Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:17 PM GMT

PDB ID	:	3THS
Title	:	Crystal structure of rat native liver Glycine N-methyltransferase complexed with 5-methyltetrahydrofolate pentaglutamate
Authors	:	Luka, Z.; Pakhomova, S.; Loukachevitch, L.V.; Newcomer, M.E.; Wagner, C.
Deposited on	:	2011-08-19
Resolution	:	2.50 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 ①) were used in the production of this report:

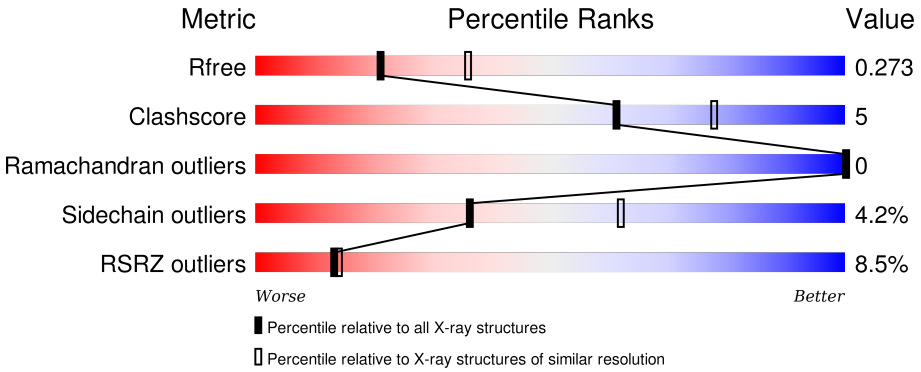
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 <=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	293	3% 86% 11%
1	B	293	83% 13%
1	C	293	24% 83% 14%
1	D	293	6% 88% 9%
2	E	6	50% 50%

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Mol	Chain	Length	Quality of chain
2	F	6	

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	GGL	F	2	-	-	X	-
3	BME	B	400[A]	-	-	-	X
3	BME	B	400[B]	-	-	-	X
4	TAM	B	293	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9091 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 Glycine N-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	284	Total	C	N	O	S	0	0	0
			2225	1415	385	414	11			
1	B	286	Total	C	N	O	S	0	0	0
			2243	1428	388	416	11			
1	C	285	Total	C	N	O	S	0	0	0
			2224	1412	386	415	11			
1	D	284	Total	C	N	O	S	0	0	0
			2226	1416	386	413	11			

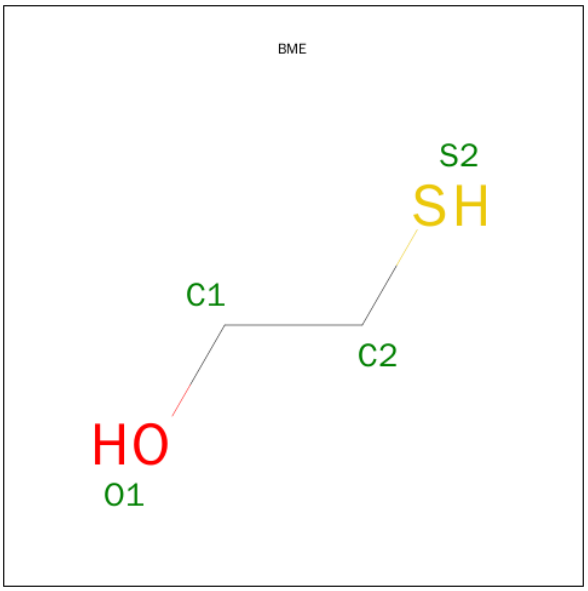
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	300	ACE	-	ACETYLATION	UNP P13255
B	300	ACE	-	ACETYLATION	UNP P13255
C	300	ACE	-	ACETYLATION	UNP P13255
D	300	ACE	-	ACETYLATION	UNP P13255

- Molecule 2 is a protein called 5-methyltetrahydrofolate pentaglutamate.

