



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:04 PM GMT

PDB ID : 1S0G
Title : Crystal structure of botulinum neurotoxin type B apo form
Authors : Eswaramoorthy, S.; Kumaran, D.; Keller, J.; Swaminathan, S.
Deposited on : 2003-12-30
Resolution : 2.60 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

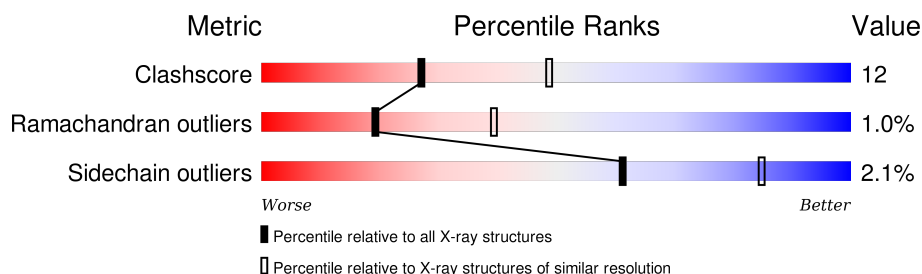
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1290	 73% 25%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10961 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 Botulinum neurotoxin type B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1288	Total	C	N	O	S	0	0	0
			10593	6832	1705	2023	33			

- Molecule 2 is water.

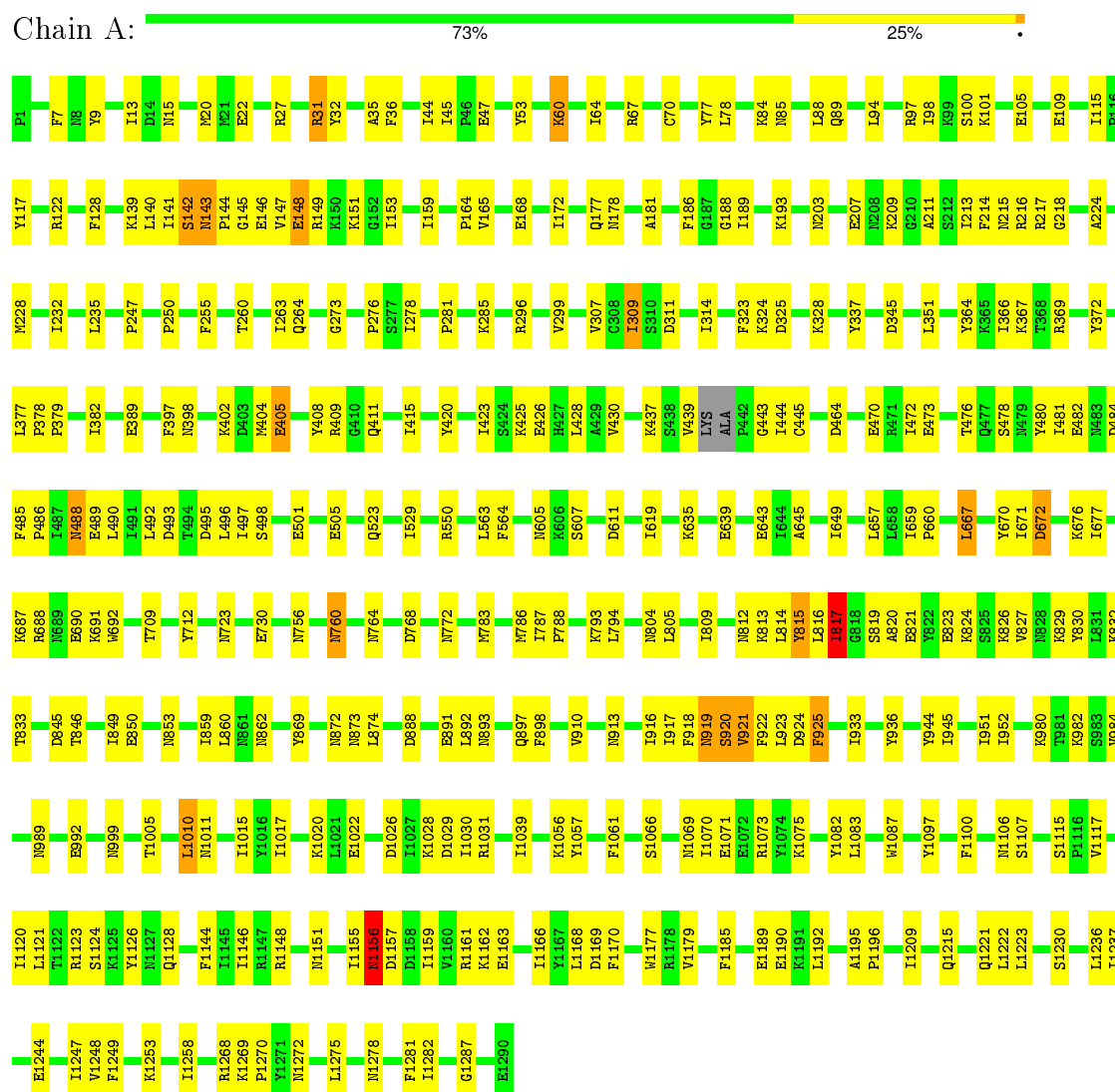
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	368	Total	O	0	0
			368	368		

