



wwPDB X-ray Structure Validation Summary Report

Mar 9, 2026 – 01:18 AM UTC

PDB ID : 5DS0 / pdb_00005ds0
Title : Crystal structure of TET aminopeptidase from marine sediment archaeon Thaumarchaeota archaeon SCGC AB-539-E09
Authors : Michalska, K.; Chhor, G.; Mootz, J.; Endres, M.; Jedrzejczak, R.; Babnigg, G.; Steen, A.; Lloyd, K.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2015-09-16
Resolution : 2.80 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

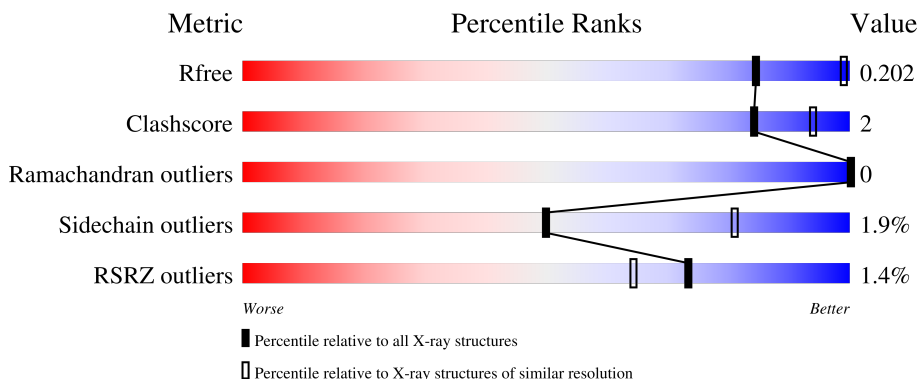
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

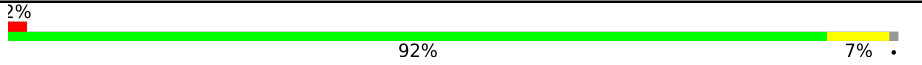
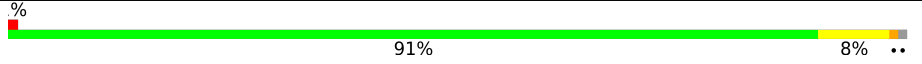
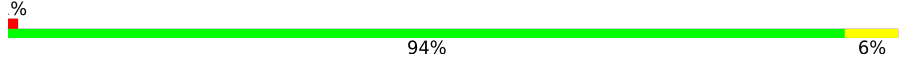
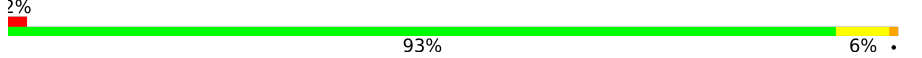
The reported resolution of this entry is 2.80 Å.

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.



