



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2020 – 11:20 PM BST

PDB ID : 6BMI
Title : Crystal Structure of GltPh R397C in complex with L-Serine
Authors : Font, J.; Scopelliti, A.J.; Vandenberg, R.J.; Boudker, O.; Ryan, R.M.
Deposited on : 2017-11-14
Resolution : 3.90 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.14.4.dev1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

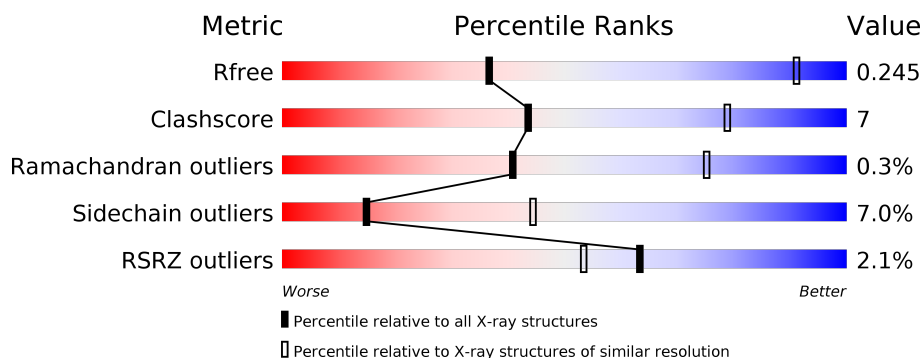
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1002 (4.14-3.66)
Clashscore	141614	1004 (4.12-3.68)
Ramachandran outliers	138981	1021 (4.14-3.66)
Sidechain outliers	138945	1014 (4.14-3.66)
RSRZ outliers	127900	1275 (4.20-3.60)

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 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	420	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>18%</div> <div>• 6%</div> </div> </div>
1	B	420	<div> <div>4%</div> <div> <div></div> <div>76%</div> <div>16%</div> <div>• 6%</div> </div> </div>
1	C	420	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>19%</div> <div>• •</div> </div> </div>

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
3	SER	A	502	-	-	-	X
3	SER	B	502	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8893 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 Glutamate transporter homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	S	0	0	0
			2935	1936	462	519	18			
1	B	396	Total	C	N	O	S	0	0	0
			2935	1936	462	519	18			
1	C	408	Total	C	N	O	S	0	0	0
			3001	1976	474	533	18			

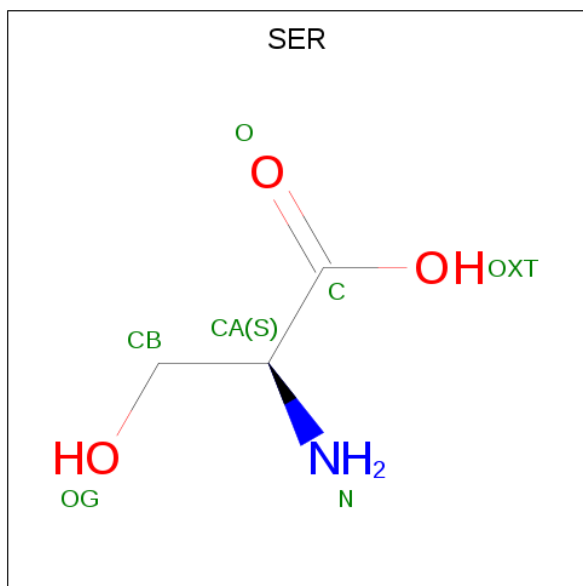
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	397	CYS	ARG	engineered mutation	UNP O59010
A	418	THR	-	expression tag	UNP O59010
A	419	LEU	-	expression tag	UNP O59010
A	420	VAL	-	expression tag	UNP O59010
B	397	CYS	ARG	engineered mutation	UNP O59010
B	418	THR	-	expression tag	UNP O59010
B	419	LEU	-	expression tag	UNP O59010
B	420	VAL	-	expression tag	UNP O59010
C	397	CYS	ARG	engineered mutation	UNP O59010
C	418	THR	-	expression tag	UNP O59010
C	419	LEU	-	expression tag	UNP O59010
C	420	VAL	-	expression tag	UNP O59010

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Na	0	0
			1	1		
2	A	1	Total	Na	0	0
			1	1		
2	C	2	Total	Na	0	0
			2	2		

- Molecule 3 is SERINE (three-letter code: SER) (formula: $C_3H_7NO_3$).