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.

Note EDS was not executed.

• Molecule 1: Botulinum neurotoxin type B



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.63 Å 123.12 Å 95.21 Å 90.00° 113.08° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60	Depositor
% Data completeness (in resolution range)	97.8 (50.00-2.60)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.210 , 0.265	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10961	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

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	0.39	0/10824	0.61	1/14622 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	1156	ASN	N-CA-C	-5.14	97.12	111.00

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	10593	0	10428	253	0
2	A	368	0	0	10	0
All	All	10961	0	10428	253	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 12.

All (253) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (\AA)	Clash overlap (\AA)
1:A:439:VAL:HB	1:A:443:GLY:HA2	1.36	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:826:LYS:HA	1:A:829:LYS:HE2	1.46	0.95
1:A:1148:ARG:HE	1:A:1155:ILE:HD12	1.35	0.91
1:A:143:ASN:HB3	1:A:144:PRO:HD2	1.54	0.90
1:A:1221:GLN:HE21	1:A:1278:ASN:HD22	1.18	0.90
1:A:1066:SER:H	1:A:1069:ASN:ND2	1.70	0.89
1:A:1066:SER:N	1:A:1069:ASN:HD22	1.72	0.87
1:A:1066:SER:H	1:A:1069:ASN:HD22	0.88	0.86
1:A:203:ASN:ND2	1:A:377:LEU:HD11	1.92	0.85
1:A:109:GLU:OE1	1:A:497:ILE:HG21	1.78	0.84
1:A:147:VAL:O	1:A:148:GLU:HB2	1.82	0.80
1:A:209:LYS:CB	1:A:218:GLY:H	1.95	0.80
1:A:1221:GLN:HE21	1:A:1278:ASN:ND2	1.79	0.78
1:A:367:LYS:H	1:A:411:GLN:HE22	1.29	0.78
1:A:255:PHE:HB2	1:A:529:ILE:CD1	2.15	0.76
1:A:309:ILE:H	1:A:309:ILE:HD13	1.52	0.74
1:A:989:ASN:HD22	1:A:992:GLU:HG2	1.54	0.72
1:A:677:ILE:HG21	1:A:816:LEU:HD21	1.72	0.71
1:A:425:LYS:HD3	1:A:428:LEU:HD12	1.73	0.71
1:A:1148:ARG:NE	1:A:1155:ILE:HD12	2.06	0.71
1:A:667:LEU:H	1:A:667:LEU:HD12	1.54	0.70
1:A:1010:LEU:HD13	1:A:1011:ASN:ND2	2.06	0.70
1:A:671:ILE:O	1:A:672:ASP:HB2	1.91	0.69
1:A:143:ASN:HB3	1:A:144:PRO:CD	2.23	0.68
1:A:255:PHE:HB2	1:A:529:ILE:HD12	1.75	0.68
1:A:1011:ASN:OD1	1:A:1028:LYS:HE2	1.93	0.68
1:A:1146:ILE:HG23	1:A:1166:ILE:HD12	1.75	0.68
1:A:485:PHE:HE2	1:A:490:LEU:HB2	1.59	0.66
1:A:670:TYR:CD1	1:A:676:LYS:HB3	2.31	0.65
1:A:402:LYS:HE3	1:A:404:MET:HE3	1.77	0.65
1:A:1126:TYR:CZ	1:A:1128:GLN:HB2	2.32	0.65
1:A:122:ARG:HH11	1:A:177:GLN:NE2	1.94	0.64