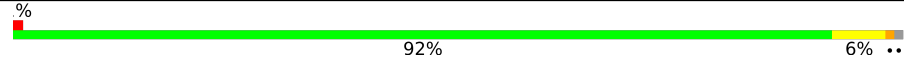
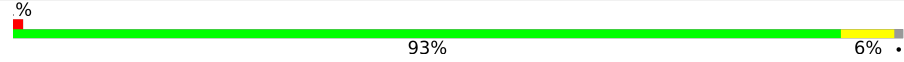
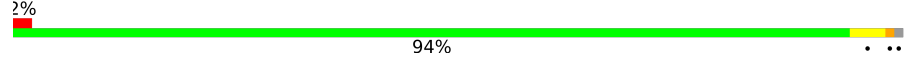
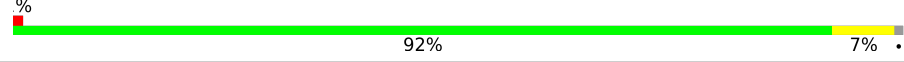
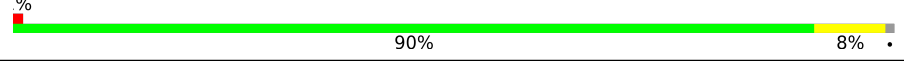
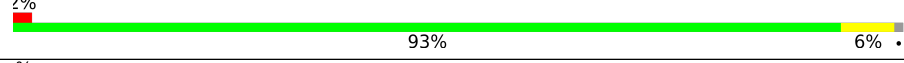
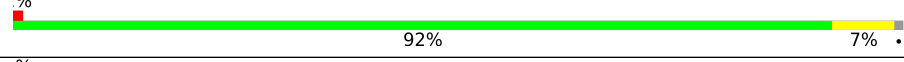
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 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	359	 2% 92% 7%
1	B	359	 1% 91% 8%
1	C	359	 1% 94% 6%
1	D	359	 2% 93% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	E	359	 % 92% 6% ..
1	F	359	 % 93% 6% .
1	G	359	 2% 94% . ..
1	H	359	 % 92% 7% .
1	I	359	 % 90% 8% .
1	J	359	 2% 93% 6% .
1	K	359	 % 92% 7% .
1	L	359	 % 91% 7% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 32797 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 Peptidase M42.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	357	2728	1720	474	517	3	14	0	0	0
1	B	356	2718	1715	472	514	3	14	0	0	0
1	C	359	2744	1731	477	519	3	14	0	0	0
1	D	358	2732	1722	475	518	3	14	0	0	0
1	E	357	2728	1720	474	517	3	14	0	0	0
1	F	356	2723	1717	473	516	3	14	0	0	0
1	G	356	2723	1717	473	516	3	14	0	0	0
1	H	356	2723	1717	473	516	3	14	0	0	0
1	I	354	2709	1710	470	512	3	14	0	0	0
1	J	356	2723	1717	473	516	3	14	0	0	0
1	K	356	2723	1717	473	516	3	14	0	0	0
1	L	355	2709	1710	471	511	3	14	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP M7T295
A	2	ASN	-	expression tag	UNP M7T295
A	3	ALA	-	expression tag	UNP M7T295
B	1	SER	-	expression tag	UNP M7T295
B	2	ASN	-	expression tag	UNP M7T295

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	3	ALA	-	expression tag	UNP M7T295
C	1	SER	-	expression tag	UNP M7T295
C	2	ASN	-	expression tag	UNP M7T295
C	3	ALA	-	expression tag	UNP M7T295
D	1	SER	-	expression tag	UNP M7T295
D	2	ASN	-	expression tag	UNP M7T295
D	3	ALA	-	expression tag	UNP M7T295
E	1	SER	-	expression tag	UNP M7T295
E	2	ASN	-	expression tag	UNP M7T295
E	3	ALA	-	expression tag	UNP M7T295
F	1	SER	-	expression tag	UNP M7T295
F	2	ASN	-	expression tag	UNP M7T295
F	3	ALA	-	expression tag	UNP M7T295
G	1	SER	-	expression tag	UNP M7T295
G	2	ASN	-	expression tag	UNP M7T295
G	3	ALA	-	expression tag	UNP M7T295
H	1	SER	-	expression tag	UNP M7T295
H	2	ASN	-	expression tag	UNP M7T295
H	3	ALA	-	expression tag	UNP M7T295
I	1	SER	-	expression tag	UNP M7T295
I	2	ASN	-	expression tag	UNP M7T295
I	3	ALA	-	expression tag	UNP M7T295
J	1	SER	-	expression tag	UNP M7T295
J	2	ASN	-	expression tag	UNP M7T295
J	3	ALA	-	expression tag	UNP M7T295
K	1	SER	-	expression tag	UNP M7T295
K	2	ASN	-	expression tag	UNP M7T295
K	3	ALA	-	expression tag	UNP M7T295
L	1	SER	-	expression tag	UNP M7T295
L	2	ASN	-	expression tag	UNP M7T295
L	3	ALA	-	expression tag	UNP M7T295

