



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2016 – 11:14 AM GMT

PDB ID : 5BRQ  
Title : Crystal structure of Bacillus licheniformis trehalose-6-phosphate hydrolase (TreA)  
Authors : Hsiao, C.-D.; Lin, M.-G.  
Deposited on : 2015-06-01  
Resolution : 2.00 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : unknown  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
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) : rb-20026982

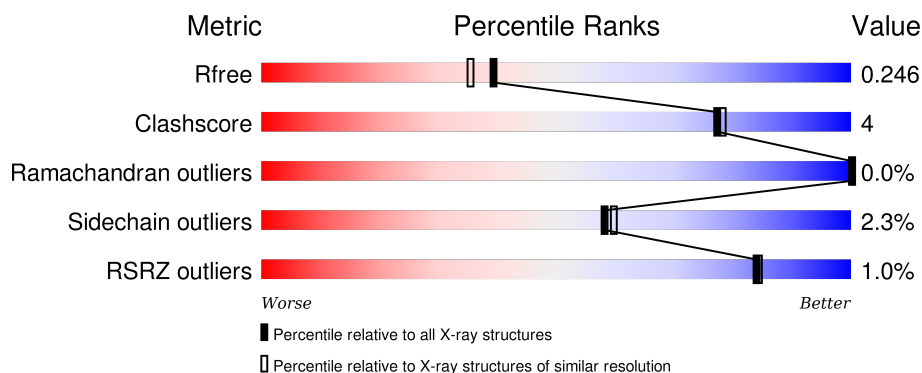
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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  $\geq 3$ , 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	568	<div> <div>90%</div> <div>7% ..</div> </div>
1	B	568	<div> <div>%</div> <div>87%</div> <div>10% ..</div> </div>
1	C	568	<div> <div>%</div> <div>87%</div> <div>10% ..</div> </div>
1	D	568	<div> <div>2%</div> <div>85%</div> <div>11% ..</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19801 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 Glycoside Hydrolase Family 13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	555	Total	C	N	O	S	0	0	0
			4588	2933	757	881	17			
1	B	555	Total	C	N	O	S	0	0	0
			4588	2933	757	881	17			
1	C	555	Total	C	N	O	S	0	0	0
			4588	2933	757	881	17			
1	D	555	Total	C	N	O	S	0	0	0
			4588	2933	757	881	17			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP Q65MI2
A	-4	HIS	-	expression tag	UNP Q65MI2
A	-3	HIS	-	expression tag	UNP Q65MI2
A	-2	HIS	-	expression tag	UNP Q65MI2
A	-1	HIS	-	expression tag	UNP Q65MI2
A	0	HIS	-	expression tag	UNP Q65MI2
B	-5	HIS	-	expression tag	UNP Q65MI2
B	-4	HIS	-	expression tag	UNP Q65MI2
B	-3	HIS	-	expression tag	UNP Q65MI2
B	-2	HIS	-	expression tag	UNP Q65MI2
B	-1	HIS	-	expression tag	UNP Q65MI2
B	0	HIS	-	expression tag	UNP Q65MI2
C	-5	HIS	-	expression tag	UNP Q65MI2
C	-4	HIS	-	expression tag	UNP Q65MI2
C	-3	HIS	-	expression tag	UNP Q65MI2
C	-2	HIS	-	expression tag	UNP Q65MI2
C	-1	HIS	-	expression tag	UNP Q65MI2
C	0	HIS	-	expression tag	UNP Q65MI2
D	-5	HIS	-	expression tag	UNP Q65MI2
D	-4	HIS	-	expression tag	UNP Q65MI2
D	-3	HIS	-	expression tag	UNP Q65MI2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	HIS	-	expression tag	UNP Q65MI2
D	-1	HIS	-	expression tag	UNP Q65MI2
D	0	HIS	-	expression tag	UNP Q65MI2