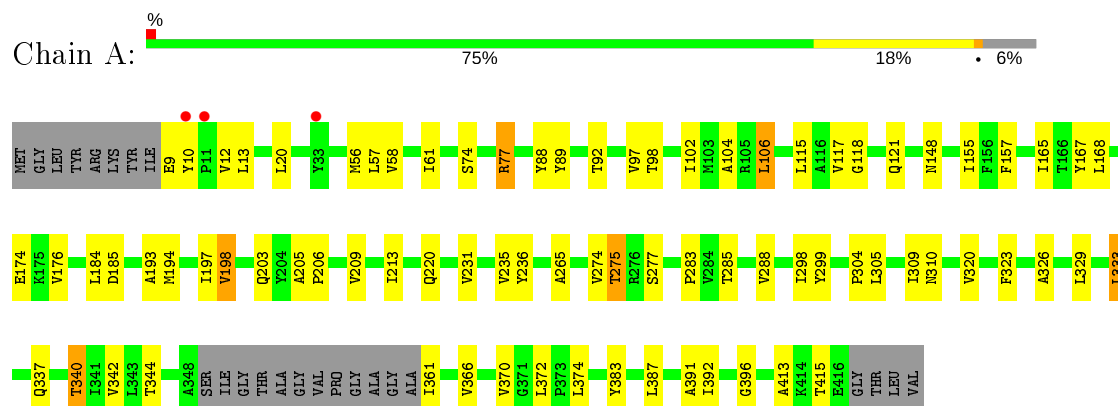


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			6	3	1	2		
3	B	1	Total	C	N	O	0	0
			6	3	1	2		
3	C	1	Total	C	N	O	0	0
			6	3	1	2		

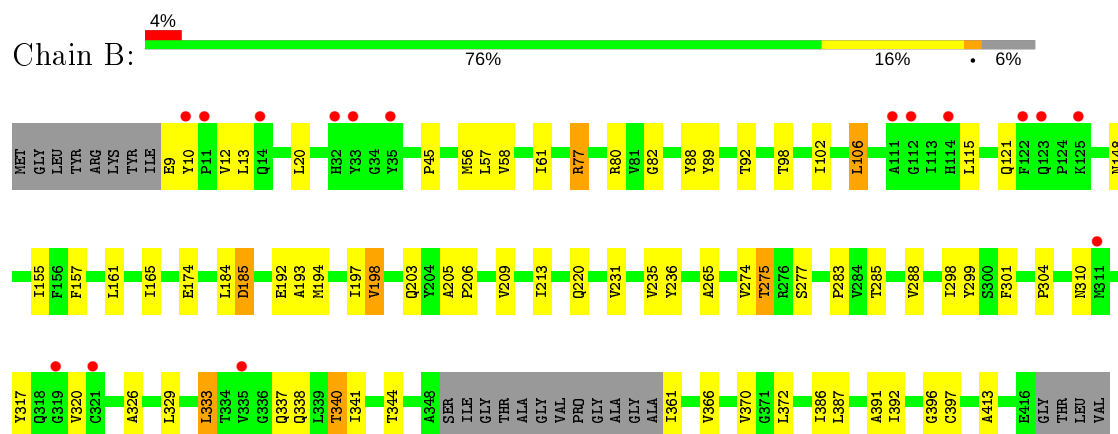
3 Residue-property plots [i](#)

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.

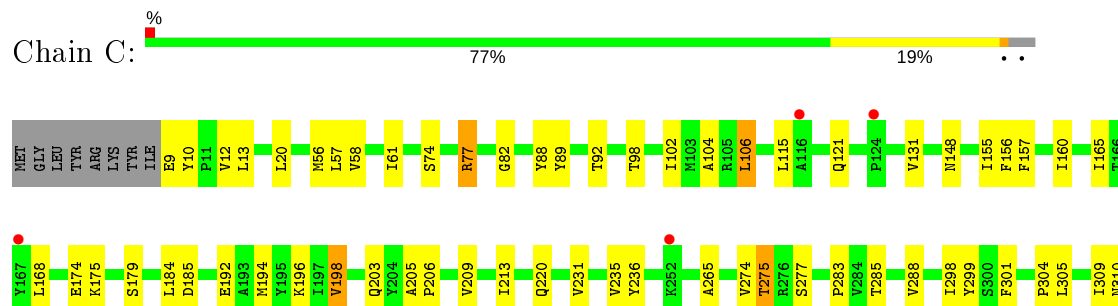
• Molecule 1: Glutamate transporter homolog