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Co 2 2	0	0
2	B	2	Total Co 2 2	0	0
2	C	2	Total Co 2 2	0	0
2	D	2	Total Co 2 2	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	E	2	Total Co 2 2	0	0
2	F	2	Total Co 2 2	0	0
2	G	2	Total Co 2 2	0	0
2	H	2	Total Co 2 2	0	0
2	I	2	Total Co 2 2	0	0
2	J	2	Total Co 2 2	0	0
2	K	2	Total Co 2 2	0	0
2	L	2	Total Co 2 2	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0

Continued on next page...

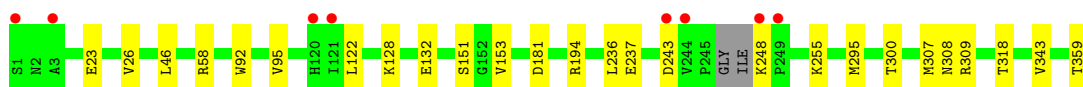
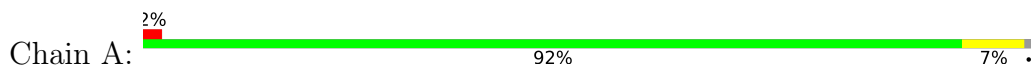
Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total 6	C 3	O 3	0	0
3	C	1	Total 6	C 3	O 3	0	0
3	E	1	Total 6	C 3	O 3	0	0
3	G	1	Total 6	C 3	O 3	0	0
3	G	1	Total 6	C 3	O 3	0	0
3	H	1	Total 6	C 3	O 3	0	0
3	H	1	Total 6	C 3	O 3	0	0
3	I	1	Total 6	C 3	O 3	0	0
3	I	1	Total 6	C 3	O 3	0	0
3	J	1	Total 6	C 3	O 3	0	0
3	K	1	Total 6	C 3	O 3	0	0
3	L	1	Total 6	C 3	O 3	0	0

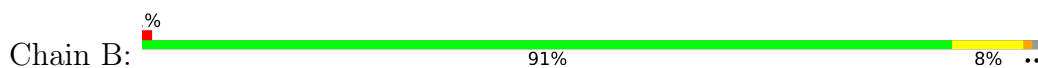
3 Residue-property plots [i](#)

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.

