



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 04:42 am GMT

PDB ID : 4X9E  
Title : DEOXYGUANOSINETRIPHOSPHATE TRIPHOSPHOHYDROLASE from  
Escherichia coli with two DNA effector molecules  
Authors : Singh, D.; Gawel, D.; Itsko, M.; Krahn, J.M.; London, R.E.; Schaaper, R.M.  
Deposited on : 2014-12-11  
Resolution : 3.10 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  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

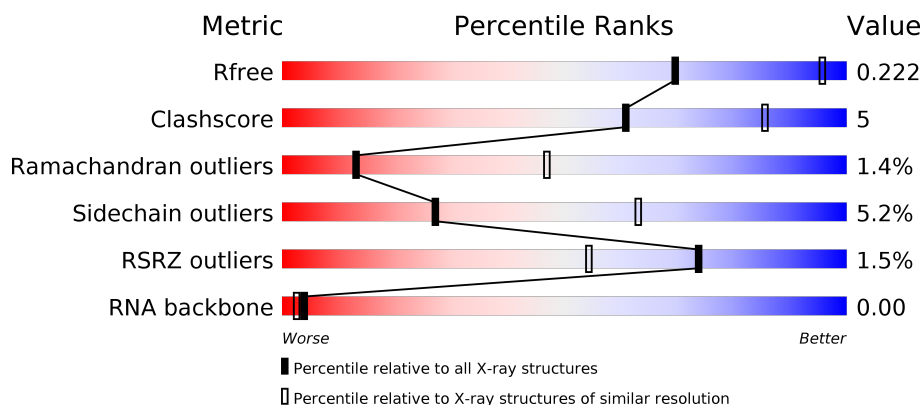
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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))
$R_{free}$	100719	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)
RNA backbone	2435	1112 (3.50-2.70)

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	505	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>19%</div> <div>..</div> </div> </div>
1	B	505	<div> <div>3%</div> <div> <div></div> <div>81%</div> <div>16%</div> <div>..</div> </div> </div>
1	C	505	<div> <div>0%</div> <div> <div></div> <div>82%</div> <div>16%</div> <div>..</div> </div> </div>
1	D	505	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>16%</div> <div>..</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	E	505	<div><div></div><div>82%</div><div>15%</div><div>••</div></div>
1	F	505	<div>%<div><div></div><div>84%</div><div>13%</div><div>••</div></div></div>
2	G	3	<div><div></div><div>33%</div><div>67%</div></div>
2	H	3	<div><div></div><div>67%</div><div>33%</div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24471 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 Deoxyguanosinetriphosphate triphosphohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	499	Total	C	N	O	S	0	0	0
			4092	2618	728	730	16			
1	B	495	Total	C	N	O	S	0	0	0
			3983	2562	709	696	16			
1	C	500	Total	C	N	O	S	0	0	0
			4107	2627	730	733	17			
1	D	501	Total	C	N	O	S	0	0	0
			4067	2606	713	732	16			
1	E	496	Total	C	N	O	S	0	0	0
			4075	2609	715	735	16			
1	F	497	Total	C	N	O	S	0	0	0
			4034	2588	715	715	16			

- Molecule 2 is a RNA chain called RNA (5'-R(P\*CP\*CP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	3	Total	C	N	O	P	0	0	0
			58	27	9	19	3			
2	H	3	Total	C	N	O	P	0	0	0
			53	27	9	15	2			

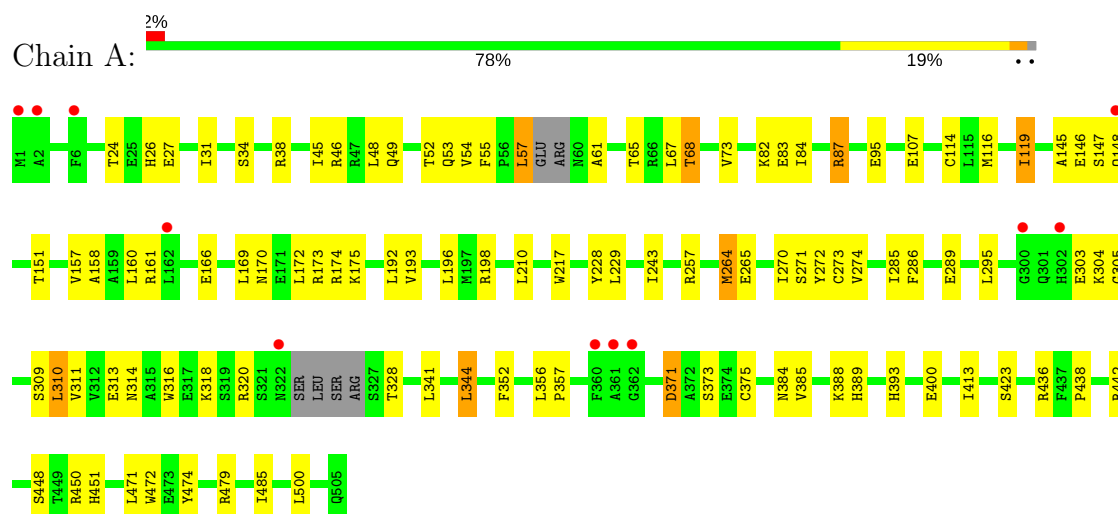
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		