1:A:13:ILE:HD13	1:A:20:MET:HG2	1.79	0.64
1:A:659:ILE:HG22	1:A:793:LYS:HG3	1.80	0.62
1:A:47:GLU:HG2	1:A:84:LYS:HE3	1.82	0.62
1:A:70:CYS:HA	1:A:430:VAL:HG12	1.80	0.62
1:A:472:ILE:O	1:A:473:GLU:HG3	2.01	0.61
1:A:845:ASP:O	1:A:849:ILE:HG12	2.01	0.61
1:A:1100:PHE:HB2	1:A:1282:ILE:HD11	1.83	0.60
1:A:1221:GLN:NE2	1:A:1278:ASN:ND2	2.50	0.60
1:A:922:PHE:O	1:A:923:LEU:HB3	2.02	0.60
1:A:639:GLU:O	1:A:643:GLU:HG3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:645:ALA:HB3	1:A:649:ILE:CG2	2.31	0.59
1:A:309:ILE:H	1:A:309:ILE:CD1	2.16	0.59
1:A:172:ILE:HD11	1:A:193:LYS:HZ2	1.67	0.59
1:A:657:LEU:HD11	1:A:786:MET:HG2	1.84	0.59
1:A:141:ILE:HD11	1:A:151:LYS:HB2	1.84	0.59
1:A:273:GLY:O	1:A:276:PRO:HD2	2.03	0.59
1:A:1272:ASN:HB3	1:A:1275:LEU:HG	1.85	0.59
1:A:263:ILE:HD13	1:A:372:TYR:CE2	2.38	0.59
1:A:203:ASN:HD22	1:A:377:LEU:HD11	1.64	0.58
1:A:486:PRO:HG2	1:A:489:GLU:HG2	1.85	0.58
1:A:951:ILE:HG13	1:A:952:ILE:HG13	1.86	0.58
1:A:263:ILE:HD13	1:A:372:TYR:HE2	1.69	0.58
1:A:309:ILE:N	1:A:309:ILE:HD13	2.19	0.57
1:A:228:MET:O	1:A:232:ILE:HG13	2.04	0.57
1:A:920:SER:O	1:A:921:VAL:HB	2.05	0.57
1:A:141:ILE:HD12	1:A:141:ILE:N	2.20	0.57
1:A:1268:ARG:HH11	1:A:1268:ARG:HG3	1.69	0.56
1:A:820:ALA:O	1:A:824:LYS:HB2	2.05	0.56
1:A:211:ALA:HB1	1:A:764:ASN:ND2	2.21	0.56
1:A:869:TYR:CE1	1:A:872:ASN:HA	2.40	0.56
1:A:667:LEU:N	1:A:667:LEU:HD12	2.19	0.56
1:A:1071:GLU:OE2	1:A:1075:LYS:HE3	2.06	0.56
1:A:812:ASN:O	1:A:816:LEU:HG	2.05	0.56
1:A:1126:TYR:CE1	1:A:1128:GLN:HB2	2.40	0.56
1:A:389:GLU:OE2	1:A:402:LYS:HD3	2.06	0.56
1:A:439:VAL:HB	1:A:443:GLY:CA	2.24	0.55
1:A:1083:LEU:HD13	1:A:1209:ILE:CD1	2.37	0.55
1:A:635:LYS:HG3	2:A:1427:HOH:O	2.07	0.55
1:A:147:VAL:O	1:A:148:GLU:CB	2.54	0.55
1:A:816:LEU:C	1:A:817:ILE:HG13	2.28	0.54
1:A:756:ASN:O	1:A:760:ASN:HB2	2.07	0.54
1:A:1185:PHE:HB3	1:A:1190:GLU:OE1	2.08	0.54
1:A:88:LEU:HB3	2:A:1578:HOH:O	2.08	0.54
1:A:379:PRO:HG2	1:A:423:ILE:HD12	1.90	0.54
1:A:1148:ARG:HE	1:A:1155:ILE:CD1	2.16	0.53
1:A:619:ILE:HG12	1:A:639:GLU:HG3	1.90	0.53
1:A:85:ASN:ND2	1:A:89:GLN:HE21	2.07	0.53
1:A:15:ASN:HD21	1:A:143:ASN:HD21	1.57	0.53
1:A:105:GLU:HG2	1:A:109:GLU:OE2	2.09	0.53
1:A:1162:LYS:O	1:A:1163:GLU:HB2	2.08	0.53
1:A:281:PRO:O	1:A:285:LYS:HG3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:TYR:HA	1:A:323:PHE:CZ	2.43	0.52
1:A:437:LYS:HD2	1:A:444:ILE:CG2	2.39	0.52
1:A:1029:ASP:HB2	2:A:1613:HOH:O	2.10	0.52
1:A:64:ILE:O	1:A:64:ILE:HD12	2.11	0.51