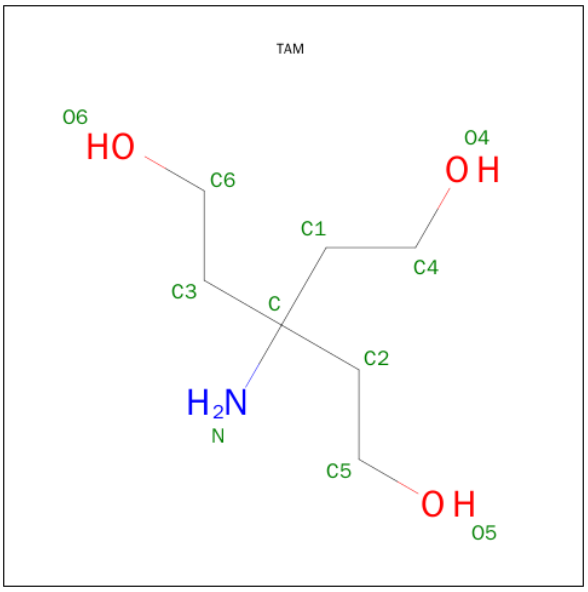
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	3	Total	C	N	O	0	0	1
			33	20	8	5			
2	F	3	Total	C	N	O	0	0	1
			33	20	8	5			

- Molecule 3 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
3	B	1	8	4	2	2	0	1

- Molecule 4 is TRIS(HYDROXYETHYL)AMINOMETHANE (three-letter code: TAM) (formula: $C_7H_{17}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	B	1	11	7	1	3	0	0

- Molecule 5 is water.

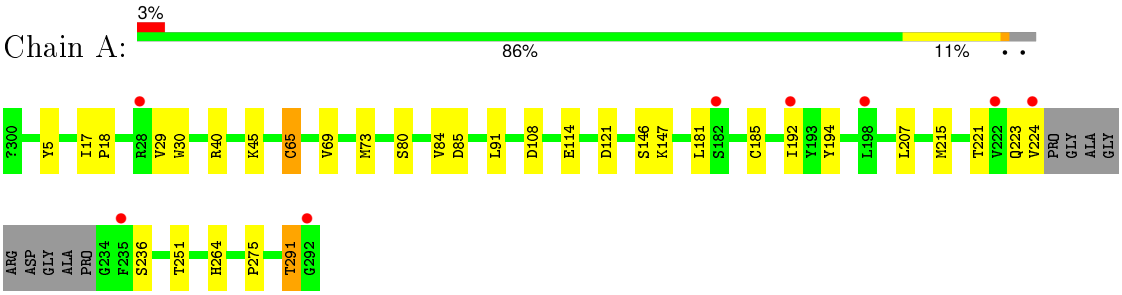
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	31	Total O 31 31	0	0
5	B	30	Total O 30 30	0	0
5	C	13	Total O 13 13	0	0
5	D	14	Total O 14 14	0	0

3 Residue-property plots (i)

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.

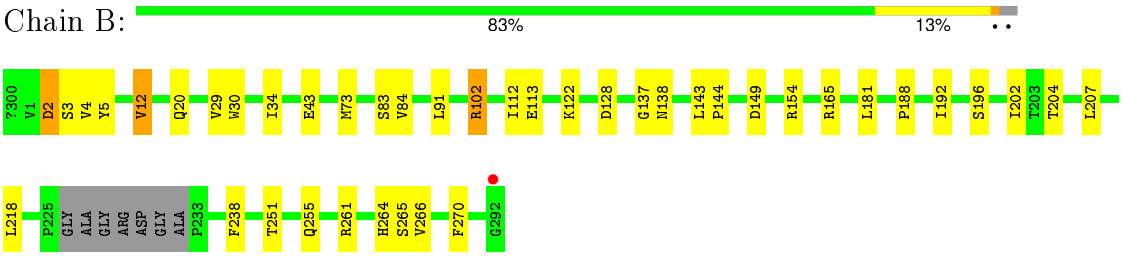
- Molecule 1: Glycine N-methyltransferase

Chain A:



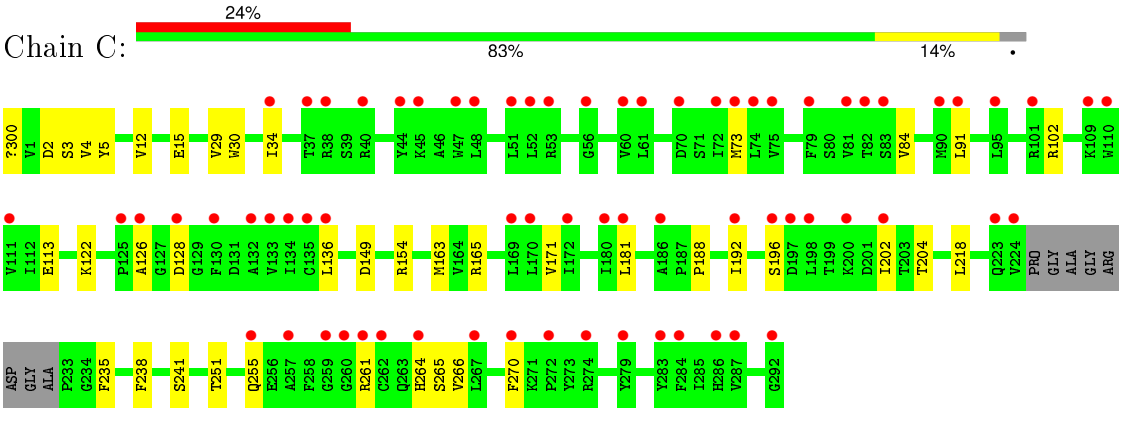
- Molecule 1: Glycine N-methyltransferase

Chain B:



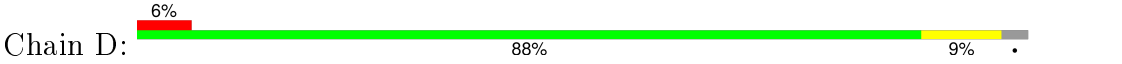
- Molecule 1: Glycine N-methyltransferase

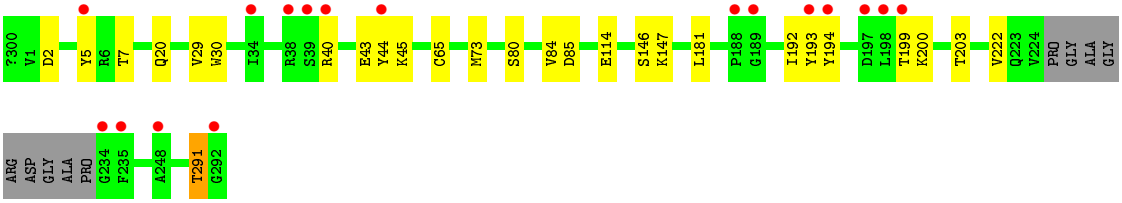
Chain C:



- Molecule 1: Glycine N-methyltransferase

Chain D:





• Molecule 2: 5-methyltetrahydrofolate pentaglutamate

Chain E:

• Molecule 2: 5-methyltetrahydrofolate pentaglutamate

Chain F:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	193.04Å 61.05Å 146.35Å 90.00° 128.92° 90.00°	Depositor
Resolution (Å)	48.22 – 2.50 48.22 – 2.49	Depositor EDS
% Data completeness (in resolution range)	98.1 (48.22-2.50) 99.3 (48.22-2.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	4.54 (at 2.48Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.228 , 0.280 0.227 , 0.273	Depositor DCC
R_{free} test set	2250 reflections (5.11%)	DCC
Wilson B-factor (Å^2)	52.5	Xtriage
Anisotropy	0.812	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 25.3	EDS
Estimated twinning fraction	0.003 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 46431 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	9091	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.68% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: GGL, TAM, 03O, ACE, BME

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	0.83	3/2276 (0.1%)	0.78	1/3086 (0.0%)
1	B	0.89	1/2296 (0.0%)	0.81	1/3113 (0.0%)
1	C	0.66	0/2275	0.72	2/3085 (0.1%)
1	D	0.82	2/2277 (0.1%)	0.78	0/3087
All	All	0.81	6/9124 (0.1%)	0.77	4/12371 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	65	CYS	CB-SG	-6.47	1.71	1.82
1	B	43	GLU	CG-CD	6.14	1.61	1.51
1	A	114	GLU	CB-CG	5.99	1.63	1.52
1	D	43	GLU	CG-CD	5.59	1.60	1.51
1	A	114	GLU	CG-CD	5.47	1.60	1.51
1	D	114	GLU	CB-CG	5.42	1.62	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	2	ASP	CB-CG-OD2	-5.93	112.97	118.30
1	C	15	GLU	OE1-CD-OE2	-5.77	116.38	123.30
1	B	2	ASP	CB-CG-OD2	-5.54	113.31	118.30
1	A	121	ASP	CB-CG-OD1	5.05	122.84	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	2225	0	2176	25	1
1	B	2243	0	2201	25	0
1	C	2224	0	2170	22	1
1	D	2226	0	2180	28	0
2	E	33	0	22	12	0
2	F	33	0	22	13	0
3	B	8	0	10	0	0
4	B	11	0	17	0	0
5	A	31	0	0	0	0
5	B	30	0	0	0	0
5	C	13	0	0	1	0
5	D	14	0	0	1	0
All	All	9091	0	8798	97	1

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 5.