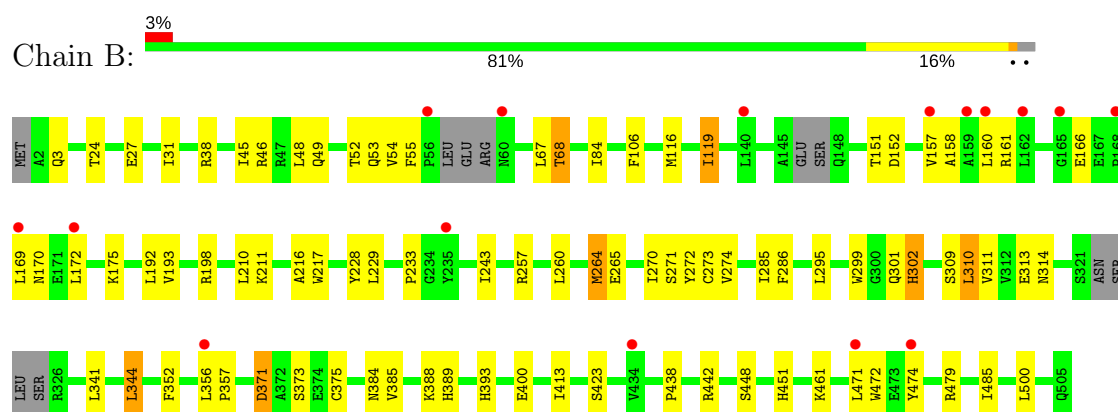
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

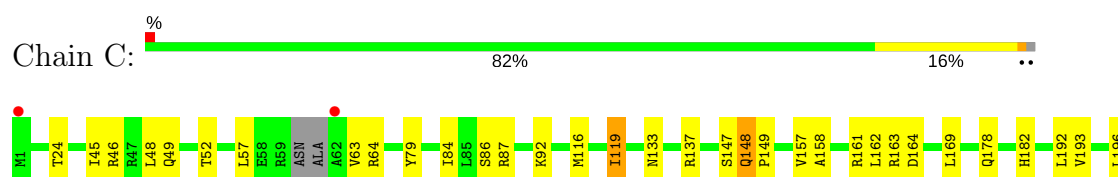
#### • Molecule 1: Deoxyguanosinetriphosphate triphosphohydrolase



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#### • Molecule 1: Deoxyguanosinetriphosphate triphosphohydrolase







- Molecule 2: RNA (5'-R(P\*CP\*CP\*C)-3')

Chain H: A horizontal bar representing the quality of Chain H, with 67% in green and 33% in yellow.



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.80Å 159.80Å 190.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.63 – 3.10 49.63 – 3.09	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.63-3.10) 95.2 (49.63-3.09)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.54 (at 3.07Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.167 , 0.223 0.167 , 0.222	Depositor DCC
$R_{free}$ test set	3876 reflections (5.11%)	DCC
Wilson B-factor (Å <sup>2</sup> )	88.3	Xtriage
Anisotropy	0.570	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 69.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	24471	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.47	0/4193	0.60	0/5674
1	B	0.42	0/4083	0.57	0/5532
1	C	0.53	0/4208	0.61	0/5692
1	D	0.47	0/4169	0.59	0/5649
1	E	0.53	0/4176	0.61	0/5651
1	F	0.48	0/4134	0.59	0/5599
2	G	1.61	1/63 (1.6%)	0.71	0/92
2	H	0.78	0/58	0.71	0/87
All	All	0.49	1/25084 (0.0%)	0.60	0/33976

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	1	C	OP3-P	-10.19	1.49	1.61

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	4092	0	4021	57	1
1	B	3983	0	3877	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4107	0	4033	41	1
1	D	4067	0	3945	45	1
1	E	4075	0	3997	43	0
1	F	4034	0	3941	34	1
2	G	58	0	34	1	0
2	H	53	0	32	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
All	All	24471	0	23880	249	2

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 5.