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

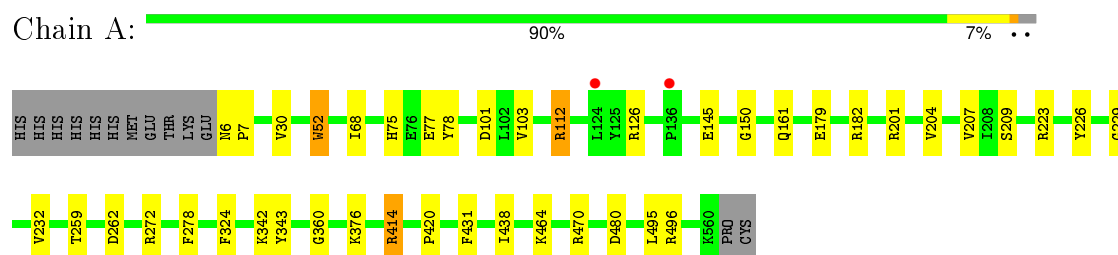
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	380	Total	O	0	0
			380	380		
3	B	386	Total	O	0	0
			386	386		
3	C	353	Total	O	0	0
			353	353		
3	D	326	Total	O	0	0
			326	326		

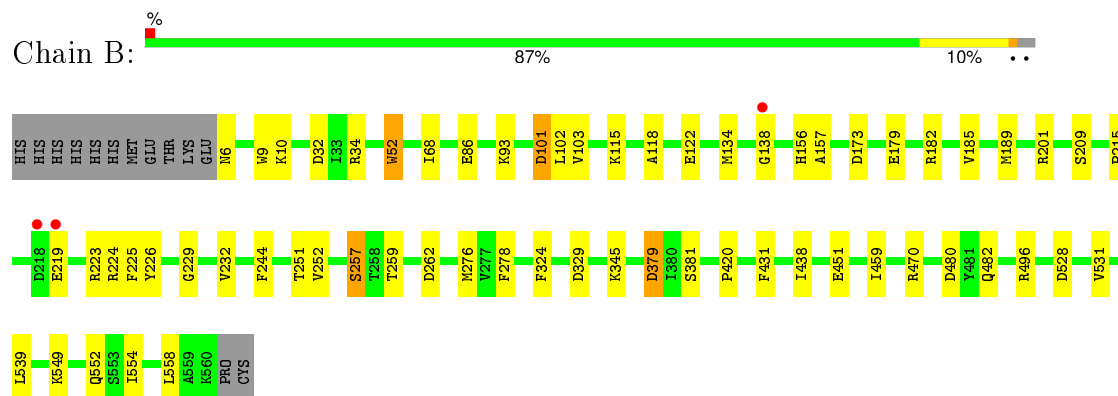
### 3 Residue-property plots [i](#)

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.

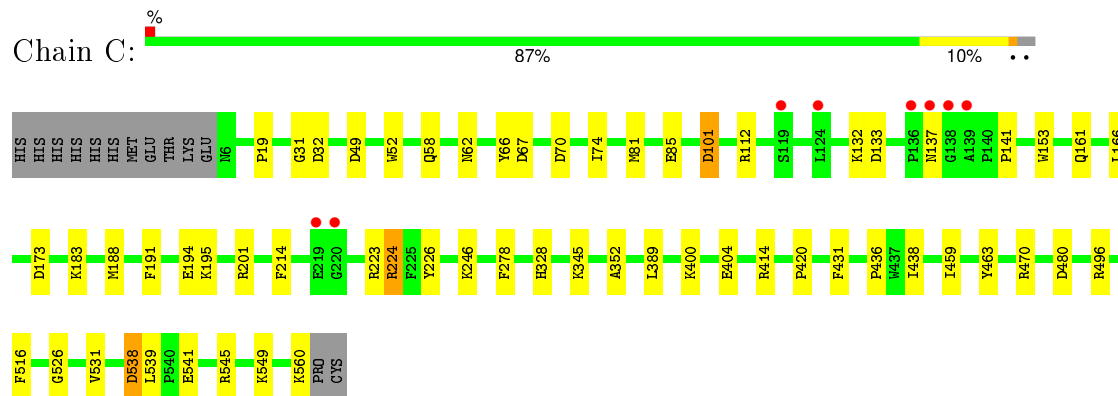
#### • Molecule 1: Glycoside Hydrolase Family 13