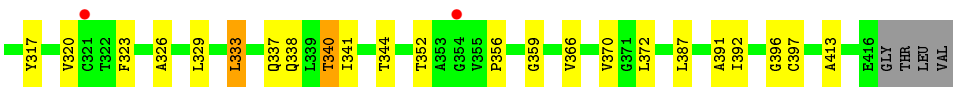


• Molecule 1: Glutamate transporter homolog



• Molecule 1: Glutamate transporter homolog





4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	114.75Å 114.75Å 322.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.90 19.88 – 3.90	Depositor EDS
% Data completeness (in resolution range)	95.0 (20.00-3.90) 95.0 (19.88-3.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 3.94Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.227 , 0.248 0.228 , 0.245	Depositor DCC
R_{free} test set	1025 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	160.7	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 109.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.077 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8893	wwPDB-VP
Average B, all atoms (Å ²)	182.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
NA

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	0/2985	0.54	0/4067
1	B	0.37	0/2985	0.51	0/4067
1	C	0.38	0/3053	0.51	0/4162
All	All	0.39	0/9023	0.52	0/12296

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

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	2935	0	3123	44	0
1	B	2935	0	3123	42	0
1	C	3001	0	3190	50	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
3	A	6	0	4	0	0
3	B	6	0	4	0	0
3	C	6	0	4	0	0
All	All	8893	0	9448	123	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 7.

