



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:11 PM GMT

PDB ID : 4R1R  
Title : RIBONUCLEOTIDE REDUCTASE R1 PROTEIN WITH SUBSTRATE,  
GDP AND EFFECTOR DTTP FROM ESCHERICHIA COLI  
Authors : Eriksson, M.; Eklund, H.  
Deposited on : 1997-07-22  
Resolution : 3.20 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:

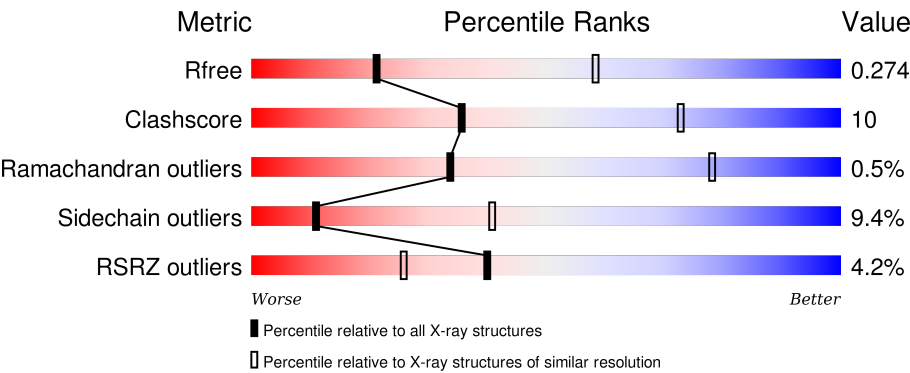
MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	761	<div><div>7%</div><div><div></div><div>70%</div><div>24%</div><div>• •</div></div></div>
1	B	761	<div><div>2%</div><div><div></div><div>70%</div><div>24%</div><div>• •</div></div></div>
1	C	761	<div><div>2%</div><div><div></div><div>70%</div><div>24%</div><div>• •</div></div></div>
2	D	20	<div><div>20%</div><div><div></div><div>65%</div><div>10%</div><div>5%</div><div>20%</div></div></div>
2	E	20	<div><div>15%</div><div><div></div><div>60%</div><div>15%</div><div>5%</div><div>20%</div></div></div>

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Mol	Chain	Length	Quality of chain
2	F	20	
2	P	20	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	TTP	A	762	-	-	-	X
4	GDP	A	763	-	-	-	X
4	GDP	B	763	-	-	-	X
4	GDP	C	763	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 18093 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 RIBONUCLEOTIDE REDUCTASE R1 PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	733	Total	C	N	O	S	0	0	0
			5836	3708	1002	1103	23			
1	B	733	Total	C	N	O	S	0	0	0
			5836	3708	1002	1103	23			
1	C	733	Total	C	N	O	S	0	0	0
			5836	3708	1002	1103	23			

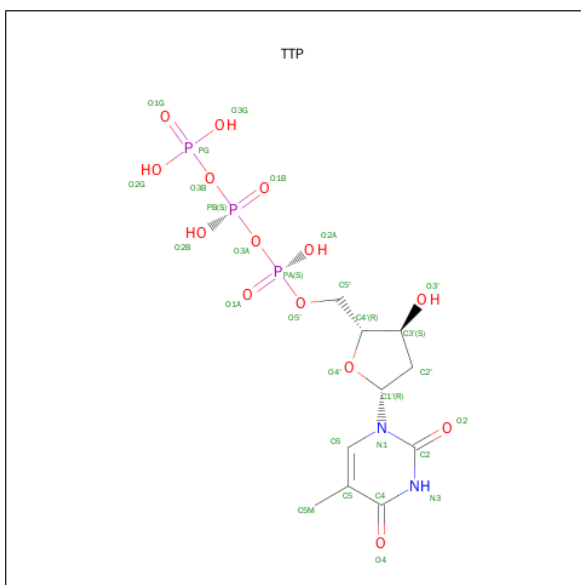
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	292	ALA	CYS	ENGINEERED	UNP P00452
B	292	ALA	CYS	ENGINEERED	UNP P00452
C	292	ALA	CYS	ENGINEERED	UNP P00452

- Molecule 2 is a protein called RIBONUCLEOTIDE REDUCTASE R2 PROTEIN.