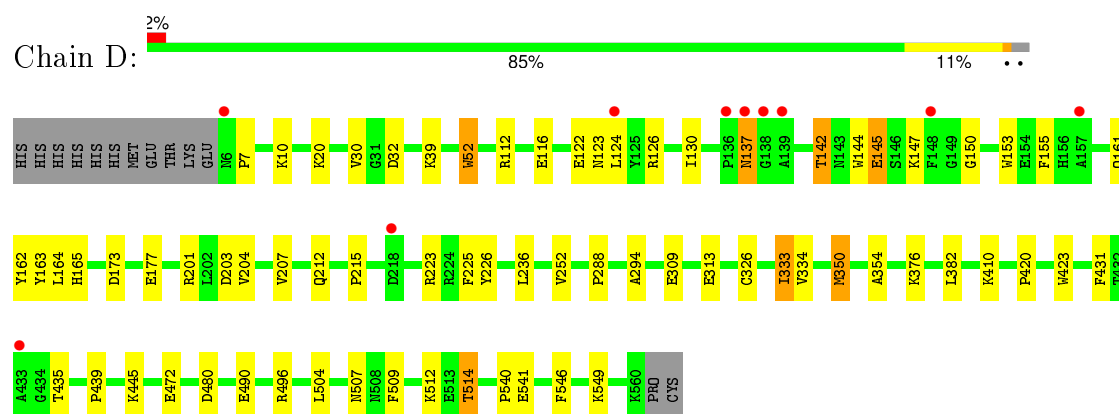
#### • Molecule 1: Glycoside Hydrolase Family 13



#### • Molecule 1: Glycoside Hydrolase Family 13



#### • Molecule 1: Glycoside Hydrolase Family 13



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.80Å 97.58Å 108.34Å 98.20° 91.44° 108.15°	Depositor
Resolution (Å)	24.30 – 2.00 24.30 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.0 (24.30-2.00) 43.6 (24.30-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.33 (at 2.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, $R_{free}$	0.181 , 0.245 0.181 , 0.246	Depositor DCC
$R_{free}$ test set	2001 reflections (1.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.5	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 43.5	EDS
Estimated twinning fraction	0.419 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 74566 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	19801	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.17% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

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

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	0.41	0/4714	0.56	0/6382
1	B	0.42	0/4714	0.56	0/6382
1	C	0.40	0/4714	0.55	0/6382
1	D	0.39	0/4714	0.55	0/6382
All	All	0.41	0/18856	0.55	0/25528

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 [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	4588	0	4357	30	0
1	B	4588	0	4357	34	0
1	C	4588	0	4357	32	0
1	D	4588	0	4357	38	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	380	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	386	0	0	3	0
3	C	353	0	0	4	0
3	D	326	0	0	0	0
All	All	19801	0	17428	131	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 4.