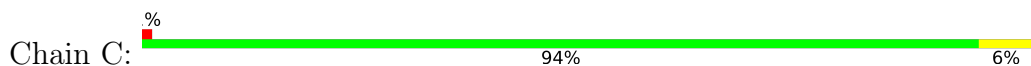
- Molecule 1: Peptidase M42



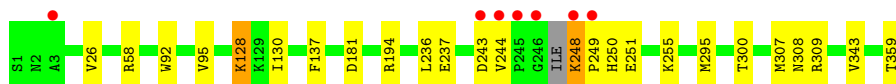
- Molecule 1: Peptidase M42



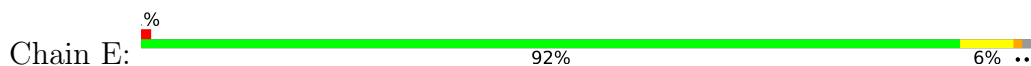
- Molecule 1: Peptidase M42



- Molecule 1: Peptidase M42



- Molecule 1: Peptidase M42



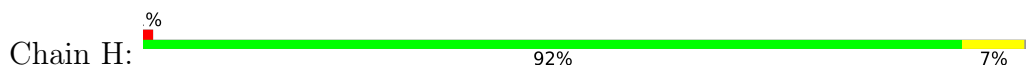
- Molecule 1: Peptidase M42



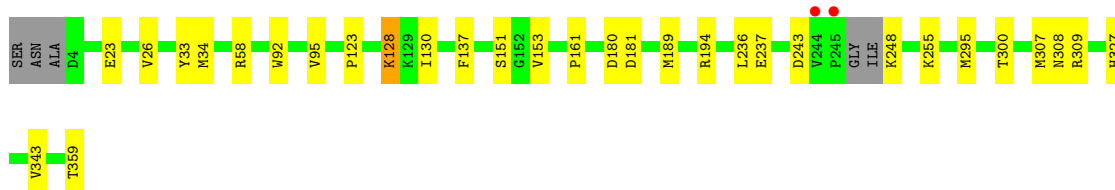
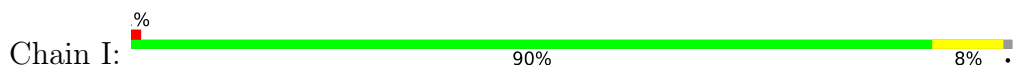
• Molecule 1: Peptidase M42



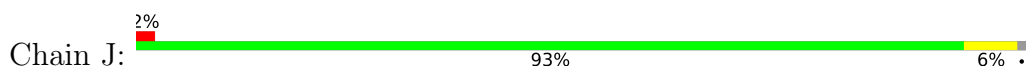
• Molecule 1: Peptidase M42



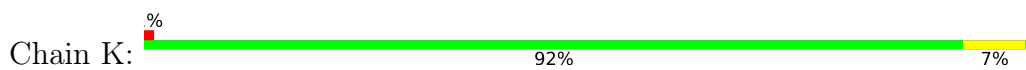
• Molecule 1: Peptidase M42



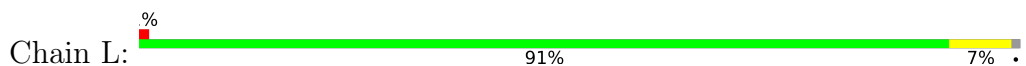
• Molecule 1: Peptidase M42

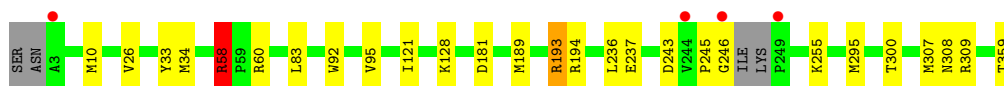


• Molecule 1: Peptidase M42



• Molecule 1: Peptidase M42





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	114.64Å 165.37Å 125.79Å 90.00° 90.87° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 30.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.00-2.80) 99.9 (30.00-2.80)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.77Å)	Xtrriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.193 , 0.206 0.194 , 0.202	Depositor DCC
R_{free} test set	1850 reflections (1.45%)	wwPDB-VP
Wilson B-factor (Å ²)	45.1	Xtrriage
Anisotropy	0.214	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 25.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.022 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	32797	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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: CO, 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	0.68	0/2764	0.86	5/3717 (0.1%)
1	B	0.72	3/2754 (0.1%)	0.92	8/3703 (0.2%)
1	C	0.67	0/2781	0.87	2/3740 (0.1%)
1	D	0.68	0/2768	0.87	5/3722 (0.1%)
1	E	0.71	1/2764 (0.0%)	0.87	6/3717 (0.2%)
1	F	0.67	0/2759	0.86	3/3709 (0.1%)
1	G	0.70	1/2759 (0.0%)	0.87	4/3709 (0.1%)
1	H	0.68	0/2759	0.86	3/3709 (0.1%)
1	I	0.70	1/2745 (0.0%)	0.86	4/3691 (0.1%)
1	J	0.67	0/2759	0.85	2/3709 (0.1%)
1	K	0.67	0/2759	0.85	3/3709 (0.1%)
1	L	0.67	0/2745	0.88	4/3690 (0.1%)
All	All	0.69	6/33116 (0.0%)	0.87	49/44525 (0.1%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	4	ASP	CA-CB	5.75	1.62	1.53
1	B	146	GLU	CA-CB	-5.75	1.44	1.53
1	I	123	PRO	CA-C	5.38	1.54	1.51
1	B	121	ILE	CA-CB	5.23	1.61	1.54
1	E	57	ASP	CA-CB	5.13	1.62	1.53

