



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:56 PM GMT

PDB ID : 4QFN
Title : Crystal structure of dipeptide binding protein from pseudoalteromonas sp. SM9913 in complex with Gly-Glu
Authors : Li, C.Y.; Zhang, Y.Z.
Deposited on : 2014-05-21
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 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

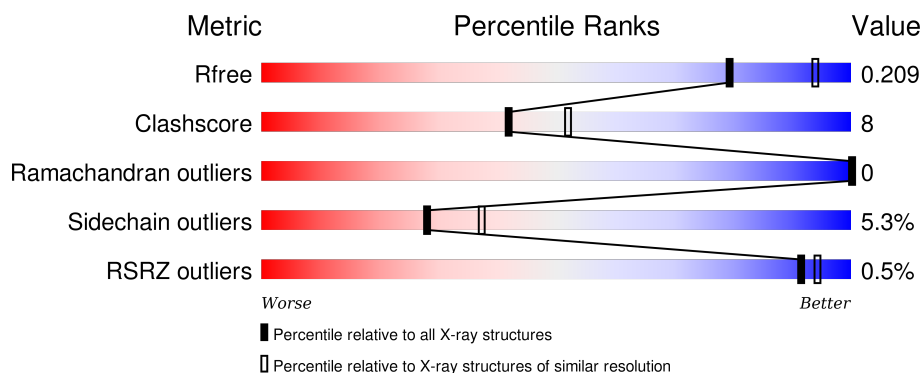
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	541	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; bottom: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 10px; background: linear-gradient(to right, red 77%, orange 77%, yellow 87%, green 97%, grey 100%);"></div> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px; background: linear-gradient(to right, red 77%, orange 77%, yellow 87%, green 97%, grey 100%);"></div> <div style="position: absolute; top: 0; left: 77%; width: 23%;"></div> <div style="position: absolute; top: 0; left: 87%; width: 10%;"></div> <div style="position: absolute; top: 0; left: 97%; width: 3%;"></div> <div style="position: absolute; top: 0; left: 99%; width: 1%;"></div> </div> <div>77% 15% • 6%</div> </div>
1	B	541	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; bottom: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 10px; background: linear-gradient(to right, red 76%, orange 76%, yellow 92%, green 100%, grey 100%);"></div> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px; background: linear-gradient(to right, red 76%, orange 76%, yellow 92%, green 100%, grey 100%);"></div> <div style="position: absolute; top: 0; left: 76%; width: 24%;"></div> <div style="position: absolute; top: 0; left: 92%; width: 8%;"></div> <div style="position: absolute; top: 0; left: 100%; width: 0%;"></div> <div style="position: absolute; top: 0; left: 100%; width: 0%;"></div> </div> <div>76% 16% • 6%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8864 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.

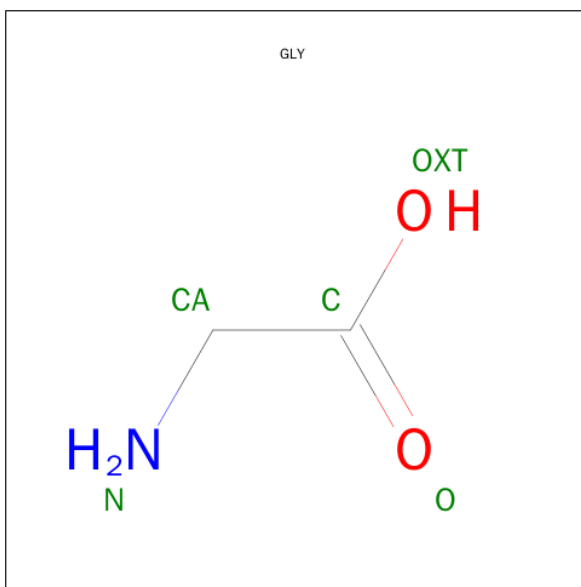
- Molecule 1 is a protein called ABC transporter periplasmic peptide-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	507	Total	C	N	O	S	0	5	0
			4124	2646	695	769	14			
1	B	507	Total	C	N	O	S	0	8	0
			4156	2662	705	775	14			