All (131) 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:C:538:ASP:OD2	1:C:549:LYS:NZ	1.95	0.97
1:D:142:THR:HG22	1:D:153:TRP:HE1	1.28	0.97
1:D:142:THR:HG23	1:D:144:TRP:H	1.42	0.84
1:B:34:ARG:NH2	1:B:86:GLU:OE2	2.21	0.72
1:C:201:ARG:HD2	1:C:278:PHE:HE2	1.55	0.71
1:C:101:ASP:OD1	1:C:201:ARG:NH1	2.25	0.70
1:C:52:TRP:CZ2	1:C:201:ARG:HD3	2.29	0.68
1:D:20:LYS:HG3	1:D:30:VAL:HG13	1.76	0.67
1:A:52:TRP:CZ2	1:A:201:ARG:HD3	2.30	0.66
1:D:142:THR:HG22	1:D:153:TRP:NE1	2.07	0.64
1:A:30:VAL:HG21	1:A:77:GLU:OE2	1.98	0.63
1:D:326:CYS:SG	1:D:333:ILE:HG13	2.41	0.60
1:A:420:PRO:HD3	1:A:438:ILE:HG23	1.84	0.59
1:D:7:PRO:HG2	1:D:10:LYS:HG2	1.84	0.58
1:A:126:ARG:NH2	1:A:161:GLN:OE1	2.34	0.57
1:D:215:PRO:HG2	1:D:225:PHE:CE1	2.40	0.56
1:A:101:ASP:OD2	1:A:201:ARG:NH1	2.39	0.56
1:A:259:THR:HG23	1:A:262:ASP:H	1.70	0.56
1:B:101:ASP:OD1	1:B:201:ARG:NH1	2.39	0.55
1:C:85:GLU:OE1	1:C:195:LYS:NZ	2.39	0.55
1:B:229:GLY:O	1:B:232:VAL:HG23	2.06	0.55
1:C:201:ARG:HD2	1:C:278:PHE:CE2	2.40	0.55
1:C:66:TYR:OH	1:C:328:HIS:NE2	2.40	0.54
1:D:490:GLU:OE2	1:D:514:THR:HG23	2.08	0.54
1:D:309:GLU:HG2	1:D:313:GLU:OE2	2.07	0.54
1:D:142:THR:CG2	1:D:153:TRP:HE1	2.13	0.54
1:A:201:ARG:NH1	1:A:201:ARG:HG2	2.23	0.53
1:C:224:ARG:NH1	3:C:704:HOH:O	2.32	0.53
1:B:219:GLU:HB2	1:B:224:ARG:HH22	1.74	0.52
1:A:376:LYS:NZ	3:A:707:HOH:O	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:ARG:HA	1:A:226:TYR:CZ	2.44	0.52
1:C:345:LYS:HA	1:C:459:ILE:HD11	1.92	0.52
1:D:137:ASN:OD1	1:D:137:ASN:N	2.31	0.52
1:A:179:GLU:HG2	1:A:182:ARG:NH1	2.24	0.52
1:D:177:GLU:HG3	1:D:212:GLN:CD	2.29	0.52
1:A:145:GLU:HG3	1:A:150:GLY:O	2.09	0.52
1:A:272:ARG:HH12	1:C:112:ARG:NH2	2.08	0.51
1:D:52:TRP:CZ2	1:D:201:ARG:HD3	2.46	0.51
1:B:209:SER:HB3	1:B:232:VAL:HG22	1.92	0.51
1:B:420:PRO:HD3	1:B:438:ILE:HG23	1.92	0.51
1:C:62:ASN:HB2	1:C:67:ASP:OD2	2.10	0.50
1:A:201:ARG:HH11	1:A:201:ARG:HG2	1.76	0.50
1:A:360:GLY:O	1:A:470:ARG:NH1	2.44	0.50
1:D:153:TRP:HB3	1:D:162:TYR:HB3	1.94	0.50
1:A:75:HIS:HB3	1:A:78:TYR:CD2	2.47	0.50
1:D:350:MET:HE3	1:D:509:PHE:CE1	2.47	0.49
1:B:223:ARG:HA	1:B:226:TYR:CZ	2.48	0.49
1:A:204:VAL:O	1:A:207:VAL:HG22	2.12	0.49
1:B:531:VAL:HG21	1:B:539:LEU:HD13	1.94	0.49
1:A:464:LYS:HE2	1:D:472:GLU:OE2	2.13	0.49
1:C:531:VAL:HG21	1:C:539:LEU:HD13	1.95	0.49
1:A:414:ARG:NH1	3:A:717:HOH:O	2.46	0.49
1:A:342:LYS:HE3	1:A:343:TYR:CZ	2.49	0.48
1:D:350:MET:CE	1:D:507:ASN:HB3	2.43	0.48
1:C:526:GLY:O	1:C:560:LYS:HB3	2.13	0.48
1:D:223:ARG:HA	1:D:226:TYR:CZ	2.48	0.48
1:B:157:ALA:N	3:B:720:HOH:O	2.45	0.48
1:B:52:TRP:CZ2	1:B:201:ARG:HD3	2.48	0.47
1:B:480:ASP:O	1:B:496:ARG:HA	2.14	0.47
1:C:420:PRO:HB3	1:C:431:PHE:CG	2.49	0.47
1:D:420:PRO:HB3	1:D:431:PHE:CG	2.49	0.47
1:C:516:PHE:O	1:C:545:ARG:HA	2.14	0.47
1:B:9:TRP:CZ3	1:B:10:LYS:HD2	2.49	0.47
1:D:480:ASP:O	1:D:496:ARG:HA	2.15	0.47
1:B:179:GLU:HG2	1:B:182:ARG:NH1	2.29	0.47
1:D:350:MET:CE	1:D:354:ALA:HB2	2.45	0.47
1:C:74:ILE:HD12	1:C:81:MET:HA	1.96	0.47
1:B:259:THR:HG22	1:B:262:ASP:OD2	2.14	0.47
1:C:19:PRO:O	1:C:31:GLY:HA3	2.15	0.46