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:D:200:LYS:NZ	1:D:222:VAL:HG12	1.20	1.45
1:D:200:LYS:NZ	1:D:222:VAL:CG1	2.02	1.21
1:D:200:LYS:HZ3	1:D:222:VAL:CG1	1.61	1.07
1:A:29:VAL:HG21	1:A:236:SER:HB2	1.51	0.93
1:A:5:TYR:CZ	2:E:2:GGL:HB2	2.08	0.87
1:A:29:VAL:HG21	1:A:236:SER:CB	2.04	0.86
1:D:200:LYS:HZ3	1:D:222:VAL:HG12	1.22	0.85
1:D:200:LYS:HZ3	1:D:222:VAL:HG11	1.43	0.82
2:E:1:03O:C11	2:E:1:03O:O4	2.31	0.77
1:D:200:LYS:HZ2	1:D:222:VAL:HG12	0.86	0.75
2:E:1:03O:H112	2:E:1:03O:O4	1.90	0.72
1:C:300:ACE:H3	1:C:3:SER:OG	1.91	0.71
1:D:5:TYR:CZ	2:F:2:GGL:HB2	2.26	0.68
1:A:185:CYS:SG	5:C:301:HOH:O	2.50	0.68
1:D:5:TYR:CE2	2:F:2:GGL:HB2	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:200:LYS:HZ2	1:D:222:VAL:CG1	1.82	0.67
1:B:207:LEU:HD22	2:E:1:03O:H71	1.77	0.67
1:C:149:ASP:O	1:C:154:ARG:NH2	2.27	0.67
1:A:45:LYS:HG3	1:A:73:MET:SD	2.35	0.66
1:A:5:TYR:CE1	2:E:2:GGL:C	2.78	0.66
1:A:5:TYR:CE2	2:E:2:GGL:HB2	2.31	0.65
1:C:29:VAL:HG12	1:C:238:PHE:CD1	2.34	0.63
2:F:1:03O:H112	2:F:1:03O:O4	1.98	0.62
1:C:4:VAL:O	1:C:4:VAL:HG23	1.99	0.61
1:D:40:ARG:HA	1:D:194:TYR:CD1	2.35	0.61
1:A:29:VAL:HG21	1:A:236:SER:HB3	1.82	0.61
1:B:149:ASP:O	1:B:154:ARG:NH2	2.34	0.60
1:D:45:LYS:HG3	1:D:73:MET:SD	2.43	0.59
1:B:5:TYR:HB2	2:F:1:03O:H91	1.85	0.58
2:F:1:03O:C11	2:F:1:03O:O4	2.54	0.55
1:D:65:CYS:HB3	1:D:85:ASP:HB2	1.90	0.53
1:D:291:THR:HG23	1:D:291:THR:O	2.08	0.53
1:C:192:ILE:HD12	1:C:270:PHE:CZ	2.43	0.53
1:C:4:VAL:O	1:C:4:VAL:CG2	2.57	0.52
1:B:264:HIS:CE1	1:B:266:VAL:HG12	2.45	0.52
1:C:264:HIS:CE1	1:C:266:VAL:HG12	2.45	0.52
1:C:84:VAL:HA	1:C:113:GLU:O	2.11	0.51
1:D:29:VAL:CG1	1:D:222:VAL:HG11	2.40	0.51
1:C:251:THR:HG23	1:C:264:HIS:CE1	2.45	0.51
1:A:291:THR:CG2	1:A:291:THR:O	2.58	0.51
1:C:29:VAL:HG12	1:C:238:PHE:HD1	1.75	0.50
1:B:251:THR:HG23	1:B:264:HIS:CE1	2.47	0.50
1:B:143:LEU:HD12	1:B:144:PRO:HD2	1.94	0.49
1:A:207:LEU:HD21	2:F:2:GGL:HA	1.94	0.49
1:B:30:TRP:CZ2	1:B:34:ILE:HG21	2.48	0.49
1:A:30:TRP:CG	1:B:12:VAL:HG22	2.48	0.49
1:D:5:TYR:CD1	2:F:2:GGL:C	2.96	0.48
1:A:291:THR:HG23	1:A:291:THR:O	2.13	0.48
1:B:29:VAL:HG12	1:B:238:PHE:HD1	1.78	0.48