1:A:464:ASP:OD1	1:A:660:PRO:HB3	2.09	0.51
1:A:235:LEU:HD21	1:A:351:LEU:CD2	2.40	0.51
1:A:377:LEU:HB3	1:A:378:PRO:HD2	1.93	0.51
1:A:922:PHE:CZ	1:A:924:ASP:HB2	2.46	0.51
1:A:405:GLU:HG2	2:A:1414:HOH:O	2.10	0.51
1:A:27:ARG:HG2	1:A:27:ARG:HH11	1.75	0.50
1:A:211:ALA:HB1	1:A:764:ASN:HD21	1.76	0.50
1:A:9:TYR:H	1:A:85:ASN:ND2	2.08	0.50
1:A:672:ASP:N	1:A:815:TYR:CD2	2.75	0.50
1:A:60:LYS:HE2	1:A:426:GLU:O	2.11	0.50
1:A:1020:LYS:HD3	1:A:1022:GLU:OE2	2.10	0.50
1:A:325:ASP:OD1	1:A:498:SER:HB2	2.12	0.50
1:A:1010:LEU:N	1:A:1010:LEU:HD12	2.26	0.50
1:A:1026:ASP:OD1	1:A:1028:LYS:HG3	2.12	0.50
1:A:437:LYS:O	1:A:443:GLY:HA3	2.12	0.50
1:A:826:LYS:HA	1:A:829:LYS:CE	2.32	0.50
1:A:892:LEU:HD23	1:A:898:PHE:CB	2.42	0.50
1:A:398:ASN:HD21	1:A:411:GLN:HE21	1.59	0.50
1:A:1075:LYS:HE2	1:A:1215:GLN:NE2	2.28	0.49
1:A:945:ILE:HD12	1:A:945:ILE:C	2.32	0.49
1:A:846:THR:O	1:A:850:GLU:HG3	2.13	0.49
1:A:285:LYS:HA	1:A:481:ILE:CD1	2.42	0.49
1:A:667:LEU:HD11	1:A:804:ASN:OD1	2.13	0.49
1:A:813:LYS:HG3	1:A:814:LEU:H	1.78	0.49
1:A:1075:LYS:HE2	1:A:1215:GLN:HE22	1.78	0.49
1:A:53:TYR:CD2	1:A:164:PRO:HG2	2.48	0.48
1:A:153:ILE:HA	1:A:505:GLU:O	2.14	0.48
1:A:67:ARG:HD3	1:A:523:GLN:HE22	1.78	0.48
1:A:22:GLU:HB2	1:A:32:TYR:CE2	2.47	0.48
1:A:178:ASN:HD22	1:A:178:ASN:N	2.10	0.48
1:A:402:LYS:HE3	1:A:404:MET:CE	2.42	0.48
1:A:181:ALA:HB1	1:A:186:PHE:HB2	1.96	0.47
1:A:823:GLU:O	1:A:827:VAL:HG23	2.14	0.47
1:A:1223:LEU:HA	1:A:1236:LEU:HD23	1.96	0.47
1:A:285:LYS:HA	1:A:481:ILE:HD11	1.96	0.47
1:A:490:LEU:HD12	1:A:496:LEU:HD22	1.97	0.47
1:A:307:VAL:HG12	2:A:1466:HOH:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:ILE:CD1	1:A:141:ILE:N	2.78	0.47
1:A:919:ASN:C	1:A:921:VAL:H	2.18	0.47
1:A:44:ILE:HD13	1:A:159:ILE:HB	1.96	0.47
1:A:9:TYR:H	1:A:85:ASN:HD22	1.63	0.47
1:A:1005:THR:HG21	1:A:1070:ILE:HG12	1.97	0.47
1:A:933:ILE:HD13	2:A:1456:HOH:O	2.15	0.47
1:A:141:ILE:CD1	1:A:151:LYS:HB2	2.45	0.47
1:A:1155:ILE:O	1:A:1156:ASN:CB	2.63	0.47
1:A:1248:VAL:HG23	1:A:1249:PHE:CD1	2.50	0.47
1:A:489:GLU:O	1:A:493:ASP:N	2.49	0.46
1:A:1030:ILE:HG12	2:A:1613:HOH:O	2.13	0.46
1:A:101:LYS:HB2	1:A:364:TYR:CZ	2.50	0.46
1:A:115:ILE:HG13	1:A:115:ILE:O	2.13	0.46
1:A:382:ILE:HD12	1:A:397:PHE:CZ	2.50	0.46
1:A:478:SER:HB2	1:A:480:TYR:CE1	2.50	0.46
1:A:480:TYR:OH	1:A:690:GLU:HA	2.15	0.46
1:A:919:ASN:OD1	1:A:919:ASN:N	2.45	0.46
1:A:1247:ILE:HG13	1:A:1248:VAL:N	2.29	0.46
1:A:1056:LYS:HE2	1:A:1057:TYR:CE1	2.50	0.46
1:A:203:ASN:OD1	1:A:203:ASN:O	2.34	0.46