There are 12 discrepancies between the modelled and reference sequences:

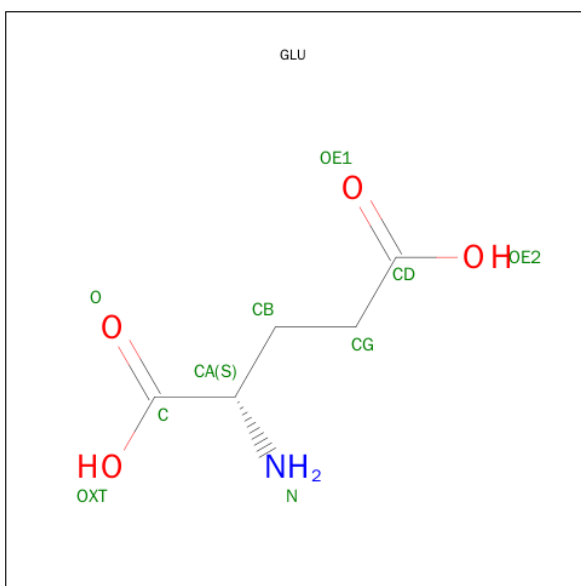
Chain	Residue	Modelled	Actual	Comment	Reference
A	536	HIS	-	EXPRESSION TAG	UNP A7Y7W1
A	537	HIS	-	EXPRESSION TAG	UNP A7Y7W1
A	538	HIS	-	EXPRESSION TAG	UNP A7Y7W1
A	539	HIS	-	EXPRESSION TAG	UNP A7Y7W1
A	540	HIS	-	EXPRESSION TAG	UNP A7Y7W1
A	541	HIS	-	EXPRESSION TAG	UNP A7Y7W1
B	536	HIS	-	EXPRESSION TAG	UNP A7Y7W1
B	537	HIS	-	EXPRESSION TAG	UNP A7Y7W1
B	538	HIS	-	EXPRESSION TAG	UNP A7Y7W1
B	539	HIS	-	EXPRESSION TAG	UNP A7Y7W1
B	540	HIS	-	EXPRESSION TAG	UNP A7Y7W1
B	541	HIS	-	EXPRESSION TAG	UNP A7Y7W1

- Molecule 2 is GLYCINE (three-letter code: GLY) (formula: C₂H₅NO₂).



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

- Molecule 3 is GLUTAMIC ACID (three-letter code: GLU) (formula: $C_5H_9NO_4$).



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

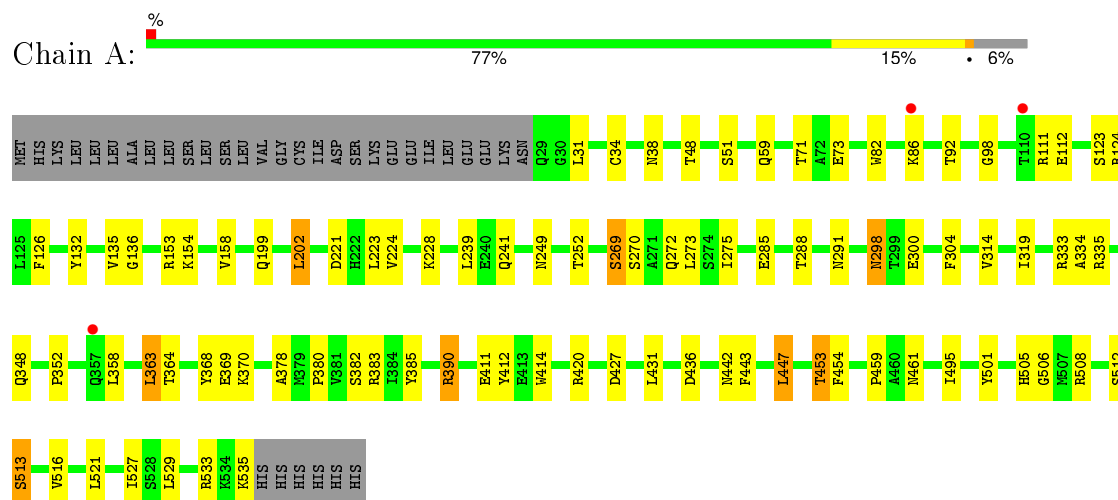
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	266	Total 266	O 266	0	0
4	B	290	Total 290	O 290	0	0

