Full wwPDB X-ray Structure Validation Report ⓘ

Jan 4, 2025 – 09:02 AM EST

PDB ID	:	2JFQ
Title	:	Crystal structure of Staphylococcus aureus glutamate racemase in complex with D- Glutamate
Authors	:	Lundqvist, T.
Deposited on	:	2007-02-04
Resolution	:	2.15 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 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:

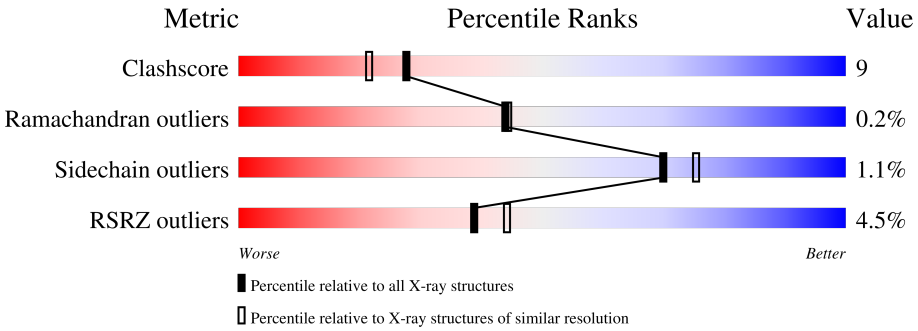
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 2.15 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))
Clashscore	180529	2047 (2.16-2.16)
Ramachandran outliers	177936	2027 (2.16-2.16)
Sidechain outliers	177891	2026 (2.16-2.16)
RSRZ outliers	164620	1882 (2.16-2.16)

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 <=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	286	5%, 76%, 16%, • 7%
1	B	286	3%, 75%, 17%, • 7%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4313 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.

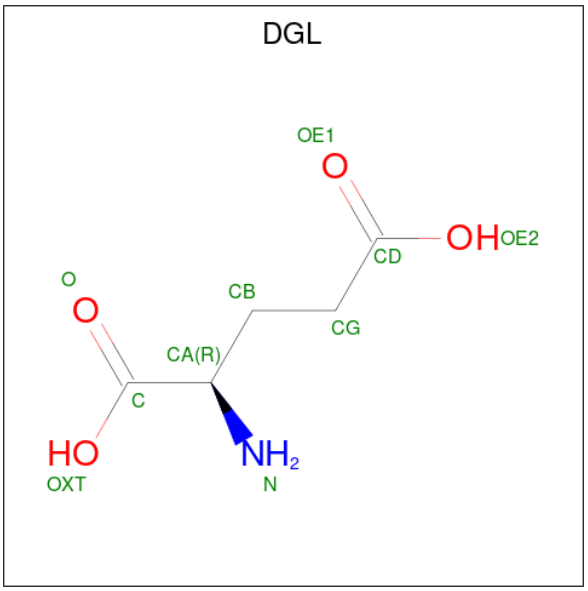
- Molecule 1 is a protein called GLUTAMATE RACEMASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	0	1
			2080	1322	360	388	10			
1	B	266	Total	C	N	O	S	0	0	1
			2080	1322	360	388	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	90	SER	PRO	conflict	UNP Q6GHT5
B	90	SER	PRO	conflict	UNP Q6GHT5

- Molecule 2 is D-GLUTAMIC ACID (three-letter code: DGL) (formula: $C_5H_9NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	5	1	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 3 is water.

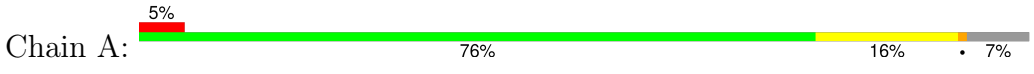
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	72	Total	O	0	0
			72	72		
3	B	61	Total	O	0	0
			61	61		

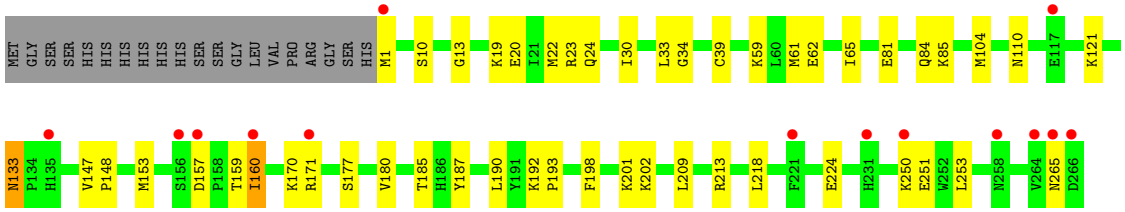
3 Residue-property plots (i)