1:A:922:PHE:HD2	1:A:1010:LEU:HB3	1.81	0.46
1:A:64:ILE:C	1:A:64:ILE:HD12	2.36	0.46
1:A:910:VAL:HB	1:A:1039:ILE:HB	1.98	0.45
1:A:1258:ILE:O	1:A:1258:ILE:HG23	2.16	0.45
1:A:913:ASN:HB3	1:A:916:ILE:HD11	1.98	0.45
1:A:140:LEU:HG	1:A:142:SER:HB3	1.97	0.45
1:A:859:ILE:O	1:A:862:ASN:HB2	2.17	0.45
1:A:178:ASN:ND2	1:A:178:ASN:N	2.64	0.45
1:A:873:ASN:ND2	1:A:874:LEU:H	2.14	0.45
1:A:925:PHE:HB2	1:A:1061:PHE:O	2.16	0.45
1:A:859:ILE:HG23	1:A:860:LEU:N	2.31	0.45
1:A:833:THR:HG22	1:A:921:VAL:HG21	1.99	0.44
1:A:1115:SER:HB2	1:A:1117:VAL:HG22	2.00	0.44
1:A:1151:ASN:O	1:A:1155:ILE:HG22	2.17	0.44
1:A:147:VAL:HG23	1:A:147:VAL:O	2.17	0.44
1:A:311:ASP:OD2	1:A:314:ILE:HG12	2.18	0.44
1:A:77:TYR:O	1:A:78:LEU:HB2	2.18	0.44
1:A:1192:LEU:HD11	1:A:1237:ILE:HG23	1.99	0.44
1:A:1169:ASP:HB3	1:A:1177:TRP:O	2.18	0.44
1:A:1269:LYS:HA	1:A:1270:PRO:C	2.36	0.44
1:A:1168:LEU:O	1:A:1179:VAL:HG23	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:488:ASN:O	1:A:492:LEU:HG	2.17	0.44
1:A:97:ARG:HH21	1:A:366:ILE:HD11	1.81	0.44
1:A:143:ASN:CB	1:A:144:PRO:CD	2.94	0.43
1:A:849:ILE:HG22	1:A:853:ASN:HD21	1.83	0.43
1:A:980:LYS:HE2	1:A:1029:ASP:HB3	2.00	0.43
1:A:768:ASP:O	1:A:772:ASN:ND2	2.51	0.43
1:A:936:TYR:HB3	1:A:944:TYR:CE1	2.53	0.43
1:A:893:ASN:HD21	1:A:897:GLN:HB2	1.84	0.43
1:A:188:GLY:O	1:A:189:ILE:C	2.56	0.43
1:A:999:ASN:ND2	1:A:1287:GLY:HA3	2.34	0.43
1:A:1082:TYR:HA	1:A:1161:ARG:HA	1.99	0.43
1:A:980:LYS:HD3	2:A:1613:HOH:O	2.18	0.43
1:A:688:ARG:O	1:A:691:LYS:HB2	2.18	0.43
1:A:819:SER:C	1:A:821:GLU:N	2.70	0.43
1:A:1155:ILE:HG12	1:A:1156:ASN:N	2.34	0.43
1:A:141:ILE:HD11	1:A:151:LYS:CB	2.47	0.43
1:A:85:ASN:O	1:A:89:GLN:HG2	2.19	0.43
1:A:35:ALA:HB2	1:A:45:ILE:HG12	2.00	0.43
1:A:891:GLU:O	1:A:898:PHE:HA	2.19	0.43
1:A:563:LEU:HD23	1:A:564:PHE:CE1	2.54	0.43
1:A:550:ARG:HG2	1:A:550:ARG:HH11	1.84	0.43
1:A:783:MET:O	1:A:788:PRO:HD3	2.19	0.43
1:A:146:GLU:O	1:A:149:ARG:HG3	2.18	0.43
1:A:1195:ALA:HB1	1:A:1196:PRO:CD	2.48	0.43
1:A:485:PHE:CE2	1:A:490:LEU:HB2	2.48	0.42
1:A:482:GLU:C	1:A:484:ASP:H	2.22	0.42
1:A:849:ILE:HG22	1:A:853:ASN:ND2	2.33	0.42
1:A:645:ALA:HB3	1:A:649:ILE:HG21	2.01	0.42
1:A:1031:ARG:HD3	1:A:1031:ARG:HA	1.77	0.42
1:A:982:LYS:HE2	2:A:1613:HOH:O	2.20	0.42
1:A:213:ILE:CB	1:A:723:ASN:OD1	2.67	0.42
1:A:139:LYS:HG3	1:A:141:ILE:HD11	2.01	0.42
1:A:1247:ILE:HG13	1:A:1248:VAL:HG13	2.01	0.42
1:A:367:LYS:HB2	1:A:408:TYR:CG	2.55	0.42
1:A:214:PHE:CD1	1:A:756:ASN:HB3	2.54	0.42