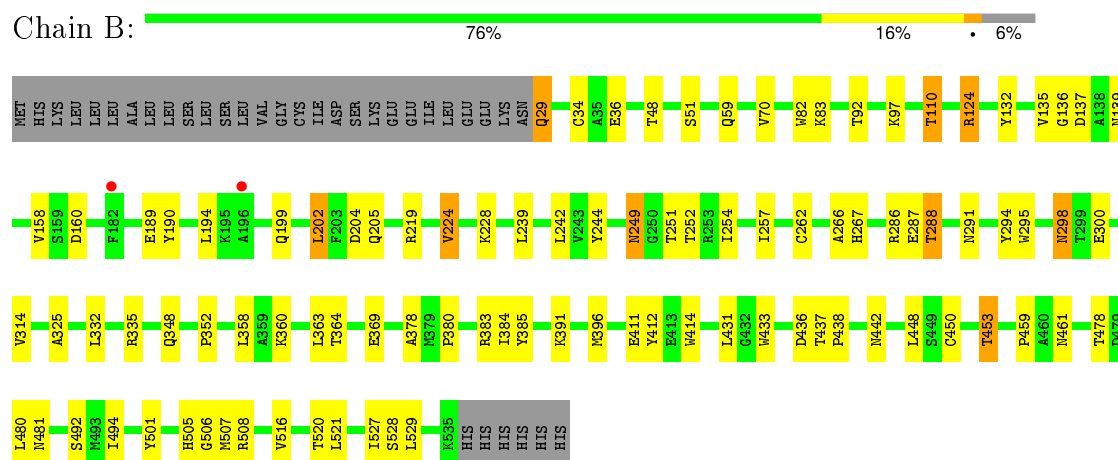
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: ABC transporter periplasmic peptide-binding protein



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4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	106.01Å 106.01Å 100.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.70 – 2.30 34.70 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.5 (34.70-2.30) 99.3 (34.70-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.11 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.151 , 0.211 0.154 , 0.209	Depositor DCC
R_{free} test set	2830 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	26.6	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.8	EDS
Estimated twinning fraction	0.019 for -h,-k,l 0.062 for h,-h-k,-l 0.025 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 55791 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8864	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.40	1/4230 (0.0%)	0.55	0/5753
1	B	0.39	0/4263	0.56	0/5796
All	All	0.40	1/8493 (0.0%)	0.55	0/11549

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	459	PRO	N-CD	5.73	1.55	1.47

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4124	0	4030	71	0
1	B	4156	0	4051	68	0
2	A	4	0	2	1	0
2	B	4	0	2	2	0
3	A	10	0	6	0	0
3	B	10	0	6	1	0
4	A	266	0	0	8	0
4	B	290	0	0	8	0
All	All	8864	0	8097	137	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 8.