All (249) 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:E:61:ALA:HB2	1:F:50:GLN:HG3	1.52	0.91
1:E:371:ASP:HB3	1:E:373:SER:H	1.48	0.79
1:F:371:ASP:HB3	1:F:373:SER:H	1.48	0.79
1:B:371:ASP:HB3	1:B:373:SER:H	1.49	0.78
1:D:371:ASP:HB3	1:D:373:SER:H	1.48	0.78
1:C:371:ASP:HB3	1:C:373:SER:H	1.48	0.76
1:A:371:ASP:HB3	1:A:373:SER:H	1.51	0.74
1:C:442:ARG:CZ	1:E:127:PHE:HZ	2.01	0.73
1:C:310:LEU:O	1:C:314:ASN:HB3	1.90	0.72
1:D:310:LEU:O	1:D:314:ASN:HB3	1.90	0.72
1:A:289:GLU:HG3	1:A:316:TRP:HH2	1.55	0.72
1:E:310:LEU:O	1:E:314:ASN:HB3	1.91	0.71
1:F:310:LEU:O	1:F:314:ASN:HB3	1.91	0.71
1:F:284:ARG:HA	1:F:284:ARG:HH11	1.56	0.70
1:A:57:LEU:HD22	1:A:65:THR:HG22	1.73	0.69
1:B:413:ILE:HG21	1:B:500:LEU:HD13	1.75	0.69
1:D:119:ILE:HG23	1:D:192:LEU:HD23	1.76	0.68
1:A:310:LEU:O	1:A:314:ASN:HB3	1.93	0.68
1:F:367:ALA:HB3	1:F:370:GLU:HB3	1.75	0.68
1:B:310:LEU:O	1:B:314:ASN:HB3	1.93	0.67
1:F:119:ILE:HG23	1:F:192:LEU:HD23	1.77	0.67
1:E:367:ALA:HB3	1:E:370:GLU:HB3	1.76	0.67
1:A:68:THR:HG21	1:B:46:ARG:HG2	1.77	0.67
1:C:367:ALA:HB3	1:C:370:GLU:HB3	1.76	0.67
1:E:119:ILE:HG23	1:E:192:LEU:HD23	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:119:ILE:HG23	1:C:192:LEU:HD23	1.78	0.65
1:D:299:TRP:HD1	1:D:302:HIS:HD1	1.44	0.65
1:D:367:ALA:HB3	1:D:370:GLU:HB3	1.78	0.65
1:A:119:ILE:HG23	1:A:192:LEU:HD23	1.78	0.64
1:D:161:ARG:HD2	1:D:163:ARG:HH22	1.61	0.64
1:B:119:ILE:HG23	1:B:192:LEU:HD23	1.79	0.64
1:A:229:LEU:HD22	1:A:257:ARG:HD3	1.78	0.64
1:D:299:TRP:HD1	1:D:302:HIS:ND1	1.96	0.64
1:A:413:ILE:HG21	1:A:500:LEU:HD13	1.80	0.63
1:A:45:ILE:O	1:A:48:LEU:HB2	2.00	0.62
1:A:46:ARG:HG2	1:B:68:THR:HG21	1.81	0.62
1:D:164:ASP:OD1	1:D:164:ASP:N	2.32	0.62
1:B:400:GLU:OE1	1:D:442:ARG:NE	2.32	0.62
1:B:229:LEU:HD22	1:B:257:ARG:HD3	1.81	0.62
1:C:448:SER:HB2	1:C:451:HIS:CD2	2.37	0.60
1:A:82:LYS:HE2	1:A:107:GLU:OE1	2.01	0.60
1:C:288:VAL:HG12	1:C:316:TRP:HZ3	1.67	0.60
1:B:45:ILE:O	1:B:48:LEU:HB2	2.01	0.59
1:C:393:HIS:CD2	1:C:394:PRO:HD2	2.37	0.59
1:D:45:ILE:O	1:D:48:LEU:HB2	2.03	0.59
1:D:95:GLU:H	1:D:95:GLU:CD	2.05	0.59
1:D:289:GLU:HG3	1:D:316:TRP:HH2	1.67	0.58
1:E:158:ALA:HA	1:E:161:ARG:HH12	1.69	0.58
1:E:413:ILE:HG21	1:E:500:LEU:HD13	1.85	0.58
1:E:448:SER:HB2	1:E:451:HIS:CD2	2.39	0.58
1:D:87:ARG:HD3	1:D:353:ILE:HD12	1.86	0.57
1:F:413:ILE:HG21	1:F:500:LEU:HD13	1.86	0.57
1:A:158:ALA:HA	1:A:161:ARG:NH1	2.20	0.56
1:D:413:ILE:HG21	1:D:500:LEU:HD13	1.87	0.56
1:F:393:HIS:CD2	1:F:394:PRO:HD2	2.41	0.56
1:C:439:ILE:HD11	1:E:404:TYR:CD1	2.41	0.55
1:A:438:PRO:O	1:A:442:ARG:HG3	2.06	0.55
1:B:49:GLN:HB3	1:B:67:LEU:HD22	1.88	0.55
1:E:3:GLN:OE1	1:E:4:ILE:N	2.38	0.55
1:C:413:ILE:HG21	1:C:500:LEU:HD13	1.88	0.55
1:E:344:LEU:HD22	1:E:375:CYS:HB3	1.90	0.54
1:F:45:ILE:O	1:F:48:LEU:HB2	2.07	0.54
1:A:49:GLN:HB3	1:A:67:LEU:HD22	1.89	0.54
1:A:160:LEU:HD23	1:A:471:LEU:HD22	1.89	0.54
1:D:84:ILE:HD13	1:D:352:PHE:CD2	2.43	0.53
1:C:84:ILE:HD13	1:C:352:PHE:CD2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:448:SER:HB2	1:D:451:HIS:CD2	2.44	0.53
1:C:424:ASP:OD1	1:C:436:ARG:NH2	2.42	0.53
1:E:84:ILE:HD13	1:E:352:PHE:CD2	2.44	0.53
1:E:45:ILE:O	1:E:48:LEU:HB2	2.08	0.53
1:C:64:ARG:NH1	1:C:279:ASP:OD1	2.42	0.52
1:A:145:ALA:O	1:A:174:ARG:HG2	2.10	0.52
1:A:175:LYS:HG2	1:A:217:TRP:CD1	2.44	0.52
1:F:84:ILE:HD13	1:F:352:PHE:CD2	2.44	0.52
1:A:303:GLU:O	1:A:305:GLY:N	2.42	0.52
1:C:45:ILE:O	1:C:48:LEU:HB2	2.07	0.52
1:B:448:SER:HB2	1:B:451:HIS:CD2	2.45	0.52
1:E:133:ASN:O	1:E:137:ARG:HB2	2.09	0.52
1:E:158:ALA:HA	1:E:161:ARG:NH1	2.25	0.52
1:E:46:ARG:O	1:E:49:GLN:HG2	2.10	0.52
1:C:158:ALA:HA	1:C:161:ARG:HH12	1.75	0.51
1:A:270:ILE:HG21	1:A:341:LEU:CD2	2.40	0.51
1:A:448:SER:HB2	1:A:451:HIS:CD2	2.46	0.51