1:C:141:PRO:HG2	1:C:153:TRP:CD2	2.51	0.46
1:A:272:ARG:NH1	1:C:112:ARG:NH2	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:345:LYS:HA	1:B:459:ILE:HD11	1.98	0.46
1:C:352:ALA:HB2	1:C:463:TYR:CZ	2.51	0.46
1:B:185:VAL:O	1:B:189:MET:HG3	2.16	0.46
1:A:68:ILE:HD12	1:A:103:VAL:HB	1.98	0.46
1:B:420:PRO:HB3	1:B:431:PHE:CG	2.51	0.46
1:C:133:ASP:OD1	1:C:161:GLN:NE2	2.39	0.45
1:D:145:GLU:HG2	1:D:150:GLY:O	2.16	0.45
1:D:382:LEU:HD22	1:D:439:PRO:HG2	1.99	0.45
1:D:130:ILE:O	1:D:163:TYR:HA	2.17	0.45
1:B:379:ASP:OD2	1:B:381:SER:OG	2.14	0.45
1:D:376:LYS:HA	1:D:410:LYS:HG2	1.99	0.45
1:A:480:ASP:O	1:A:496:ARG:HA	2.16	0.45
1:D:126:ARG:NH2	1:D:161:GLN:OE1	2.40	0.44
1:D:350:MET:HE3	1:D:507:ASN:HB3	1.99	0.44
1:D:39:LYS:HE2	1:D:423:TRP:CE3	2.53	0.44
1:B:215:PRO:HG2	1:B:225:PHE:CE1	2.52	0.44
1:C:49:ASP:HB2	3:C:822:HOH:O	2.17	0.44
1:A:112:ARG:NH2	3:A:724:HOH:O	2.50	0.44
1:D:204:VAL:O	1:D:207:VAL:HG22	2.17	0.44
1:B:252:VAL:HG23	1:B:276:MET:HG3	1.99	0.44
1:C:188:MET:O	1:C:191:PHE:HB3	2.17	0.44
1:B:278:PHE:HD2	1:B:324:PHE:CE1	2.36	0.44
1:C:58:GLN:HB3	1:C:70:ASP:HB3	2.00	0.43
1:B:482:GLN:NE2	3:B:715:HOH:O	2.43	0.43
1:B:552:GLN:NE2	1:B:554:ILE:HD11	2.33	0.43
1:B:201:ARG:HA	1:B:252:VAL:HG13	1.99	0.43
1:C:436:PRO:HB2	1:C:438:ILE:O	2.18	0.43
1:A:229:GLY:O	1:A:232:VAL:HG23	2.19	0.43
1:B:134:MET:SD	1:B:138:GLY:HA2	2.59	0.43
1:B:223:ARG:NH1	1:B:257:SER:OG	2.52	0.42
1:C:480:ASP:O	1:C:496:ARG:HA	2.19	0.42
1:A:209:SER:HB3	1:A:232:VAL:HG22	2.00	0.42
1:B:179:GLU:HG2	1:B:182:ARG:CZ	2.49	0.42
1:D:112:ARG:O	1:D:116:GLU:HG2	2.20	0.42
1:C:132:LYS:HE2	1:C:214:PHE:CD2	2.54	0.42
1:A:179:GLU:HG2	1:A:182:ARG:HH12	1.85	0.42
1:B:118:ALA:HB1	1:B:156:HIS:CE1	2.55	0.42
1:C:400:LYS:HE3	1:C:404:GLU:HB3	2.02	0.42
1:B:244:PHE:CG	1:B:251:THR:HG21	2.55	0.42
1:B:93:LYS:HB2	1:B:93:LYS:HE3	1.74	0.41
1:A:420:PRO:HB3	1:A:431:PHE:CG	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:ASN:HA	1:A:7:PRO:HD3	1.89	0.41
1:D:123:ASN:OD1	1:D:124:LEU:N	2.54	0.41
1:C:414:ARG:HG3	3:C:776:HOH:O	2.21	0.41
1:B:451:GLU:OE2	3:B:701:HOH:O	2.22	0.41
1:D:142:THR:HG21	1:D:144:TRP:CD2	2.56	0.41
1:A:201:ARG:HD2	1:A:278:PHE:HE2	1.85	0.41
1:C:223:ARG:HA	1:C:226:TYR:CZ	2.55	0.41
1:B:528:ASP:O	1:B:558:LEU:HA	2.21	0.41
1:B:68:ILE:HD12	1:B:103:VAL:HB	2.02	0.41
1:D:540:PRO:HG3	1:D:546:PHE:CD2	2.56	0.41
1:D:288:PRO:HG2	1:D:294:ALA:HB3	2.03	0.41
1:C:414:ARG:HD2	3:C:871:HOH:O	2.21	0.40
1:D:165:HIS:O	1:D:165:HIS:CG	2.74	0.40
1:D:549:LYS:HE2	1:D:549:LYS:HB3	1.88	0.40
1:D:236:LEU:HD23	1:D:236:LEU:HA	1.81	0.40
1:B:549:LYS:HB3	1:B:549:LYS:HE2	1.89	0.40
1:A:278:PHE:HD1	1:A:324:PHE:CE1	2.40	0.40
1:D:490:GLU:OE1	1:D:512:LYS:HG3	2.22	0.40
1:C:166:LEU:HG	1:C:173:ASP:OD2	2.22	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	553/568 (97%)	539 (98%)	14 (2%)	0	100	100
1	B	553/568 (97%)	539 (98%)	13 (2%)	1 (0%)	52	48
1	C	553/568 (97%)	533 (96%)	20 (4%)	0	100	100
1	D	553/568 (97%)	533 (96%)	20 (4%)	0	100	100
All	All	2212/2272 (97%)	2144 (97%)	67 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	257	SER