All (137) 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:291:ASN:HD21	1:A:506:GLY:H	1.17	0.91
1:A:275:ILE:HD12	1:A:275:ILE:H	1.35	0.91
1:A:249:ASN:HD22	1:A:252:THR:H	1.15	0.90
1:B:291:ASN:HD21	1:B:506:GLY:H	1.19	0.88
1:A:272:GLN:HA	1:A:275:ILE:HD13	1.55	0.87
1:A:59:GLN:NE2	1:A:529:LEU:H	1.79	0.81
1:A:199:GLN:HB3	1:A:202:LEU:HD22	1.61	0.81
1:B:59:GLN:NE2	1:B:529:LEU:H	1.79	0.79
1:B:364:THR:HG22	1:B:369:GLU:HA	1.67	0.76
1:A:98:GLY:HA2	1:A:112:GLU:OE1	1.85	0.75
1:A:132:TYR:HA	1:A:135:VAL:HG23	1.67	0.75
1:B:83:LYS:HE3	4:B:797:HOH:O	1.86	0.74
1:A:38:ASN:ND2	1:A:221:ASP:H	1.87	0.72
1:B:314:VAL:HG11	1:B:352:PRO:HG3	1.71	0.72
1:A:453:THR:HG22	1:A:454:PHE:CD1	2.27	0.70
1:B:124:ARG:NH1	4:B:973:HOH:O	2.08	0.69
1:A:390:ARG:HG3	1:A:390:ARG:HH11	1.58	0.68
1:A:275:ILE:N	1:A:275:ILE:HD12	2.10	0.67
1:A:275:ILE:CD1	1:A:275:ILE:H	2.08	0.67
1:A:86[A]:LYS:HA	1:A:86[A]:LYS:NZ	2.09	0.67
1:A:249:ASN:ND2	1:A:252:THR:H	1.89	0.67
1:A:363:LEU:HD22	1:A:368:TYR:HB2	1.78	0.66
1:B:291:ASN:O	1:B:505:HIS:HD2	1.78	0.66
1:B:348:GLN:HE22	1:B:492:SER:HB3	1.61	0.65
1:A:38:ASN:HD21	1:A:221:ASP:H	1.44	0.65
1:B:132:TYR:HA	1:B:135:VAL:HG23	1.80	0.64
1:A:269:SER:HA	4:A:956:HOH:O	1.97	0.64
1:A:71:THR:OG1	1:A:73:GLU:HG2	1.98	0.63
1:B:286:ARG:HB2	1:B:507:MET:HE3	1.79	0.63
1:B:433:TRP:HE1	1:B:442:ASN:ND2	1.96	0.63
1:A:508:ARG:NH2	1:A:527:ILE:HD12	2.14	0.62
1:A:298:ASN:HD21	1:A:461:ASN:HD22	1.47	0.61
1:B:325:ALA:O	1:B:391:LYS:HE3	2.01	0.61
1:B:298:ASN:HD21	1:B:461:ASN:HD22	1.46	0.61
1:B:36:GLU:OE2	1:B:383:ARG:NH2	2.33	0.61
1:B:505:HIS:HE1	4:B:969:HOH:O	1.85	0.60
1:A:298:ASN:HD22	1:A:298:ASN:C	2.03	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:SER:HB3	4:A:899:HOH:O	2.03	0.59
1:B:204:ASP:OD2	4:B:973:HOH:O	2.17	0.58
1:A:512:SER:HB2	1:A:516[A]:VAL:HG21	1.84	0.58
1:B:135:VAL:HG12	1:B:136:GLY:N	2.19	0.58
1:A:314[A]:VAL:HG11	1:A:352:PRO:HG2	1.85	0.58
1:A:291:ASN:HD22	1:A:385:TYR:HB3	1.68	0.57
1:A:333:ARG:NH1	1:B:481:ASN:HD21	2.03	0.56
1:A:314[A]:VAL:HG13	1:A:501:TYR:CE2	2.40	0.56
1:A:132:TYR:HA	1:A:135:VAL:CG2	2.36	0.56
1:A:153:ARG:HH21	1:A:154:LYS:HE2	1.71	0.56
1:B:437:THR:HB	1:B:438:PRO:HD2	1.87	0.55
1:A:124:ARG:NH2	4:A:950:HOH:O	2.39	0.55
1:A:508:ARG:HH21	1:A:527:ILE:HD12	1.70	0.55
1:B:266:ALA:HA	4:B:979:HOH:O	2.05	0.54
1:B:436:ASP:H	1:B:442:ASN:ND2	2.04	0.54
1:A:86[A]:LYS:HA	1:A:86[A]:LYS:HZ2	1.71	0.54
1:B:298:ASN:C	1:B:298:ASN:HD22	2.11	0.54
1:B:298:ASN:HD22	1:B:300:GLU:H	1.53	0.54
1:A:123:SER:HA	1:A:126:PHE:CE2	2.44	0.53
1:A:436:ASP:H	1:A:442:ASN:HD21	1.57	0.52
1:B:380:PRO:HG3	1:B:412:TYR:O	2.10	0.52
1:A:436:ASP:H	1:A:442:ASN:ND2	2.08	0.52
1:B:59:GLN:HE21	1:B:529:LEU:H	1.55	0.52
1:B:124:ARG:NH2	4:B:973:HOH:O	2.43	0.51
1:A:59:GLN:HE22	1:A:529:LEU:H	1.55	0.51
1:B:383:ARG:HD3	3:B:602:GLU:OXT	2.10	0.51
1:A:82:TRP:HA	1:A:92:THR:O	2.10	0.51
1:B:228:LYS:HB2	1:B:239:LEU:O	2.11	0.51
1:A:291:ASN:O	1:A:505:HIS:HD2	1.93	0.50
1:B:249:ASN:ND2	1:B:252:THR:H	2.10	0.50
1:B:249:ASN:HD22	1:B:249:ASN:C	2.15	0.50
1:B:520:THR:OG1	1:B:528:SER:HB3	2.11	0.49
1:B:29:GLN:NE2	1:B:29:GLN:HA	2.26	0.49
1:A:51:SER:HG	1:A:414:TRP:HE1	1.58	0.49
1:B:224:VAL:HG13	1:B:244:TYR:HB2	1.93	0.49