1:E:314:ASN:O	1:E:318:LYS:HB2	2.09	0.51
1:B:175:LYS:HG2	1:B:217:TRP:CD1	2.46	0.51
1:B:160:LEU:HD23	1:B:471:LEU:HD22	1.91	0.51
1:C:393:HIS:CG	1:C:394:PRO:HD2	2.46	0.51
1:C:442:ARG:NH1	1:E:127:PHE:HZ	2.08	0.51
1:F:448:SER:HB2	1:F:451:HIS:CD2	2.44	0.51
1:B:158:ALA:HA	1:B:161:ARG:NH1	2.26	0.51
1:C:269:ASP:O	1:C:272:TYR:HB3	2.10	0.50
1:B:285:ILE:HG23	1:B:393:HIS:HD2	1.74	0.50
1:F:344:LEU:HD22	1:F:375:CYS:HB3	1.93	0.50
1:A:228:TYR:OH	1:A:265:GLU:OE1	2.28	0.50
1:B:270:ILE:HG21	1:B:341:LEU:CD2	2.41	0.50
1:F:269:ASP:O	1:F:272:TYR:HB3	2.11	0.50
1:F:303:GLU:O	1:F:306:SER:HB3	2.12	0.50
1:A:116:MET:HB2	1:A:119:ILE:HD12	1.94	0.50
1:C:147:SER:OG	1:C:148:GLN:N	2.43	0.50
1:E:393:HIS:CD2	1:E:394:PRO:HD2	2.47	0.49
1:A:27:GLU:O	1:A:31:ILE:HG13	2.12	0.49
1:A:289:GLU:HG3	1:A:316:TRP:CH2	2.42	0.49
1:D:46:ARG:O	1:D:49:GLN:HG2	2.12	0.49
1:F:427:GLU:CD	1:F:436:ARG:HH22	2.16	0.49
1:C:442:ARG:CZ	1:E:127:PHE:CZ	2.90	0.49
1:C:442:ARG:NE	1:E:400:GLU:OE1	2.39	0.49
1:D:158:ALA:HA	1:D:161:ARG:HH12	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:344:LEU:HD22	1:D:375:CYS:HB3	1.95	0.49
1:A:67:LEU:HD23	1:B:67:LEU:HD23	1.94	0.48
1:B:228:TYR:OH	1:B:265:GLU:OE1	2.30	0.48
1:B:84:ILE:HD13	1:B:352:PHE:CD2	2.48	0.48
1:C:344:LEU:HD22	1:C:375:CYS:HB3	1.95	0.48
1:C:46:ARG:O	1:C:49:GLN:HG2	2.13	0.48
1:D:158:ALA:HA	1:D:161:ARG:NH1	2.29	0.48
1:E:147:SER:OG	1:E:148:GLN:N	2.46	0.48
1:F:123:PRO:HG3	1:F:488:MET:O	2.14	0.48
1:B:270:ILE:HG21	1:B:341:LEU:HD23	1.95	0.48
1:C:158:ALA:HA	1:C:161:ARG:NH1	2.28	0.48
1:E:388:LYS:HB3	1:E:389:HIS:CD2	2.49	0.48
1:B:388:LYS:HB3	1:B:389:HIS:CD2	2.48	0.47
1:F:133:ASN:O	1:F:137:ARG:HB2	2.15	0.47
1:C:133:ASN:O	1:C:137:ARG:HB2	2.15	0.47
1:F:158:ALA:HA	1:F:161:ARG:HH12	1.79	0.47
1:E:269:ASP:O	1:E:272:TYR:HB3	2.14	0.47
1:D:269:ASP:O	1:D:272:TYR:HB3	2.13	0.47
1:D:393:HIS:CD2	1:D:394:PRO:HD2	2.50	0.47
1:B:27:GLU:O	1:B:31:ILE:HG13	2.15	0.47
1:B:169:LEU:HA	1:B:169:LEU:HD23	1.74	0.46
1:F:147:SER:HB3	1:F:148:GLN:H	1.50	0.46
1:F:46:ARG:O	1:F:49:GLN:HG2	2.15	0.46
1:A:172:LEU:HD23	1:A:471:LEU:HD12	1.96	0.46
1:A:273:CYS:SG	1:A:274:VAL:N	2.88	0.46
1:B:116:MET:HB2	1:B:119:ILE:HD12	1.96	0.46
1:E:289:GLU:HG3	1:E:316:TRP:HH2	1.81	0.46
1:A:73:VAL:HG12	1:A:114:CYS:HB3	1.98	0.46
1:D:192:LEU:HD12	1:D:196:LEU:HB2	1.98	0.46
1:D:388:LYS:HB3	1:D:389:HIS:CD2	2.51	0.46
1:F:393:HIS:CG	1:F:394:PRO:HD2	2.50	0.46
1:B:438:PRO:O	1:B:442:ARG:HG3	2.16	0.46
1:A:344:LEU:HD22	1:A:375:CYS:HB3	1.97	0.46
1:C:309:SER:O	1:C:313:GLU:HB3	2.16	0.46
1:A:84:ILE:HD13	1:A:352:PHE:CD2	2.52	0.45
1:D:289:GLU:HG3	1:D:316:TRP:CH2	2.49	0.45
1:C:157:VAL:HG21	1:C:474:TYR:CE2	2.52	0.45
1:A:388:LYS:HB3	1:A:389:HIS:CD2	2.51	0.45
1:F:116:MET:HB2	1:F:119:ILE:HD12	1.98	0.45
1:F:309:SER:O	1:F:313:GLU:HB3	2.17	0.45
1:D:133:ASN:O	1:D:137:ARG:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:116:MET:HB2	1:E:119:ILE:HD12	1.98	0.45
1:A:356:LEU:N	1:A:357:PRO:HD2	2.32	0.45
1:F:158:ALA:HA	1:F:161:ARG:NH1	2.32	0.45
1:B:172:LEU:HD23	1:B:471:LEU:HD12	2.00	0.44
1:A:53:GLN:HG3	1:A:54:VAL:HG23	1.99	0.44
1:C:169:LEU:HD23	1:C:169:LEU:HA	1.76	0.44
1:C:178:GLN:O	1:C:182:HIS:HD2	2.00	0.44
1:D:116:MET:HB2	1:D:119:ILE:HD12	1.98	0.44
1:D:356:LEU:N	1:D:357:PRO:HD2	2.32	0.44
1:E:393:HIS:CG	1:E:394:PRO:HD2	2.52	0.44
1:C:501:MET:HA	1:E:405:ARG:HD2	1.99	0.44
1:A:158:ALA:HA	1:A:161:ARG:HH12	1.81	0.44
1:D:52:THR:HG22	1:D:57:LEU:HG	2.00	0.44
1:C:388:LYS:HB3	1:C:389:HIS:CD2	2.52	0.44
1:E:327:SER:O	1:E:331:GLN:HG2	2.18	0.44
1:A:166:GLU:O	1:A:170:ASN:ND2	2.50	0.44
1:B:344:LEU:HD22	1:B:375:CYS:HB3	1.99	0.44
1:D:27:GLU:O	1:D:31:ILE:HG13	2.17	0.44
1:E:309:SER:O	1:E:313:GLU:HB3	2.18	0.44