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 RACEMASE

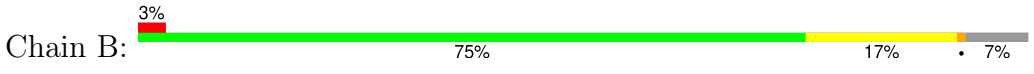
Chain A:

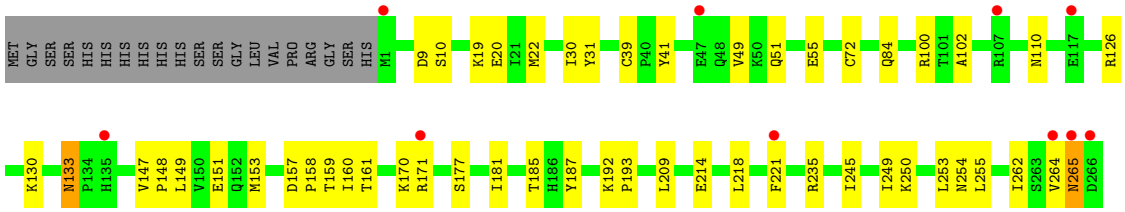




• Molecule 1: GLUTAMATE RACEMASE

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	96.43Å 88.87Å 96.56Å 90.00° 109.00° 90.00°	Depositor
Resolution (Å)	34.00 – 2.15 34.00 – 2.15	Depositor EDS
% Data completeness (in resolution range)	(Not available) (34.00-2.15) 99.2 (34.00-2.15)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.18 (at 2.13Å)	Xtriage
Refinement program	CNX 2000.2	Depositor
R, R_{free}	0.202 , 0.229 0.201 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	23.0	Xtriage
Anisotropy	0.322	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 46.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4313	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.71% 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, 0.333 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: DGL

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	0.58	3/2123 (0.1%)	0.61	0/2887
1	B	0.47	3/2123 (0.1%)	0.62	2/2887 (0.1%)
All	All	0.53	6/4246 (0.1%)	0.61	2/5774 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	159	THR	C-N	-17.60	0.93	1.34
1	B	159	THR	C-N	-12.82	1.04	1.34
1	A	84	GLN	C-N	-9.01	1.13	1.34
1	A	160	ILE	C-N	-8.73	1.14	1.34
1	B	160	ILE	C-N	-5.98	1.20	1.34
1	B	84	GLN	C-N	-5.79	1.20	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	160	ILE	O-C-N	-7.74	110.32	122.70
1	B	160	ILE	CA-C-N	6.15	130.74	117.20

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	2080	0	2107	44	0
1	B	2080	0	2108	34	0
2	A	10	0	7	0	0
2	B	10	0	7	1	0
3	A	72	0	0	2	0
3	B	61	0	0	0	0
All	All	4313	0	4229	75	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 9.