### 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	490/503 (97%)	486 (99%)	4 (1%)	86	89
1	B	490/503 (97%)	479 (98%)	11 (2%)	60	62
1	C	490/503 (97%)	479 (98%)	11 (2%)	60	62
1	D	490/503 (97%)	470 (96%)	20 (4%)	37	32
All	All	1960/2012 (97%)	1914 (98%)	46 (2%)	58	60

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	TRP
1	A	112	ARG
1	A	414	ARG
1	A	495	LEU
1	B	6	ASN
1	B	32	ASP
1	B	52	TRP
1	B	101	ASP
1	B	102	LEU
1	B	115	LYS
1	B	122	GLU
1	B	173	ASP
1	B	329	ASP
1	B	379	ASP
1	B	470	ARG
1	C	32	ASP
1	C	101	ASP
1	C	137	ASN
1	C	183	LYS

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Mol	Chain	Res	Type
1	C	194	GLU
1	C	224	ARG
1	C	246	LYS
1	C	389	LEU
1	C	470	ARG
1	C	538	ASP
1	C	541	GLU
1	D	32	ASP
1	D	52	TRP
1	D	122	GLU
1	D	137	ASN
1	D	142	THR
1	D	145	GLU
1	D	147	LYS
1	D	155	PHE
1	D	164	LEU
1	D	173	ASP
1	D	203	ASP
1	D	252	VAL
1	D	333	ILE
1	D	334	VAL
1	D	350	MET
1	D	435	THR
1	D	445	LYS
1	D	504	LEU
1	D	514	THR
1	D	541	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	555/568 (97%)	-0.59	2 (0%) 93 93	5, 19, 35, 49	0
1	B	555/568 (97%)	-0.59	3 (0%) 91 92	4, 17, 36, 60	0
1	C	555/568 (97%)	-0.54	8 (1%) 78 78	3, 21, 42, 70	0
1	D	555/568 (97%)	-0.52	10 (1%) 71 72	8, 23, 41, 59	0
All	All	2220/2272 (97%)	-0.56	23 (1%) 84 84	3, 20, 39, 70	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	136	PRO	4.5
1	C	136	PRO	3.4
1	A	136	PRO	3.4
1	B	219	GLU	3.3
1	C	124	LEU	3.2
1	D	124	LEU	3.1
1	D	137	ASN	2.7
1	D	6	ASN	2.6
1	C	119	SER	2.5
1	C	137	ASN	2.5
1	A	124	LEU	2.5
1	C	219	GLU	2.4
1	D	139	ALA	2.3
1	D	157	ALA	2.3
1	B	138	GLY	2.3
1	C	220	GLY	2.2
1	D	218	ASP	2.2
1	D	148	PHE	2.1
1	D	433	ALA	2.1
1	B	218	ASP	2.1
1	C	139	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	138	GLY	2.0
1	C	138	GLY	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	MG	D	601	1/1	0.95	0.17	1.40	26,26,26,26	0
2	MG	C	601	1/1	0.93	0.09	-0.27	27,27,27,27	0
2	MG	A	601	1/1	0.97	0.04	-1.39	19,19,19,19	0
2	MG	B	601	1/1	0.99	0.03	-2.40	11,11,11,11	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.