1:F:356:LEU:N	1:F:357:PRO:HD2	2.32	0.44
1:B:157:VAL:HG21	1:B:474:TYR:CE2	2.53	0.44
1:D:296:HIS:CD2	1:D:302:HIS:CE1	3.05	0.44
1:A:172:LEU:HD11	1:A:472:TRP:CZ2	2.53	0.44
1:B:309:SER:O	1:B:313:GLU:HB3	2.18	0.44
1:E:169:LEU:HA	1:E:169:LEU:HD23	1.84	0.44
1:A:243:ILE:HA	1:A:243:ILE:HD13	1.80	0.43
1:B:53:GLN:HG3	1:B:54:VAL:HG23	1.98	0.43
1:C:116:MET:HB2	1:C:119:ILE:HD12	1.99	0.43
1:C:356:LEU:N	1:C:357:PRO:HD2	2.32	0.43
1:A:320:ARG:HB3	1:A:320:ARG:HE	1.66	0.43
1:C:192:LEU:HD12	1:C:196:LEU:HB2	1.99	0.43
1:C:79:TYR:CD1	1:C:345:VAL:HG21	2.53	0.43
1:D:411:LEU:HA	1:D:411:LEU:HD23	1.89	0.43
1:D:79:TYR:CD1	1:D:345:VAL:HG21	2.54	0.43
1:A:270:ILE:HG21	1:A:341:LEU:HD23	2.00	0.43
1:B:166:GLU:O	1:B:170:ASN:ND2	2.51	0.43
1:A:400:GLU:OE1	1:E:442:ARG:NE	2.51	0.43
1:F:192:LEU:HD12	1:F:196:LEU:HB2	1.99	0.43
1:A:83:GLU:O	1:A:87:ARG:HB2	2.19	0.43
1:C:52:THR:HG22	1:C:57:LEU:HG	2.01	0.43
1:A:46:ARG:O	1:A:49:GLN:HG2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:295:LEU:HD23	1:B:385:VAL:HG21	2.01	0.43
1:E:67:LEU:HD23	1:F:67:LEU:HD23	2.00	0.43
1:A:46:ARG:O	1:A:49:GLN:N	2.52	0.43
1:E:203:TRP:CE2	1:E:249:GLU:HG3	2.54	0.43
1:F:27:GLU:O	1:F:31:ILE:HG13	2.19	0.43
1:E:356:LEU:N	1:E:357:PRO:HD2	2.34	0.43
1:A:309:SER:O	1:A:313:GLU:HB3	2.19	0.42
1:A:38:ARG:CZ	2:G:2:C:H2'	2.49	0.42
1:B:172:LEU:HD11	1:B:472:TRP:CZ2	2.54	0.42
1:A:169:LEU:HA	1:A:169:LEU:HD23	1.69	0.42
1:A:442:ARG:HE	1:C:397:GLU:HG2	1.84	0.42
1:D:316:TRP:O	1:D:319:SER:N	2.52	0.42
1:A:295:LEU:HD23	1:A:385:VAL:HG21	2.01	0.42
1:B:273:CYS:SG	1:B:274:VAL:N	2.93	0.42
1:F:327:SER:O	1:F:331:GLN:HG2	2.19	0.42
1:B:106:PHE:CE1	1:B:260:LEU:HD21	2.54	0.42
1:C:149:PRO:HB3	1:C:162:LEU:HB3	2.01	0.42
1:A:285:ILE:HG23	1:A:393:HIS:HD2	1.84	0.42
1:A:52:THR:HB	1:A:55:PHE:O	2.20	0.42
1:B:356:LEU:N	1:B:357:PRO:HD2	2.35	0.42
1:E:438:PRO:O	1:E:442:ARG:HG3	2.19	0.42
1:A:157:VAL:HG21	1:A:474:TYR:CE2	2.55	0.42
1:E:295:LEU:HD23	1:E:385:VAL:HG21	2.01	0.42
1:F:46:ARG:O	1:F:49:GLN:N	2.51	0.42
1:C:428:LEU:HD11	1:C:441:SER:HA	2.02	0.41
1:F:320:ARG:HA	1:F:320:ARG:HD2	1.43	0.41
1:B:46:ARG:O	1:B:49:GLN:HG2	2.19	0.41
1:D:161:ARG:HB3	1:D:163:ARG:HH12	1.85	0.41
1:D:393:HIS:CG	1:D:394:PRO:HD2	2.54	0.41
1:B:264:MET:HG3	1:B:265:GLU:N	2.35	0.41
1:B:461:LYS:HB2	1:B:461:LYS:HE3	1.57	0.41
1:A:169:LEU:O	1:A:173:ARG:HG3	2.21	0.41
1:B:211:LYS:O	1:B:257:ARG:HD2	2.20	0.41
1:E:192:LEU:HD12	1:E:196:LEU:HB2	2.02	0.41
1:E:172:LEU:HD23	1:E:471:LEU:HD12	2.03	0.41
1:A:192:LEU:HD12	1:A:196:LEU:HB2	2.03	0.41
1:A:31:ILE:O	1:A:34:SER:HB3	2.21	0.41
1:C:163:ARG:HD3	1:C:163:ARG:HA	1.91	0.41
1:D:157:VAL:HG21	1:D:474:TYR:CE2	2.55	0.41
1:F:273:CYS:HB2	1:F:382:TYR:HB3	2.02	0.41
1:A:229:LEU:CD2	1:A:257:ARG:HD3	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:ALA:HA	1:B:233:PRO:HB3	2.02	0.41
1:D:273:CYS:HB2	1:D:382:TYR:HB3	2.02	0.41
1:A:264:MET:HG3	1:A:265:GLU:N	2.36	0.41
1:E:479:ARG:HA	1:E:479:ARG:HD3	1.91	0.41
1:A:270:ILE:HG21	1:A:341:LEU:HD21	2.02	0.41
1:B:243:ILE:HA	1:B:243:ILE:HD13	1.82	0.41
1:E:157:VAL:HG21	1:E:474:TYR:CE2	2.56	0.41
1:B:52:THR:HB	1:B:55:PHE:O	2.21	0.40
1:C:278:GLU:HA	1:C:333:PHE:CZ	2.56	0.40
1:F:52:THR:HG22	1:F:57:LEU:HG	2.02	0.40
1:B:38:ARG:CZ	2:H:2:C:H2'	2.50	0.40
1:D:73:VAL:HG22	1:D:271:SER:HB2	2.02	0.40
1:D:309:SER:O	1:D:313:GLU:HB3	2.21	0.40
1:D:327:SER:OG	1:D:330:ASP:HB2	2.22	0.40
1:E:52:THR:HG22	1:E:57:LEU:HG	2.03	0.40
1:D:14:ARG:HG3	1:D:19:PRO:HD2	2.02	0.40
1:D:169:LEU:HD23	1:D:169:LEU:HA	1.81	0.40
1:D:438:PRO:O	1:D:442:ARG:HG3	2.21	0.40
1:D:127:PHE:HZ	1:F:442:ARG:CZ	2.35	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:ASP:O	1:F:8:LYS:NZ[3_644]	2.03	0.17
1:A:26:HIS:NE2	1:C:465:ASP:OD2[3_544]	2.15	0.05