All (75) 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:157:ASP:OD1	1:A:160:ILE:HD12	1.61	1.00
1:A:20:GLU:HG2	1:A:209:LEU:HA	1.49	0.93
1:B:170:LYS:HG3	1:B:171:ARG:HD2	1.53	0.91
1:A:198:PHE:O	1:A:201:LYS:HG2	1.80	0.82
1:A:250:LYS:HD2	3:A:2065:HOH:O	1.82	0.79
1:A:170:LYS:HG3	1:A:171:ARG:HD2	1.67	0.76
1:B:110:ASN:HB3	1:B:177:SER:HA	1.68	0.75
1:A:153:MET:HE1	1:A:251:GLU:HG2	1.71	0.72
1:A:19:LYS:HB2	1:A:253:LEU:CD2	2.23	0.68
1:A:20:GLU:HG3	1:A:24:GLN:HE21	1.57	0.68
1:A:192:LYS:HB3	1:A:193:PRO:HD3	1.80	0.64
1:A:157:ASP:OD1	1:A:160:ILE:CD1	2.43	0.64
1:B:192:LYS:HB3	1:B:193:PRO:HD3	1.81	0.62
1:A:20:GLU:HG3	1:A:24:GLN:NE2	2.16	0.59
1:A:180:VAL:CG2	1:A:202:LYS:HD3	2.34	0.58
1:A:147:VAL:HB	1:A:148:PRO:HD3	1.86	0.58
1:A:170:LYS:HD2	1:A:171:ARG:NH1	2.20	0.57
1:A:19:LYS:HB2	1:A:253:LEU:HD22	1.85	0.57
1:A:20:GLU:CG	1:A:24:GLN:HE21	2.20	0.55
1:A:177:SER:O	1:A:202:LYS:HE3	2.07	0.55
1:A:61:MET:HG2	1:A:65:ILE:HD11	1.89	0.55
1:A:59:LYS:HD2	1:A:62:GLU:OE2	2.06	0.54
1:A:190:LEU:O	1:A:193:PRO:HD2	2.09	0.52
1:B:100:ARG:HB2	1:B:100:ARG:NH1	2.25	0.51
1:A:20:GLU:OE1	1:A:23:ARG:NH1	2.44	0.51
1:B:10:SER:O	1:B:39:CYS:HB3	2.10	0.51
1:B:250:LYS:O	1:B:254:ASN:HA	2.11	0.51
1:A:22:MET:HA	3:A:2004:HOH:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:MET:HG3	1:B:30:ILE:HD12	1.93	0.50
1:A:153:MET:CE	1:A:251:GLU:HG2	2.39	0.50
1:A:10:SER:O	1:A:39:CYS:HB3	2.11	0.49
1:B:147:VAL:HB	1:B:148:PRO:HD3	1.93	0.49
1:A:20:GLU:OE1	1:A:209:LEU:HD12	2.13	0.49
1:A:110:ASN:HB3	1:A:177:SER:HA	1.95	0.49
1:A:170:LYS:HG3	1:A:171:ARG:N	2.29	0.48
1:A:187:TYR:CD1	1:A:187:TYR:N	2.82	0.48
1:B:31:TYR:CZ	1:B:235:ARG:HD3	2.49	0.48
1:B:157:ASP:O	1:B:161:THR:HG23	2.13	0.48
1:B:19:LYS:HB2	1:B:253:LEU:CD2	2.44	0.48
1:B:51:GLN:O	1:B:55:GLU:HG3	2.13	0.47
1:B:187:TYR:CD1	1:B:187:TYR:N	2.83	0.47
1:B:133:ASN:C	1:B:133:ASN:HD22	2.18	0.47
1:B:100:ARG:NH1	1:B:214:GLU:OE1	2.48	0.46
1:A:33:LEU:HD23	1:A:34:GLY:N	2.30	0.46
1:B:149:LEU:HG	1:B:153:MET:HE3	1.99	0.45
1:A:213:ARG:HH11	1:A:213:ARG:HG2	1.80	0.45
1:A:30:ILE:HD12	1:A:30:ILE:N	2.31	0.44
1:B:102:ALA:HB2	1:B:181:ILE:HD11	2.00	0.44
1:A:190:LEU:C	1:A:193:PRO:HD2	2.38	0.44
1:B:262:ILE:C	1:B:262:ILE:HD12	2.38	0.44
1:A:104:MET:HE3	1:B:209:LEU:O	2.17	0.44
1:B:264:VAL:O	1:B:265:ASN:C	2.55	0.44
1:B:253:LEU:O	1:B:255:LEU:HD13	2.18	0.44
1:A:33:LEU:HD23	1:A:33:LEU:C	2.39	0.44
1:A:81:GLU:CG	1:A:85:LYS:HE2	2.48	0.43
1:B:100:ARG:HH11	1:B:100:ARG:CB	2.32	0.43
1:A:13:GLY:C	1:A:185:THR:HB	2.39	0.43
1:A:218:LEU:HD11	1:B:221:PHE:CE1	2.54	0.42
1:A:1:MET:HE2	1:A:224:GLU:OE1	2.19	0.42
1:B:185:THR:HG23	2:B:1267:DGL:O	2.20	0.42
1:A:133:ASN:C	1:A:133:ASN:HD22	2.23	0.42
1:A:198:PHE:CG	1:A:202:LYS:HD2	2.54	0.42
1:A:170:LYS:HD2	1:A:171:ARG:CZ	2.50	0.42
1:B:245:ILE:O	1:B:249:ILE:HG13	2.20	0.42
1:B:41:TYR:CD2	1:B:49:VAL:HG13	2.55	0.41
1:B:149:LEU:HG	1:B:153:MET:CE	2.49	0.41
1:B:157:ASP:HA	1:B:158:PRO:HD3	1.95	0.41
1:A:121:LYS:HE3	1:A:121:LYS:HB2	1.89	0.41
1:B:9:ASP:OD1	1:B:72:CYS:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:ARG:NH1	1:B:100:ARG:CB	2.83	0.41
1:B:126:ARG:O	1:B:130:LYS:HG2	2.20	0.41
1:A:104:MET:HE2	1:B:209:LEU:HG	2.03	0.40
1:B:20:GLU:HG3	1:B:209:LEU:HA	2.03	0.40
1:B:22:MET:HG3	1:B:30:ILE:CD1	2.51	0.40
1:A:81:GLU:HG2	1:A:85:LYS:HE2	2.02	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	264/286 (92%)	257 (97%)	7 (3%)	0	100	100
1	B	264/286 (92%)	254 (96%)	9 (3%)	1 (0%)	30	27
All	All	528/572 (92%)	511 (97%)	16 (3%)	1 (0%)	44	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	265	ASN