All (123) 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:275:THR:HG23	1:A:277:SER:H	1.47	0.79
1:A:235:VAL:HG22	1:A:320:VAL:HG11	1.64	0.77
1:B:275:THR:HG23	1:B:277:SER:H	1.47	0.77
1:C:275:THR:HG23	1:C:277:SER:H	1.49	0.75
1:C:235:VAL:HG22	1:C:320:VAL:HG11	1.68	0.75
1:C:337:GLN:O	1:C:340:THR:HG22	1.90	0.71
1:B:235:VAL:HG22	1:B:320:VAL:HG11	1.72	0.71
1:B:155:ILE:HD11	1:B:304:PRO:HB2	1.72	0.71
1:B:337:GLN:O	1:B:340:THR:HG22	1.91	0.71
1:A:337:GLN:O	1:A:340:THR:HG22	1.91	0.70
1:A:155:ILE:HD11	1:A:304:PRO:HB2	1.74	0.69
1:A:61:ILE:HG13	1:A:194:MET:HB3	1.76	0.68
1:C:155:ILE:HD11	1:C:304:PRO:HB2	1.75	0.67
1:B:61:ILE:HG13	1:B:194:MET:HB3	1.77	0.66
1:A:236:TYR:HE1	1:A:396:GLY:HA3	1.59	0.66
1:C:61:ILE:HG13	1:C:194:MET:HB3	1.78	0.66
1:A:209:VAL:HG13	1:A:274:VAL:HG21	1.79	0.65
1:B:209:VAL:HG13	1:B:274:VAL:HG21	1.79	0.64
1:A:157:PHE:HD1	1:C:56:MET:HE2	1.61	0.64
1:C:209:VAL:HG13	1:C:274:VAL:HG21	1.79	0.63
1:C:12:VAL:HG11	1:C:203:GLN:HE21	1.63	0.63
1:C:352:THR:HG23	1:C:359:GLY:HA2	1.80	0.62
1:C:265:ALA:HA	1:C:288:VAL:HG11	1.81	0.62
1:C:61:ILE:CG1	1:C:194:MET:HB3	2.29	0.62
1:A:298:ILE:HD13	1:A:413:ALA:HA	1.82	0.61
1:B:61:ILE:CG1	1:B:194:MET:HB3	2.32	0.60
1:B:298:ILE:HD13	1:B:413:ALA:HA	1.84	0.59
1:B:236:TYR:HE1	1:B:396:GLY:HA3	1.66	0.59
1:C:12:VAL:HG11	1:C:203:GLN:NE2	2.19	0.58
1:A:61:ILE:CG1	1:A:194:MET:HB3	2.34	0.58
1:B:12:VAL:HG11	1:B:203:GLN:HE21	1.66	0.58
1:B:265:ALA:HA	1:B:288:VAL:HG11	1.84	0.58
1:A:157:PHE:HD1	1:C:56:MET:CE	2.17	0.58
1:C:236:TYR:HE1	1:C:396:GLY:HA3	1.69	0.57
1:A:12:VAL:HG11	1:A:203:GLN:HE21	1.68	0.57
1:C:57:LEU:HD13	1:C:198:VAL:HG12	1.86	0.57
1:B:165:ILE:HG21	1:B:184:LEU:HB2	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:ALA:HA	1:A:288:VAL:HG11	1.87	0.57
1:C:298:ILE:HD13	1:C:413:ALA:HA	1.87	0.57
1:A:89:TYR:CG	1:A:310:ASN:HB2	2.40	0.56
1:C:165:ILE:HG21	1:C:184:LEU:HB2	1.87	0.56
1:A:165:ILE:HG21	1:A:184:LEU:HB2	1.87	0.56
1:C:89:TYR:CG	1:C:310:ASN:HB2	2.42	0.54
1:B:57:LEU:HD13	1:B:198:VAL:HG12	1.87	0.54
1:B:89:TYR:CG	1:B:310:ASN:HB2	2.42	0.54
1:A:89:TYR:CD1	1:A:310:ASN:HB2	2.43	0.53
1:B:20:LEU:O	1:B:213:ILE:HD11	2.07	0.53
1:C:20:LEU:O	1:C:213:ILE:HD11	2.08	0.53
1:B:56:MET:HE2	1:C:157:PHE:HD1	1.73	0.52
1:B:89:TYR:CD1	1:B:310:ASN:HB2	2.44	0.52
1:A:57:LEU:HD13	1:A:198:VAL:HG12	1.91	0.52
1:A:20:LEU:O	1:A:213:ILE:HD11	2.10	0.52
1:B:220:GLN:HE22	1:B:391:ALA:N	2.08	0.52
1:B:12:VAL:HG11	1:B:203:GLN:NE2	2.24	0.51
1:A:209:VAL:HA	1:A:274:VAL:HG11	1.93	0.51
1:B:88:TYR:CZ	1:B:92:THR:HG21	2.45	0.51
1:A:12:VAL:HG11	1:A:203:GLN:NE2	2.25	0.51
1:C:205:ALA:N	1:C:206:PRO:HD2	2.26	0.50
1:B:220:GLN:HE22	1:B:391:ALA:H	1.59	0.50
1:C:89:TYR:CD1	1:C:310:ASN:HB2	2.46	0.50
1:B:209:VAL:HA	1:B:274:VAL:HG11	1.93	0.50
1:A:102:ILE:O	1:A:106:LEU:HB2	2.12	0.50
1:A:88:TYR:CZ	1:A:92:THR:HG21	2.47	0.49
1:B:205:ALA:N	1:B:206:PRO:HD2	2.27	0.49