## 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	493/505 (98%)	454 (92%)	32 (6%)	7 (1%)	13 47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	487/505 (96%)	453 (93%)	28 (6%)	6 (1%)	15	51
1	C	494/505 (98%)	468 (95%)	20 (4%)	6 (1%)	15	51
1	D	497/505 (98%)	465 (94%)	24 (5%)	8 (2%)	11	43
1	E	490/505 (97%)	466 (95%)	19 (4%)	5 (1%)	18	57
1	F	491/505 (97%)	462 (94%)	21 (4%)	8 (2%)	11	43
All	All	2952/3030 (97%)	2768 (94%)	144 (5%)	40 (1%)	13	47

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	148	GLN
1	A	304	LYS
1	B	301	GLN
1	D	326	ARG
1	F	301	GLN
1	A	310	LEU
1	A	311	VAL
1	B	310	LEU
1	B	311	VAL
1	C	272	TYR
1	C	304	LYS
1	C	310	LEU
1	D	272	TYR
1	D	325	SER
1	E	272	TYR
1	E	301	GLN
1	E	311	VAL
1	F	272	TYR
1	A	146	GLU
1	A	210	LEU
1	B	210	LEU
1	B	302	HIS
1	C	311	VAL
1	D	310	LEU
1	D	311	VAL
1	E	310	LEU
1	F	149	PRO
1	F	306	SER
1	F	310	LEU
1	C	319	SER