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	194	ARG	NE-CZ-NH2	-8.36	111.67	119.20
1	B	194	ARG	NE-CZ-NH1	8.15	129.65	121.50
1	E	194	ARG	NE-CZ-NH2	-7.87	112.11	119.20
1	L	194	ARG	NE-CZ-NH2	-7.79	112.19	119.20
1	D	194	ARG	NE-CZ-NH2	-7.73	112.25	119.20

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	2728	0	2752	10	0
1	B	2718	0	2741	21	0
1	C	2744	0	2778	11	0
1	D	2732	0	2755	23	0
1	E	2728	0	2752	15	0
1	F	2723	0	2751	14	0
1	G	2723	0	2751	8	0
1	H	2723	0	2751	15	0
1	I	2709	0	2733	24	0
1	J	2723	0	2751	13	0
1	K	2723	0	2751	14	0
1	L	2709	0	2736	18	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
3	A	6	0	8	0	0
3	B	12	0	16	0	0
3	C	12	0	16	0	0
3	E	6	0	8	0	0
3	G	12	0	16	0	0
3	H	12	0	16	0	0
3	I	12	0	16	1	0
3	J	6	0	8	0	0
3	K	6	0	8	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	6	0	8	0	0
All	All	32797	0	33122	151	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.

The worst 5 of 151 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:I:34:MSE:HG2	1:I:189:MSE:HE3	1.31	1.10
1:D:248:LYS:CB	1:D:249:PRO:HD2	1.81	1.10
1:B:130:ILE:HG13	1:D:130:ILE:HG22	1.54	0.87
1:I:34:MSE:CG	1:I:189:MSE:HE3	2.05	0.86
1:D:248:LYS:CB	1:D:249:PRO:CD	2.56	0.82

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	353/359 (98%)	341 (97%)	12 (3%)	0	100	100
1	B	352/359 (98%)	341 (97%)	11 (3%)	0	100	100
1	C	357/359 (99%)	344 (96%)	13 (4%)	0	100	100
1	D	354/359 (99%)	343 (97%)	11 (3%)	0	100	100
1	E	353/359 (98%)	341 (97%)	12 (3%)	0	100	100
1	F	352/359 (98%)	339 (96%)	13 (4%)	0	100	100
1	G	352/359 (98%)	340 (97%)	12 (3%)	0	100	100
1	H	352/359 (98%)	340 (97%)	12 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	350/359 (98%)	338 (97%)	12 (3%)	0	100	100
1	J	352/359 (98%)	339 (96%)	13 (4%)	0	100	100
1	K	352/359 (98%)	341 (97%)	11 (3%)	0	100	100
1	L	351/359 (98%)	339 (97%)	12 (3%)	0	100	100
All	All	4230/4308 (98%)	4086 (97%)	144 (3%)	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	298/286 (104%)	293 (98%)	5 (2%)	53	83
1	B	296/286 (104%)	289 (98%)	7 (2%)	43	77
1	C	300/286 (105%)	294 (98%)	6 (2%)	48	80
1	D	298/286 (104%)	293 (98%)	5 (2%)	53	83
1	E	298/286 (104%)	292 (98%)	6 (2%)	48	80
1	F	298/286 (104%)	292 (98%)	6 (2%)	48	80
1	G	298/286 (104%)	292 (98%)	6 (2%)	48	80
1	H	298/286 (104%)	293 (98%)	5 (2%)	53	83
1	I	296/286 (104%)	291 (98%)	5 (2%)	53	83
1	J	298/286 (104%)	295 (99%)	3 (1%)	68	88
1	K	298/286 (104%)	292 (98%)	6 (2%)	48	80
1	L	295/286 (103%)	288 (98%)	7 (2%)	43	77
All	All	3571/3432 (104%)	3504 (98%)	67 (2%)	50	81