1:A:1157:ASP:OD1	1:A:1159:ILE:HG13	2.20	0.42
1:A:172:ILE:HD11	1:A:193:LYS:NZ	2.33	0.42
1:A:813:LYS:HG3	1:A:814:LEU:N	2.33	0.42
1:A:1107:SER:HA	1:A:1121:LEU:O	2.20	0.42
1:A:31:ARG:HG2	1:A:32:TYR:N	2.35	0.42
1:A:224:ALA:O	1:A:228:MET:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:GLY:O	1:A:149:ARG:HD2	2.20	0.42
1:A:278:ILE:HG22	1:A:278:ILE:O	2.20	0.42
1:A:809:ILE:HG23	1:A:816:LEU:CD1	2.50	0.42
1:A:611:ASP:OD2	1:A:643:GLU:OE2	2.38	0.42
1:A:470:GLU:OE2	1:A:687:LYS:HD2	2.20	0.42
1:A:605:ASN:C	1:A:607:SER:H	2.21	0.42
1:A:215:ASN:OD1	1:A:216:ARG:N	2.51	0.42
1:A:165:VAL:CG1	1:A:168:GLU:HB2	2.50	0.42
1:A:444:ILE:HG12	1:A:445:CYS:N	2.35	0.42
1:A:892:LEU:HD23	1:A:898:PHE:HB3	2.02	0.42
1:A:142:SER:OG	1:A:147:VAL:HA	2.20	0.41
1:A:787:ILE:HB	1:A:788:PRO:HD3	2.02	0.41
1:A:1195:ALA:HB1	1:A:1196:PRO:HD2	2.01	0.41
1:A:216:ARG:HD3	1:A:420:TYR:OH	2.20	0.41
1:A:324:LYS:HD3	1:A:337:TYR:HE2	1.84	0.41
1:A:830:TYR:C	1:A:832:LYS:H	2.22	0.41
1:A:177:GLN:HB2	1:A:177:GLN:HE21	1.63	0.41
1:A:31:ARG:HH11	1:A:31:ARG:CG	2.34	0.41
1:A:478:SER:HB2	1:A:480:TYR:HE1	1.85	0.41
1:A:1073:ARG:HH11	1:A:1073:ARG:HG3	1.85	0.41
1:A:247:PRO:HB3	1:A:264:GLN:NE2	2.35	0.41
1:A:667:LEU:HD21	1:A:805:LEU:HD23	2.02	0.41
1:A:1073:ARG:HG3	1:A:1073:ARG:NH1	2.36	0.41
1:A:402:LYS:HB3	1:A:404:MET:HE3	2.03	0.41
1:A:27:ARG:HG2	1:A:27:ARG:NH1	2.35	0.41
1:A:1017:ILE:CG1	1:A:1022:GLU:HG3	2.51	0.41
1:A:1106:ASN:HA	1:A:1123:ARG:HD2	2.02	0.41
1:A:36:PHE:N	1:A:36:PHE:CD1	2.89	0.41
1:A:1097:TYR:CG	1:A:1281:PHE:HB3	2.55	0.41
1:A:409:ARG:NH1	1:A:415:ILE:HD13	2.35	0.41
1:A:922:PHE:O	1:A:923:LEU:CB	2.68	0.41
1:A:1107:SER:HB3	1:A:1120:ILE:CG2	2.50	0.41
1:A:296:ARG:O	1:A:299:VAL:HG12	2.21	0.41
1:A:692:TRP:CE3	1:A:794:LEU:HD13	2.56	0.41
1:A:77:TYR:CD2	1:A:78:LEU:HG	2.56	0.40
1:A:482:GLU:HG2	2:A:1443:HOH:O	2.21	0.40
1:A:250:PRO:HG3	1:A:260:THR:CG2	2.50	0.40
1:A:1010:LEU:HD12	1:A:1011:ASN:H	1.85	0.40
1:A:493:ASP:OD1	1:A:496:LEU:HB2	2.21	0.40
1:A:328:LYS:HA	1:A:328:LYS:HD3	1.90	0.40
1:A:139:LYS:HG3	1:A:141:ILE:CD1	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:999:ASN:HB3	1:A:1087:TRP:CZ3	2.56	0.40
1:A:94:LEU:O	1:A:98:ILE:HG13	2.21	0.40
1:A:984:VAL:HG13	1:A:1015:ILE:CD1	2.51	0.40
1:A:1244:GLU:OE1	1:A:1253:LYS:HD2	2.22	0.40
1:A:709:THR:O	1:A:712:TYR:HB3	2.21	0.40
1:A:1144:PHE:CD2	1:A:1170:PHE:HB3	2.57	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	1284/1290 (100%)	1189 (93%)	82 (6%)	13 (1%)	19	39