1:C:88:TYR:CZ	1:C:92:THR:HG21	2.48	0.49
1:B:58:VAL:HG22	1:B:283:PRO:HD3	1.95	0.49
1:B:45:PRO:HG3	1:C:131:VAL:HG21	1.95	0.49
1:C:209:VAL:HA	1:C:274:VAL:HG11	1.96	0.48
1:A:167:TYR:HB3	1:C:196:LYS:HE2	1.96	0.48
1:A:58:VAL:HG22	1:A:283:PRO:HD3	1.94	0.48
1:A:205:ALA:N	1:A:206:PRO:HD2	2.29	0.48
1:C:220:GLN:HE22	1:C:391:ALA:N	2.12	0.48
1:C:102:ILE:O	1:C:106:LEU:HB2	2.14	0.47
1:A:220:GLN:HE22	1:A:391:ALA:N	2.11	0.47
1:A:56:MET:HE2	1:B:157:PHE:HD1	1.78	0.47
1:A:168:LEU:HD21	1:C:192:GLU:HB2	1.96	0.47
1:B:102:ILE:O	1:B:106:LEU:HB2	2.15	0.46
1:C:58:VAL:HG22	1:C:283:PRO:HD3	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:LEU:HD21	1:C:192:GLU:CB	2.46	0.46
1:A:236:TYR:CE1	1:A:396:GLY:HA3	2.47	0.46
1:A:193:ALA:O	1:A:197:ILE:HG13	2.15	0.46
1:B:77:ARG:HG3	1:B:80:ARG:HH22	1.80	0.45
1:A:235:VAL:HG22	1:A:320:VAL:CG1	2.39	0.45
1:C:235:VAL:HG22	1:C:320:VAL:CG1	2.43	0.45
1:B:231:VAL:O	1:B:235:VAL:HG23	2.17	0.45
1:B:56:MET:CE	1:C:157:PHE:HD1	2.29	0.45
1:B:185:ASP:OD1	1:C:175:LYS:HE2	2.16	0.44
1:B:192:GLU:HB2	1:C:168:LEU:HD21	2.00	0.44
1:A:333:LEU:HA	1:A:337:GLN:OE1	2.17	0.44
1:C:231:VAL:O	1:C:235:VAL:HG23	2.17	0.44
1:B:185:ASP:O	1:C:179:SER:HB2	2.18	0.44
1:A:117:VAL:HG12	1:A:118:GLY:N	2.32	0.44
1:A:344:THR:HB	1:A:366:VAL:HG23	1.99	0.44
1:B:338:GLN:HA	1:B:341:ILE:HD12	2.00	0.44
1:C:220:GLN:HE22	1:C:391:ALA:H	1.65	0.44
1:C:344:THR:HB	1:C:366:VAL:HG23	1.99	0.43
1:C:338:GLN:HA	1:C:341:ILE:HD12	2.00	0.43
1:B:333:LEU:HA	1:B:337:GLN:OE1	2.18	0.43
1:A:176:VAL:HG22	1:C:192:GLU:OE1	2.18	0.43
1:B:344:THR:HB	1:B:366:VAL:HG23	2.01	0.43
1:C:333:LEU:HA	1:C:337:GLN:OE1	2.19	0.42
1:C:74:SER:HB2	1:C:77:ARG:HB2	2.01	0.42
1:B:317:TYR:HB2	1:B:397:CYS:SG	2.59	0.42
1:B:386:ILE:HA	1:B:386:ILE:HD13	1.90	0.42
1:A:305:LEU:HG	1:A:309:ILE:HD12	2.01	0.42
1:B:326:ALA:CB	1:B:333:LEU:HD11	2.50	0.42
1:A:220:GLN:HE22	1:A:391:ALA:H	1.68	0.42
1:B:161:LEU:O	1:B:165:ILE:HG12	2.20	0.42
1:A:74:SER:HB2	1:A:77:ARG:HB2	2.01	0.42
1:C:326:ALA:CB	1:C:333:LEU:HD11	2.50	0.41
1:A:97:VAL:HG11	1:A:342:VAL:HA	2.02	0.41
1:B:193:ALA:O	1:B:197:ILE:HG13	2.20	0.41
1:A:231:VAL:O	1:A:235:VAL:HG23	2.21	0.41
1:A:104:ALA:HB1	1:A:323:PHE:CB	2.51	0.41
1:A:374:LEU:HD11	1:A:383:TYR:CD1	2.56	0.41
1:B:82:GLY:HA2	1:B:301:PHE:HE1	1.85	0.41
1:C:82:GLY:HA2	1:C:301:PHE:HE1	1.86	0.41
1:C:317:TYR:HB2	1:C:397:CYS:SG	2.61	0.40
1:C:156:PHE:O	1:C:160:ILE:HG12	2.20	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:305:LEU:HG	1:C:309:ILE:HD12	2.03	0.40
1:C:104:ALA:HB1	1:C:323:PHE:CB	2.52	0.40
1:A:326:ALA:CB	1:A:333:LEU:HD11	2.52	0.40
1:C:352:THR:HG23	1:C:359:GLY:CA	2.50	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	392/420 (93%)	380 (97%)	11 (3%)	1 (0%)	41	75
1	B	392/420 (93%)	382 (97%)	9 (2%)	1 (0%)	41	75
1	C	406/420 (97%)	392 (97%)	12 (3%)	2 (0%)	29	67
All	All	1190/1260 (94%)	1154 (97%)	32 (3%)	4 (0%)	41	75