5 of 67 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	307	MSE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	K	353	GLU
1	L	295	MSE
1	E	58	ARG
1	E	49	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	170	ASN
1	J	226	HIS
1	J	111	HIS
1	K	111	HIS
1	D	198	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 39 ligands modelled in this entry, 24 are monoatomic - leaving 15 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
3	GOL	A	403	-	5,5,5	0.29	0	5,5,5	0.62	0
3	GOL	C	404	-	5,5,5	0.51	0	5,5,5	0.71	0
3	GOL	H	403	-	5,5,5	0.51	0	5,5,5	0.14	0
3	GOL	B	403	-	5,5,5	0.53	0	5,5,5	0.62	0
3	GOL	J	403	-	5,5,5	0.57	0	5,5,5	0.61	0
3	GOL	C	403	-	5,5,5	0.38	0	5,5,5	0.70	0
3	GOL	K	403	-	5,5,5	0.27	0	5,5,5	0.53	0
3	GOL	E	403	-	5,5,5	0.68	0	5,5,5	0.94	0
3	GOL	B	404	-	5,5,5	0.50	0	5,5,5	0.47	0
3	GOL	I	404	-	5,5,5	0.25	0	5,5,5	0.58	0
3	GOL	G	403	-	5,5,5	0.20	0	5,5,5	0.70	0
3	GOL	L	403	-	5,5,5	0.26	0	5,5,5	0.25	0
3	GOL	H	404	-	5,5,5	0.48	0	5,5,5	0.40	0
3	GOL	I	403	-	5,5,5	0.56	0	5,5,5	0.89	0
3	GOL	G	404	-	5,5,5	0.36	0	5,5,5	0.53	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
3	GOL	A	403	-	-	2/4/4/4	-
3	GOL	C	404	-	-	4/4/4/4	-
3	GOL	H	403	-	-	4/4/4/4	-
3	GOL	B	403	-	-	3/4/4/4	-
3	GOL	J	403	-	-	2/4/4/4	-
3	GOL	C	403	-	-	2/4/4/4	-
3	GOL	K	403	-	-	4/4/4/4	-
3	GOL	E	403	-	-	4/4/4/4	-
3	GOL	B	404	-	-	0/4/4/4	-
3	GOL	I	404	-	-	0/4/4/4	-
3	GOL	G	403	-	-	4/4/4/4	-
3	GOL	L	403	-	-	2/4/4/4	-
3	GOL	H	404	-	-	2/4/4/4	-
3	GOL	I	403	-	-	2/4/4/4	-
3	GOL	G	404	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	403	GOL	O1-C1-C2-C3
3	C	403	GOL	O1-C1-C2-C3
3	C	404	GOL	C1-C2-C3-O3
3	G	403	GOL	O1-C1-C2-O2
3	G	403	GOL	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	K	403	GOL	1	0
3	I	404	GOL	1	0

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	343/359 (95%)	-0.23	8 (2%) 61 51	29, 43, 84, 123	0
1	B	342/359 (95%)	-0.20	5 (1%) 72 63	28, 48, 79, 111	0
1	C	345/359 (96%)	-0.25	3 (0%) 81 74	28, 41, 81, 117	0
1	D	344/359 (95%)	-0.23	7 (2%) 65 56	27, 42, 80, 124	0
1	E	343/359 (95%)	-0.20	5 (1%) 72 63	31, 44, 78, 112	0
1	F	342/359 (95%)	-0.17	3 (0%) 81 74	31, 49, 88, 122	0
1	G	342/359 (95%)	-0.19	6 (1%) 67 58	26, 47, 84, 115	0
1	H	342/359 (95%)	-0.29	3 (0%) 81 74	23, 41, 71, 128	0
1	I	340/359 (94%)	-0.34	2 (0%) 85 80	24, 38, 70, 104	0
1	J	342/359 (95%)	-0.16	6 (1%) 67 58	27, 48, 85, 113	0
1	K	342/359 (95%)	-0.22	5 (1%) 72 63	28, 46, 77, 110	0
1	L	341/359 (94%)	-0.23	4 (1%) 76 68	26, 44, 81, 115	0
All	All	4108/4308 (95%)	-0.23	57 (1%) 73 64	23, 44, 82, 128	0