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	148	GLU
1	A	1156	ASN
1	A	142	SER
1	A	476	THR
1	A	921	VAL
1	A	143	ASN
1	A	501	GLU
1	A	817	ILE
1	A	920	SER
1	A	207	GLU
1	A	672	ASP
1	A	1230	SER
1	A	917	ILE

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	1177/1189 (99%)	1152 (98%)	25 (2%)	61 85

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	PHE
1	A	31	ARG
1	A	60	LYS
1	A	100	SER
1	A	128	PHE
1	A	217	ARG
1	A	309	ILE
1	A	345	ASP
1	A	369	ARG
1	A	405	GLU
1	A	488	ASN
1	A	495	ASP
1	A	667	LEU
1	A	730	GLU
1	A	760	ASN
1	A	815	TYR
1	A	817	ILE
1	A	888	ASP
1	A	918	PHE
1	A	919	ASN
1	A	925	PHE
1	A	1010	LEU
1	A	1124	SER
1	A	1189	GLU
1	A	1222	LEU

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	15	ASN
1	A	16	ASN
1	A	85	ASN
1	A	177	GLN
1	A	178	ASN
1	A	203	ASN
1	A	411	GLN
1	A	475	ASN
1	A	523	GLN
1	A	605	ASN
1	A	683	ASN
1	A	689	ASN
1	A	764	ASN
1	A	772	ASN
1	A	799	ASN
1	A	853	ASN
1	A	862	ASN
1	A	873	ASN
1	A	943	ASN
1	A	953	ASN
1	A	957	ASN
1	A	989	ASN
1	A	999	ASN
1	A	1024	ASN
1	A	1069	ASN
1	A	1215	GLN
1	A	1278	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.