1:C:126:ALA:HB2	1:C:163:MET:CE	2.43	0.48
1:A:207:LEU:CD2	2:F:2:GGL:HA	2.43	0.48
1:D:5:TYR:CE1	2:F:2:GGL:C	2.95	0.48
1:B:5:TYR:CD1	2:F:1:03O:H16	2.49	0.48
1:A:251:THR:HG23	1:A:264:HIS:CE1	2.49	0.48
1:B:204:THR:HG23	1:B:218:LEU:CD2	2.44	0.48
1:C:5:TYR:HB2	2:E:1:03O:C11	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:291:THR:CG2	1:D:291:THR:O	2.62	0.48
1:A:65:CYS:HB3	1:A:85:ASP:HB2	1.96	0.47
1:A:29:VAL:CG2	1:A:236:SER:HB2	2.33	0.47
1:D:44:TYR:CD1	1:D:193:TYR:HD2	2.33	0.47
1:B:188:PRO:HB3	1:B:202:ILE:HD12	1.96	0.47
1:B:4:VAL:HG23	1:B:4:VAL:O	2.14	0.47
1:B:84:VAL:HA	1:B:113:GLU:O	2.15	0.47
1:C:12:VAL:HG22	1:D:30:TRP:CG	2.49	0.46
1:D:29:VAL:HG11	1:D:222:VAL:HG13	1.97	0.46
1:D:29:VAL:CG1	1:D:222:VAL:CG1	2.94	0.46
1:B:2:ASP:OD2	1:D:20:GLN:HG2	2.16	0.46
1:B:83:SER:O	1:B:112:ILE:HA	2.16	0.46
1:A:108:ASP:OD1	1:B:102:ARG:NH1	2.48	0.46
1:A:5:TYR:CB	2:E:1:03O:C17	2.95	0.45
1:B:137:GLY:O	1:B:138:ASN:HB3	2.16	0.45
1:A:215:MET:HE1	2:F:2:GGL:OXT	2.17	0.45
1:B:192:ILE:HD12	1:B:270:PHE:CZ	2.51	0.45
1:B:29:VAL:HG12	1:B:238:PHE:CD1	2.52	0.45
1:C:5:TYR:HB2	2:E:1:03O:H111	1.98	0.45
1:C:136:LEU:HD21	1:C:171:VAL:HG12	2.00	0.44
1:B:20:GLN:HG2	1:D:2:ASP:OD2	2.16	0.44
1:B:207:LEU:CD2	2:E:1:03O:H71	2.45	0.43
1:C:235:PHE:CG	1:C:235:PHE:O	2.71	0.43
1:A:223:GLN:O	1:A:224:VAL:HG23	2.19	0.43
1:C:126:ALA:HB2	1:C:163:MET:HE2	2.00	0.43
1:D:199:THR:O	1:D:200:LYS:HD3	2.18	0.43
1:A:5:TYR:HB3	2:E:1:03O:C17	2.50	0.42
1:D:5:TYR:CE1	2:F:2:GGL:HB2	2.54	0.42
1:A:40:ARG:HA	1:A:194:TYR:CD1	2.55	0.42
1:C:30:TRP:CZ2	1:C:34:ILE:HG21	2.55	0.41
1:C:29:VAL:HG12	1:C:238:PHE:CE1	2.54	0.41
1:A:5:TYR:OH	2:E:3:GGL:N	2.53	0.41
1:C:204:THR:HG23	1:C:218:LEU:CD2	2.50	0.41
1:B:20:GLN:HA	1:D:2:ASP:OD1	2.21	0.41
1:C:241:SER:HB2	1:D:7:THR:HG23	2.01	0.41
1:A:17:ILE:HA	1:A:18:PRO:HD3	1.96	0.41
1:B:3:SER:HB2	2:F:1:03O:O4	2.21	0.41
1:A:29:VAL:CG2	1:A:236:SER:CB	2.89	0.41
1:B:4:VAL:CG2	1:B:4:VAL:O	2.69	0.41
1:D:203:THR:HG22	5:D:297:HOH:O	2.20	0.40
1:C:188:PRO:HB3	1:C:202:ILE:HD12	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:PRO:O	1:C:154:ARG:NH1[2_556]	2.17	0.03