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Mol	Chain	Res	Type
1	D	210	LEU
1	F	300	GLY
1	F	304	LYS
1	F	311	VAL
1	A	61	ALA
1	C	210	LEU
1	D	301	GLN
1	B	299	TRP
1	E	210	LEU
1	D	270	ILE

### 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	430/450 (96%)	406 (94%)	24 (6%)	25	61
1	B	405/450 (90%)	386 (95%)	19 (5%)	30	67
1	C	432/450 (96%)	408 (94%)	24 (6%)	25	61
1	D	422/450 (94%)	400 (95%)	22 (5%)	27	63
1	E	431/450 (96%)	411 (95%)	20 (5%)	31	68
1	F	418/450 (93%)	396 (95%)	22 (5%)	26	63
All	All	2538/2700 (94%)	2407 (95%)	131 (5%)	27	63

All (131) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	THR
1	A	57	LEU
1	A	68	THR
1	A	87	ARG
1	A	95	GLU
1	A	119	ILE
1	A	147	SER
1	A	151	THR

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Mol	Chain	Res	Type
1	A	193	VAL
1	A	198	ARG
1	A	264	MET
1	A	271	SER
1	A	272	TYR
1	A	286	PHE
1	A	318	LYS
1	A	328	THR
1	A	344	LEU
1	A	371	ASP
1	A	384	ASN
1	A	423	SER
1	A	436	ARG
1	A	450	ARG
1	A	479	ARG
1	A	485	ILE
1	B	3	GLN
1	B	24	THR
1	B	68	THR
1	B	119	ILE
1	B	151	THR
1	B	152	ASP
1	B	193	VAL
1	B	198	ARG
1	B	264	MET
1	B	271	SER
1	B	272	TYR
1	B	286	PHE
1	B	302	HIS
1	B	344	LEU
1	B	371	ASP
1	B	384	ASN
1	B	423	SER
1	B	479	ARG
1	B	485	ILE
1	C	24	THR
1	C	63	VAL
1	C	86	SER
1	C	87	ARG
1	C	92	LYS
1	C	119	ILE
1	C	148	GLN