1:A:390:ARG:HG3	1:A:390:ARG:NH1	2.26	0.49
1:B:132:TYR:HA	1:B:135:VAL:CG2	2.42	0.49
1:B:199:GLN:HB3	1:B:202:LEU:HD22	1.94	0.49
1:B:48:THR:O	2:B:601:GLY:HA3	2.13	0.49
1:A:513:SER:O	1:A:516[A]:VAL:HG22	2.12	0.49
1:A:380:PRO:HG3	1:A:412:TYR:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:267:HIS:HE1	1:B:384:ILE:HG13	1.78	0.48
1:B:450:CYS:O	1:B:453:THR:HG22	2.13	0.48
1:A:443:PHE:O	1:A:447:LEU:HB2	2.13	0.48
1:A:48:THR:O	2:A:601:GLY:HA3	2.13	0.48
1:A:31:LEU:HD23	1:A:31:LEU:C	2.34	0.48
1:A:390:ARG:CG	1:A:390:ARG:NH1	2.76	0.48
1:A:505:HIS:HE1	4:A:946:HOH:O	1.96	0.48
1:A:364:THR:HG23	1:A:369:GLU:HB3	1.95	0.48
1:B:291:ASN:HD22	1:B:385:TYR:HB3	1.79	0.48
1:B:82:TRP:HA	1:B:92:THR:O	2.13	0.48
1:A:382:SER:O	1:A:383:ARG:HD2	2.14	0.48
1:B:378:ALA:O	1:B:411:GLU:HG2	2.14	0.48
1:B:294:TYR:OH	1:B:459:PRO:HG2	2.13	0.48
1:B:219:ARG:HG2	1:B:219:ARG:HH11	1.78	0.48
1:A:86[B]:LYS:HG2	4:A:954:HOH:O	2.14	0.47
1:B:360:LYS:O	1:B:364:THR:HG23	2.14	0.47
1:B:348:GLN:NE2	1:B:492:SER:HA	2.30	0.47
1:B:314:VAL:HG13	1:B:501:TYR:CE2	2.49	0.47
1:B:135:VAL:CG1	1:B:136:GLY:N	2.77	0.47
1:B:124:ARG:CZ	4:B:973:HOH:O	2.59	0.47
1:A:319:ILE:HG21	1:A:333:ARG:NH2	2.28	0.47
1:B:254:ILE:O	1:B:257:ILE:HG22	2.15	0.47
1:A:132:TYR:CD2	1:A:135:VAL:HG21	2.51	0.46
1:A:86[A]:LYS:HA	1:A:86[A]:LYS:HZ3	1.80	0.46
1:A:135:VAL:HG12	1:A:136:GLY:N	2.31	0.46
1:A:319:ILE:HG21	1:A:333:ARG:CZ	2.46	0.46
1:B:348:GLN:NE2	1:B:492:SER:HB3	2.27	0.46
1:B:433:TRP:CZ3	2:B:601:GLY:HA2	2.51	0.46
1:B:521:LEU:HD23	1:B:521:LEU:N	2.30	0.46
1:B:249:ASN:HD22	1:B:252:THR:H	1.64	0.45
1:B:508:ARG:NH2	1:B:527:ILE:HD12	2.31	0.45
1:A:314[A]:VAL:HG13	1:A:501:TYR:CZ	2.51	0.44
1:A:270:SER:HA	1:A:273:LEU:HG	2.00	0.44
1:A:135:VAL:HG12	4:A:950:HOH:O	2.16	0.44
1:A:223:LEU:O	1:A:223:LEU:HD12	2.17	0.44
1:A:124:ARG:O	1:A:124:ARG:HG2	2.17	0.44
1:A:348:GLN:HG3	1:A:495:ILE:HG13	1.99	0.44
1:B:521:LEU:H	1:B:521:LEU:HD23	1.82	0.43
1:B:190:TYR:CZ	1:B:194:LEU:HD11	2.53	0.43
1:B:287:GLU:HG3	1:B:521:LEU:O	2.19	0.43
1:A:228:LYS:HB2	1:A:239:LEU:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:PHE:CE2	1:A:427:ASP:HB3	2.54	0.43
1:B:51:SER:HG	1:B:414:TRP:HE1	1.67	0.42
1:A:363:LEU:HA	1:A:363:LEU:HD23	1.91	0.42
1:A:298:ASN:HD22	1:A:300:GLU:H	1.67	0.42
1:B:110:THR:HG22	1:B:189:GLU:OE2	2.19	0.42
1:A:378:ALA:O	1:A:411:GLU:HG3	2.20	0.41
1:B:295:TRP:CD2	1:B:396:MET:HE3	2.56	0.41
1:A:412:TYR:CE1	1:A:420:ARG:NH1	2.89	0.41
4:A:744:HOH:O	1:B:288:THR:CG2	2.68	0.41
1:A:334:ALA:HA	1:A:505:HIS:CE1	2.56	0.41
1:B:291:ASN:O	1:B:505:HIS:CD2	2.66	0.41
1:B:383:ARG:HD2	1:B:414:TRP:CZ2	2.56	0.41
1:B:448:LEU:HD13	1:B:494[A]:ILE:CD1	2.51	0.41
1:A:288:THR:HG22	1:B:288:THR:HG21	2.02	0.40
1:B:257:ILE:HD12	1:B:262:CYS:O	2.20	0.40
1:A:223:LEU:HD12	1:A:223:LEU:C	2.41	0.40
1:B:348:GLN:HB3	4:B:850:HOH:O	2.21	0.40
4:A:845:HOH:O	1:B:335:ARG:HD3	2.20	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	510/541 (94%)	498 (98%)	12 (2%)	0	100	100
1	B	513/541 (95%)	497 (97%)	16 (3%)	0	100	100
All	All	1023/1082 (94%)	995 (97%)	28 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	445/472 (94%)	424 (95%)	21 (5%)	32	43
1	B	448/472 (95%)	422 (94%)	26 (6%)	25	33
All	All	893/944 (95%)	846 (95%)	47 (5%)	28	37