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	280/293 (96%)	272 (97%)	8 (3%)	0	100	100
1	B	282/293 (96%)	273 (97%)	9 (3%)	0	100	100
1	C	281/293 (96%)	269 (96%)	12 (4%)	0	100	100
1	D	280/293 (96%)	273 (98%)	7 (2%)	0	100	100
All	All	1123/1172 (96%)	1087 (97%)	36 (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	236/242 (98%)	226 (96%)	10 (4%)	36	62
1	B	239/242 (99%)	227 (95%)	12 (5%)	30	53
1	C	235/242 (97%)	224 (95%)	11 (5%)	32	56
1	D	236/242 (98%)	229 (97%)	7 (3%)	48	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	946/968 (98%)	906 (96%)	40 (4%)	36 62

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	VAL
1	A	80	SER
1	A	84	VAL
1	A	91	LEU
1	A	146	SER
1	A	147	LYS
1	A	181	LEU
1	A	192	ILE
1	A	221	THR
1	A	291	THR
1	B	12	VAL
1	B	73	MET
1	B	91	LEU
1	B	102	ARG
1	B	122	LYS
1	B	128	ASP
1	B	165	ARG
1	B	181	LEU
1	B	196	SER
1	B	255	GLN
1	B	261	ARG
1	B	265	SER
1	C	73	MET
1	C	91	LEU
1	C	102	ARG
1	C	122	LYS
1	C	128	ASP
1	C	165	ARG
1	C	181	LEU
1	C	196	SER
1	C	255	GLN
1	C	261	ARG
1	C	265	SER
1	D	80	SER
1	D	84	VAL
1	D	146	SER
1	D	147	LYS

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Mol	Chain	Res	Type
1	D	181	LEU
1	D	192	ILE
1	D	291	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	255	GLN
1	B	255	GLN
1	C	150	GLN
1	C	211	ASN
1	C	255	GLN
1	D	138	ASN
1	D	263	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)

Of 4 non-standard protein/DNA/RNA residues modelled in this entry, 2 are modelled with single atom - leaving 2 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	$\#\|Z\| > 2$
2	GGL	E	2	2	5,8,9	0.77	0	2,9,11	0.56	0
2	GGL	F	2	2	5,8,9	0.87	0	2,9,11	1.62	1 (50%)

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	GGL	E	2	2	-	0/3/8/9	0/0/0/0
2	GGL	F	2	2	-	0/3/8/9	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	2	GGL	CB-CA-N	2.16	116.65	110.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	2	GGL	3	0
2	F	2	GGL	8	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

3 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	$\#\|Z\| > 2$
4	TAM	B	293	-	7,10,10	1.59	1 (14%)	9,12,12	2.32	4 (44%)
3	BME	B	400[A]	1	3,3,3	0.95	0	2,2,2	1.07	0
3	BME	B	400[B]	1	3,3,3	0.28	0	2,2,2	0.71	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
4	TAM	B	293	-	-	0/12/12/12	0/0/0/0
3	BME	B	400[A]	1	-	0/1/1/1	0/0/0/0
3	BME	B	400[B]	1	-	0/1/1/1	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	293	TAM	C1-C4	3.61	1.60	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	293	TAM	C3-C-N	-3.81	100.40	108.28
4	B	293	TAM	C3-C-C2	2.52	114.53	110.50
4	B	293	TAM	O5-C5-C2	3.04	118.08	111.14
4	B	293	TAM	O4-C4-C1	3.52	119.17	111.14

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, 95^{th} 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	283/293 (96%)	0.51	8 (2%) 56 61	30, 39, 57, 68	1 (0%)
1	B	285/293 (97%)	0.28	1 (0%) 93 93	28, 37, 48, 57	0
1	C	284/293 (96%)	1.24	70 (24%) 1 1	28, 37, 48, 57	1 (0%)
1	D	283/293 (96%)	0.69	17 (6%) 25 28	30, 39, 57, 68	0
2	E	0/6	-	-	-	-
2	F	0/6	-	-	-	-
All	All	1135/1184 (95%)	0.68	96 (8%) 13 14	28, 38, 53, 68	2 (0%)