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Mol	Chain	Res	Type
1	C	164	ASP
1	C	193	VAL
1	C	238	SER
1	C	264	MET
1	C	273	CYS
1	C	286	PHE
1	C	302	HIS
1	C	330	ASP
1	C	344	LEU
1	C	371	ASP
1	C	384	ASN
1	C	423	SER
1	C	436	ARG
1	C	450	ARG
1	C	479	ARG
1	C	485	ILE
1	C	495	ASP
1	D	24	THR
1	D	68	THR
1	D	86	SER
1	D	95	GLU
1	D	119	ILE
1	D	139	ARG
1	D	150	LEU
1	D	164	ASP
1	D	193	VAL
1	D	238	SER
1	D	264	MET
1	D	273	CYS
1	D	286	PHE
1	D	330	ASP
1	D	344	LEU
1	D	371	ASP
1	D	384	ASN
1	D	423	SER
1	D	436	ARG
1	D	479	ARG
1	D	485	ILE
1	D	495	ASP
1	E	24	THR
1	E	68	THR
1	E	86	SER

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Mol	Chain	Res	Type
1	E	90	GLU
1	E	119	ILE
1	E	167	GLU
1	E	193	VAL
1	E	238	SER
1	E	264	MET
1	E	273	CYS
1	E	286	PHE
1	E	330	ASP
1	E	344	LEU
1	E	371	ASP
1	E	384	ASN
1	E	423	SER
1	E	450	ARG
1	E	479	ARG
1	E	485	ILE
1	E	495	ASP
1	F	24	THR
1	F	68	THR
1	F	86	SER
1	F	119	ILE
1	F	147	SER
1	F	193	VAL
1	F	238	SER
1	F	264	MET
1	F	273	CYS
1	F	284	ARG
1	F	286	PHE
1	F	320	ARG
1	F	327	SER
1	F	330	ASP
1	F	344	LEU
1	F	371	ASP
1	F	384	ASN
1	F	423	SER
1	F	450	ARG
1	F	479	ARG
1	F	485	ILE
1	F	495	ASP

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	302	HIS
1	A	384	ASN
1	B	302	HIS
1	B	384	ASN
1	C	13	HIS
1	C	141	HIS
1	C	182	HIS
1	C	384	ASN
1	C	393	HIS
1	C	505	GLN
1	D	13	HIS
1	D	141	HIS
1	D	182	HIS
1	D	227	HIS
1	D	296	HIS
1	D	384	ASN
1	E	13	HIS
1	E	141	HIS
1	E	182	HIS
1	E	384	ASN
1	E	505	GLN
1	F	13	HIS
1	F	141	HIS
1	F	182	HIS
1	F	227	HIS
1	F	384	ASN
1	F	393	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	G	0/3	-	-
2	H	0/3	-	-
All	All	0/6	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 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 2 ligands modelled in this entry, 2 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	499/505 (98%)	-0.21	11 (2%) 62 41	61, 104, 156, 212	0
1	B	495/505 (98%)	-0.02	16 (3%) 48 25	73, 125, 176, 213	0
1	C	500/505 (99%)	-0.34	3 (0%) 89 77	55, 89, 140, 204	0
1	D	501/505 (99%)	-0.08	8 (1%) 72 51	59, 113, 180, 217	0
1	E	496/505 (98%)	-0.34	1 (0%) 94 89	56, 84, 139, 193	0
1	F	497/505 (98%)	-0.17	6 (1%) 79 61	65, 110, 175, 219	0
2	G	3/3 (100%)	-0.00	0 100 100	95, 95, 109, 155	0
2	H	3/3 (100%)	0.46	0 100 100	117, 117, 119, 204	0
All	All	2994/3036 (98%)	-0.19	45 (1%) 74 54	55, 104, 166, 219	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1	MET	7.5
1	D	323	SER	4.4
1	B	168	PRO	4.4
1	B	162	LEU	3.6
1	D	164	ASP	3.6
1	A	1	MET	3.5
1	A	302	HIS	3.5
1	A	2	ALA	3.4
1	B	60	ASN	3.4
1	F	162	LEU	3.4
1	A	322	ASN	3.1
1	D	162	LEU	3.0
1	B	160	LEU	2.9
1	A	6	PHE	2.8
1	D	151	THR	2.8
1	C	305	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	F	305	GLY	2.8
1	B	169	LEU	2.6
1	F	2	ALA	2.6
1	D	62	ALA	2.6
1	B	172	LEU	2.6
1	D	472	TRP	2.5
1	D	58	GLU	2.5
1	B	434	VAL	2.5
1	B	474	TYR	2.5
1	F	389	HIS	2.5
1	A	362	GLY	2.4
1	A	162	LEU	2.4
1	B	165	GLY	2.4
1	B	235	TYR	2.3
1	F	147	SER	2.3
1	D	163	ARG	2.3
1	B	157	VAL	2.3
1	A	360	PHE	2.3
1	A	361	ALA	2.3
1	B	56	PRO	2.3
1	E	302	HIS	2.2
1	B	356	LEU	2.2
1	B	140	LEU	2.2
1	A	148	GLN	2.1
1	C	62	ALA	2.1
1	A	300	GLY	2.1
1	F	295	LEU	2.1
1	B	159	ALA	2.0
1	B	471	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

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( $\text{\AA}^2$ )	Q<0.9
3	MG	A	1000	1/1	0.93	0.24	0.14	120,120,120,120	0
3	MG	B	1000	1/1	0.76	0.29	-	134,134,134,134	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.