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	CYS
1	A	111	ARG
1	A	158	VAL
1	A	202	LEU
1	A	224	VAL
1	A	241	GLN
1	A	269	SER
1	A	285	GLU
1	A	298	ASN
1	A	335	ARG
1	A	358	LEU
1	A	363	LEU
1	A	370	LYS
1	A	390	ARG
1	A	431	LEU
1	A	447	LEU
1	A	453	THR
1	A	513	SER
1	A	521	LEU
1	A	533	ARG
1	A	535	LYS
1	B	29	GLN
1	B	34	CYS
1	B	70	VAL
1	B	97	LYS
1	B	110	THR
1	B	124	ARG

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Mol	Chain	Res	Type
1	B	137	ASP
1	B	139	ASN
1	B	158	VAL
1	B	160	ASP
1	B	202	LEU
1	B	205	GLN
1	B	224	VAL
1	B	242	LEU
1	B	249	ASN
1	B	251	THR
1	B	288	THR
1	B	298	ASN
1	B	332	LEU
1	B	358	LEU
1	B	363	LEU
1	B	431	LEU
1	B	453	THR
1	B	478	THR
1	B	480	LEU
1	B	516	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	58	ASN
1	A	59	GLN
1	A	139	ASN
1	A	249	ASN
1	A	291	ASN
1	A	298	ASN
1	A	311	GLN
1	A	348	GLN
1	A	357	GLN
1	A	442	ASN
1	A	497	GLN
1	A	505	HIS
1	B	29	GLN
1	B	58	ASN
1	B	59	GLN
1	B	139	ASN
1	B	249	ASN