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	356	PRO
1	B	10	TYR
1	A	10	TYR
1	C	10	TYR

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	311/328 (95%)	288 (93%)	23 (7%)	13	43
1	B	311/328 (95%)	289 (93%)	22 (7%)	14	44
1	C	316/328 (96%)	295 (93%)	21 (7%)	16	46
All	All	938/984 (95%)	872 (93%)	66 (7%)	15	44

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	GLU
1	A	13	LEU
1	A	77	ARG
1	A	98	THR
1	A	106	LEU
1	A	115	LEU
1	A	121	GLN
1	A	148	ASN
1	A	174	GLU
1	A	185	ASP
1	A	198	VAL
1	A	275	THR
1	A	285	THR
1	A	299	TYR
1	A	329	LEU
1	A	333	LEU
1	A	340	THR
1	A	361	ILE
1	A	370	VAL
1	A	372	LEU
1	A	387	LEU
1	A	392	ILE
1	A	415	THR
1	B	9	GLU
1	B	13	LEU
1	B	77	ARG
1	B	98	THR
1	B	106	LEU
1	B	115	LEU
1	B	121	GLN
1	B	148	ASN
1	B	174	GLU
1	B	185	ASP
1	B	198	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	275	THR
1	B	285	THR
1	B	299	TYR
1	B	329	LEU
1	B	333	LEU
1	B	340	THR
1	B	361	ILE
1	B	370	VAL
1	B	372	LEU
1	B	387	LEU
1	B	392	ILE
1	C	9	GLU
1	C	13	LEU
1	C	77	ARG
1	C	98	THR
1	C	106	LEU
1	C	115	LEU
1	C	121	GLN
1	C	148	ASN
1	C	174	GLU
1	C	185	ASP
1	C	198	VAL
1	C	275	THR
1	C	285	THR
1	C	299	TYR
1	C	329	LEU
1	C	333	LEU
1	C	340	THR
1	C	370	VAL
1	C	372	LEU
1	C	387	LEU
1	C	392	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	203	GLN
1	A	220	GLN
1	A	327	ASN
1	B	14	GLN
1	B	203	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	220	GLN
1	B	327	ASN
1	B	338	GLN
1	C	14	GLN
1	C	203	GLN
1	C	220	GLN
1	C	327	ASN
1	C	338	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 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	SER	A	502	-	4,5,6	0.49	0	0,5,7	0.00	-
3	SER	B	502	-	4,5,6	0.52	0	0,5,7	0.00	-
3	SER	C	503	-	4,5,6	0.49	0	0,5,7	0.00	-

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	SER	A	502	-	-	0/2/4/6	-
3	SER	B	502	-	-	0/2/4/6	-
3	SER	C	503	-	-	0/2/4/6	-

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	396/420 (94%)	-0.51	3 (0%) 86 79	112, 143, 186, 219	0
1	B	396/420 (94%)	-0.32	16 (4%) 38 30	132, 199, 260, 288	0
1	C	408/420 (97%)	-0.42	6 (1%) 73 64	141, 199, 263, 300	0
All	All	1200/1260 (95%)	-0.42	25 (2%) 63 53	112, 178, 253, 300	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	321	CYS	4.4
1	B	311	MET	3.8
1	C	321	CYS	3.7
1	B	33	TYR	3.6
1	A	11	PRO	3.5
1	B	111	ALA	3.5
1	B	11	PRO	3.4
1	B	10	TYR	3.3
1	B	112	GLY	3.1
1	B	35	TYR	2.8
1	B	319	GLY	2.7
1	B	114	HIS	2.4
1	C	354	GLY	2.4
1	A	33	TYR	2.4
1	A	10	TYR	2.3
1	B	123	GLN	2.3
1	B	32	HIS	2.2
1	C	124	PRO	2.1
1	B	335	VAL	2.1
1	B	125	LYS	2.1
1	C	252	LYS	2.1
1	B	14	GLN	2.1
1	C	116	ALA	2.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	167	TYR	2.0
1	B	122	PHE	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 monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SER	B	502	6/7	0.62	0.56	161,164,165,167	0
3	SER	A	502	6/7	0.80	0.51	121,121,121,122	0
2	NA	B	501	1/1	0.81	0.50	150,150,150,150	0
3	SER	C	503	6/7	0.92	0.45	158,161,164,167	0
2	NA	C	502	1/1	0.93	0.17	130,130,130,130	0
2	NA	C	501	1/1	0.97	0.27	152,152,152,152	0
2	NA	A	501	1/1	1.00	0.30	99,99,99,99	0

6.5 Other polymers [i](#)

There are no such residues in this entry.