (88%)	383 (98%)	6 (2%)	72	85
1	E	392/440 (89%)	387 (99%)	5 (1%)	76	87
1	F	394/440 (90%)	388 (98%)	6 (2%)	72	85
All	All	2371/2640 (90%)	2339 (99%)	32 (1%)	74	87

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	SER
1	A	205	GLU
1	A	252	HIS
1	A	320	LYS
1	A	367	ARG
1	B	205	GLU
1	B	252	HIS

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Mol	Chain	Res	Type
1	B	367	ARG
1	B	386	GLU
1	C	13	SER
1	C	32	LEU
1	C	34	SER
1	C	252	HIS
1	C	266	MET
1	C	408	LYS
1	D	32	LEU
1	D	239	ARG
1	D	252	HIS
1	D	266	MET
1	D	371	LYS
1	D	386	GLU
1	E	34	SER
1	E	252	HIS
1	E	266	MET
1	E	452	SER
1	E	473	THR
1	F	2	THR
1	F	34	SER
1	F	221	ILE
1	F	252	HIS
1	F	269	ARG
1	F	274	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	125	ASN
1	E	176	HIS
1	F	427	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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

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	490/529 (92%)	-0.37	6 (1%) 81 89	22, 37, 63, 89	0
1	B	490/529 (92%)	-0.43	3 (0%) 90 95	17, 31, 51, 99	0
1	C	492/529 (93%)	-0.47	1 (0%) 95 98	21, 38, 61, 94	0
1	D	491/529 (92%)	-0.31	6 (1%) 81 89	22, 43, 72, 114	0
1	E	489/529 (92%)	-0.23	11 (2%) 65 77	27, 47, 76, 116	0
1	F	490/529 (92%)	-0.25	4 (0%) 87 93	27, 46, 72, 96	0
All	All	2942/3174 (92%)	-0.34	31 (1%) 82 90	17, 40, 70, 116	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	60	TYR	5.4
1	A	60	TYR	3.9
1	F	217	SER	3.9
1	D	103	PHE	3.1
1	E	318	ASN	3.0
1	B	462	TYR	2.9
1	F	60	TYR	2.8
1	E	317	THR	2.8
1	A	63	ASP	2.7
1	E	319	ALA	2.7
1	B	460	ARG	2.6
1	E	331	VAL	2.6
1	C	63	ASP	2.6
1	E	103	PHE	2.5
1	E	100	GLN	2.5
1	D	458	ASP	2.5
1	A	317	THR	2.4
1	E	316	LEU	2.2
1	D	105	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	459	GLY	2.2
1	D	2	THR	2.1
1	D	319	ALA	2.1
1	A	61	GLU	2.1
1	E	220	VAL	2.1
1	A	360	LEU	2.1
1	B	360	LEU	2.0
1	E	332	ILE	2.0
1	F	321	TRP	2.0
1	F	461	THR	2.0
1	E	321	TRP	2.0
1	A	316	LEU	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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q < 0.9
2	MG	F	601	1/1	0.97	0.07	-1.91	68,68,68,68	0
2	MG	E	601	1/1	0.96	0.05	-3.00	48,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.