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Mol	Chain	Res	Type
1	B	291	ASN
1	B	298	ASN
1	B	311	GLN
1	B	348	GLN
1	B	419	GLN
1	B	442	ASN
1	B	485	GLN
1	B	497	GLN
1	B	505	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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	GLY	A	601	3	3,3,4	0.73	0	0,2,4	0.00	-
3	GLU	A	602	2	3,9,9	0.33	0	2,11,11	0.15	0
2	GLY	B	601	3	3,3,4	0.68	0	0,2,4	0.00	-
3	GLU	B	602	2	3,9,9	0.38	0	2,11,11	0.18	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	GLY	A	601	3	-	0/0/1/2	0/0/0/0
3	GLU	A	602	2	-	0/3/9/9	0/0/0/0
2	GLY	B	601	3	-	0/0/1/2	0/0/0/0
3	GLU	B	602	2	-	0/3/9/9	0/0/0/0

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.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	GLY	1	0
2	B	601	GLY	2	0
3	B	602	GLU	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	507/541 (93%)	-0.41	3 (0%) 90 93	16, 26, 43, 59	0
1	B	507/541 (93%)	-0.35	2 (0%) 93 95	16, 26, 46, 60	0
All	All	1014/1082 (93%)	-0.38	5 (0%) 91 94	16, 26, 45, 60	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	110	THR	2.4
1	B	196	ALA	2.1
1	A	86[A]	LYS	2.0
1	A	357	GLN	2.0
1	B	182	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 carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	GLY	A	601	4/5	0.98	0.21	1.29	22,23,24,26	0
2	GLY	B	601	4/5	0.99	0.22	0.87	22,28,28,31	0
3	GLU	A	602	10/10	0.98	0.13	-0.60	20,25,28,31	0
3	GLU	B	602	10/10	0.98	0.13	-0.70	16,24,28,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.