All (96) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	292	GLY	7.7
1	C	270	PHE	6.7
1	C	126	ALA	6.2
1	D	188	PRO	6.2
1	D	189	GLY	5.8
1	C	255	GLN	5.6
1	C	132	ALA	5.4
1	C	292	GLY	5.3
1	C	48	LEU	5.2
1	D	199	THR	5.2
1	D	39	SER	5.1
1	C	134	ILE	5.0
1	D	38	ARG	5.0
1	C	61	LEU	4.7
1	C	60	VAL	4.6
1	D	40	ARG	4.6
1	C	274	ARG	4.5
1	C	259	GLY	4.5
1	C	128	ASP	4.5

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Mol	Chain	Res	Type	RSRZ
1	C	125	PRO	4.5
1	C	186	ALA	4.4
1	C	135	CYS	4.4
1	C	197	ASP	4.3
1	D	197	ASP	4.2
1	D	235	PHE	4.2
1	C	52	LEU	4.1
1	C	136	LEU	4.1
1	C	44	TYR	3.9
1	C	169	LEU	3.8
1	A	192	ILE	3.8
1	C	198	LEU	3.6
1	C	73	MET	3.6
1	C	284	PHE	3.4
1	C	75	VAL	3.4
1	C	34	ILE	3.3
1	C	257	ALA	3.3
1	C	47	TRP	3.3
1	C	81	VAL	3.3
1	D	198	LEU	3.2
1	C	279	TYR	3.2
1	A	222	VAL	3.1
1	C	53	ARG	3.1
1	C	70	ASP	3.0
1	C	37	THR	2.9
1	C	56	GLY	2.8
1	C	130	PHE	2.8
1	D	44	TYR	2.8
1	B	292	GLY	2.8
1	C	74	LEU	2.7
1	C	272	PRO	2.7
1	C	40	ARG	2.7
1	C	79	PHE	2.7
1	C	286	HIS	2.7
1	C	111	VAL	2.6
1	C	83	SER	2.6
1	C	91	LEU	2.6
1	D	194	TYR	2.6
1	D	234	GLY	2.5
1	C	283	TYR	2.5
1	A	28	ARG	2.5
1	C	110	TRP	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	261	ARG	2.5
1	C	262	CYS	2.5
1	C	196	SER	2.5
1	C	170	LEU	2.4
1	D	248	ALA	2.4
1	C	287	VAL	2.4
1	C	109	LYS	2.4
1	C	260	GLY	2.4
1	D	5	TYR	2.4
1	C	133	VAL	2.4
1	C	267	LEU	2.4
1	C	172	ILE	2.4
1	D	193	TYR	2.3
1	C	224	VAL	2.3
1	C	45	LYS	2.3
1	C	72	ILE	2.3
1	A	182	SER	2.3
1	C	38	ARG	2.3
1	C	202	ILE	2.2
1	C	95	LEU	2.2
1	C	181	LEU	2.2
1	A	292	GLY	2.2
1	A	224	VAL	2.2
1	A	235	PHE	2.2
1	D	34	ILE	2.1
1	C	200	LYS	2.1
1	C	180	ILE	2.1
1	C	82	THR	2.1
1	C	223	GLN	2.1
1	C	51	LEU	2.1
1	C	90	MET	2.0
1	C	192	ILE	2.0
1	C	264	HIS	2.0
1	A	198	LEU	2.0
1	C	101	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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	GGL	E	2	9/10	0.74	0.30	-	95,96,98,98	0
2	GGL	F	3	1/10	0.30	0.68	-	98,98,98,98	0
2	GGL	E	3	1/10	0.78	0.14	-	99,99,99,99	0
2	GGL	F	2	9/10	0.70	0.47	-	96,97,99,99	0

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, 95^{th} 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
3	BME	B	400[B]	4/4	0.64	0.35	4.60	33,40,45,52	4
3	BME	B	400[A]	4/4	0.64	0.35	4.18	43,45,45,50	4
4	TAM	B	293	11/11	0.66	0.30	3.40	62,67,68,72	0

6.5 Other polymers (i)

There are no such residues in this entry.