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	249	PRO	4.5
1	F	249	PRO	4.4
1	G	249	PRO	4.2
1	D	246	GLY	4.1
1	L	249	PRO	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 oligosaccharides 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
3	GOL	E	403	6/6	0.84	0.14	49,54,58,60	0
3	GOL	G	403	6/6	0.87	0.17	62,63,67,70	0
3	GOL	A	403	6/6	0.88	0.11	45,46,50,52	0
3	GOL	H	403	6/6	0.88	0.12	44,46,48,49	0
3	GOL	H	404	6/6	0.88	0.16	55,57,61,62	0
3	GOL	C	404	6/6	0.89	0.16	64,64,65,66	0
3	GOL	J	403	6/6	0.89	0.11	56,62,64,64	0
3	GOL	K	403	6/6	0.89	0.14	54,56,57,59	0
3	GOL	B	404	6/6	0.90	0.11	41,48,51,51	0
3	GOL	B	403	6/6	0.91	0.08	43,46,48,50	0
3	GOL	I	404	6/6	0.91	0.11	44,46,48,48	0
3	GOL	I	403	6/6	0.92	0.11	43,46,46,48	0
3	GOL	G	404	6/6	0.92	0.09	48,54,55,57	0
3	GOL	L	403	6/6	0.93	0.10	50,52,55,60	0
3	GOL	C	403	6/6	0.95	0.07	40,44,50,55	0
2	CO	K	401	1/1	0.98	0.03	31,31,31,31	0
2	CO	B	401	1/1	0.98	0.04	35,35,35,35	0
2	CO	L	402	1/1	0.99	0.02	26,26,26,26	0
2	CO	A	401	1/1	0.99	0.02	28,28,28,28	0
2	CO	C	402	1/1	0.99	0.03	29,29,29,29	0
2	CO	D	402	1/1	0.99	0.02	30,30,30,30	0
2	CO	E	402	1/1	0.99	0.03	30,30,30,30	0
2	CO	F	401	1/1	0.99	0.02	38,38,38,38	0
2	CO	G	401	1/1	0.99	0.02	24,24,24,24	0
2	CO	G	402	1/1	0.99	0.02	30,30,30,30	0
2	CO	H	401	1/1	0.99	0.03	27,27,27,27	0
2	CO	I	401	1/1	0.99	0.03	26,26,26,26	0
2	CO	I	402	1/1	0.99	0.03	22,22,22,22	0
2	CO	J	401	1/1	0.99	0.03	29,29,29,29	0
2	CO	J	402	1/1	0.99	0.02	25,25,25,25	0
2	CO	A	402	1/1	0.99	0.02	23,23,23,23	0
2	CO	K	402	1/1	0.99	0.02	26,26,26,26	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CO	L	401	1/1	0.99	0.02	28,28,28,28	0
2	CO	H	402	1/1	1.00	0.02	24,24,24,24	0
2	CO	D	401	1/1	1.00	0.03	23,23,23,23	0
2	CO	F	402	1/1	1.00	0.03	26,26,26,26	0
2	CO	C	401	1/1	1.00	0.01	22,22,22,22	0
2	CO	E	401	1/1	1.00	0.02	27,27,27,27	0
2	CO	B	402	1/1	1.00	0.02	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.