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	232/250 (93%)	230 (99%)	2 (1%)	75 81
1	B	232/250 (93%)	229 (99%)	3 (1%)	65 71
All	All	464/500 (93%)	459 (99%)	5 (1%)	70 75

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	133	ASN
1	A	265	ASN
1	B	133	ASN
1	B	151	GLU
1	B	218	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	133	ASN
1	A	135	HIS
1	A	139	HIS
1	A	166	HIS
1	A	244	HIS
1	A	265	ASN
1	B	133	ASN
1	B	139	HIS
1	B	166	HIS
1	B	247	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	$\#\|Z\| > 2$
2	DGL	A	1267	-	8,9,9	1.28	2 (25%)	8,11,11	1.19	0
2	DGL	B	1267	-	8,9,9	1.26	2 (25%)	8,11,11	1.14	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
2	DGL	A	1267	-	-	2/9/9/9	-
2	DGL	B	1267	-	-	2/9/9/9	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1267	DGL	OE2-CD	-2.59	1.22	1.30
2	A	1267	DGL	OE2-CD	-2.43	1.22	1.30
2	A	1267	DGL	O-C	2.16	1.28	1.22
2	B	1267	DGL	O-C	2.11	1.28	1.22

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1267	DGL	OE2-CD-CG-CB
2	A	1267	DGL	OE1-CD-CG-CB
2	B	1267	DGL	OE2-CD-CG-CB
2	B	1267	DGL	OE1-CD-CG-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1267	DGL	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3
1	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	160:ILE	C	161:THR	N	1.20
1	A	160:ILE	C	161:THR	N	1.14
1	A	84:GLN	C	85:LYS	N	1.13
1	B	159:THR	C	160:ILE	N	1.04
1	A	159:THR	C	160:ILE	N	0.93

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	266/286 (93%)	-0.05	14 (5%)	33	38	12, 23, 44, 73	0
1	B	266/286 (93%)	0.09	10 (3%)	44	50	14, 26, 45, 75	0
All	All	532/572 (93%)	0.02	24 (4%)	39	44	12, 24, 45, 75	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	266	ASP	3.5
1	A	266	ASP	3.3
1	B	221	PHE	3.2
1	B	265	ASN	3.2
1	A	1	MET	3.1
1	A	265	ASN	3.0
1	B	1	MET	2.9
1	B	171	ARG	2.9
1	A	160	ILE	2.8
1	B	264	VAL	2.7
1	A	231	HIS	2.6
1	A	117	GLU	2.5
1	B	135	HIS	2.5
1	B	107	ARG	2.5
1	B	117	GLU	2.5
1	A	171	ARG	2.5
1	A	264	VAL	2.5
1	A	221	PHE	2.4
1	A	135	HIS	2.4
1	A	250	LYS	2.3
1	A	258	ASN	2.2
1	A	156	SER	2.1
1	A	157	ASP	2.1
1	B	47	GLU	2.1

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, 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	B-factors(Å^2)	Q<0.9
2	DGL	A	1267	10/10	0.95	0.07	16,18,20,20	0
2	DGL	B	1267	10/10	0.97	0.07	19,21,22,23	0

6.5 Other polymers (i)

There are no such residues in this entry.