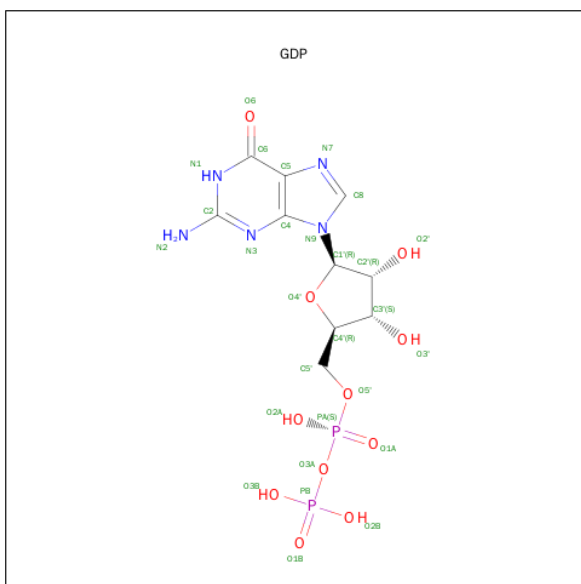
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	16	Total	C	N	O	0	0	0
			129	77	19	33			
2	E	16	Total	C	N	O	0	0	0
			129	77	19	33			
2	F	16	Total	C	N	O	0	0	0
			129	77	19	33			
2	P	3	Total	C	N	O	0	0	0
			27	20	3	4			

- Molecule 3 is THYMIDINE-5'-TRIPHOSPHATE (three-letter code: TTP) (formula:  $C_{10}H_{17}N_2O_{14}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 29	C 10	N 2	O 14	P 3	0	0
3	B	1	Total 29	C 10	N 2	O 14	P 3	0	0
3	C	1	Total 29	C 10	N 2	O 14	P 3	0	0

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{11}\text{P}_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 28	C 10	N 5	O 11	P 2	0	0
4	B	1	Total 28	C 10	N 5	O 11	P 2	0	0
4	C	1	Total 28	C 10	N 5	O 11	P 2	0	0

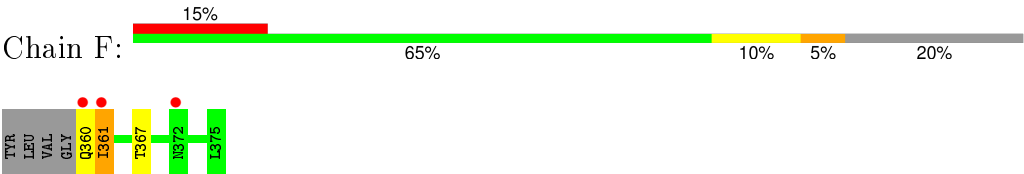








● Molecule 2: RIBONUCLEOTIDE REDUCTASE R2 PROTEIN



● Molecule 2: RIBONUCLEOTIDE REDUCTASE R2 PROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	224.02Å 224.02Å 335.97Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.20 64.67 – 3.02	Depositor EDS
% Data completeness (in resolution range)	96.1 (20.00-3.20) 95.8 (64.67-3.02)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.28 (at 3.01Å)	Xtriage
Refinement program	REFMAC, TNT	Depositor
R, $R_{free}$	0.278 , 0.308 0.266 , 0.274	Depositor DCC
$R_{free}$ test set	859 reflections (1.68%)	DCC
Wilson B-factor (Å <sup>2</sup> )	57.2	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 19.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 61188 reflections	Xtriage
$F_o, F_c$ correlation	0.85	EDS
Total number of atoms	18093	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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

### 5.1 Standard geometry

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

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	0.37	0/5964	0.90	4/8078 (0.0%)
1	B	0.37	0/5964	0.90	4/8078 (0.0%)
1	C	0.37	0/5964	0.90	4/8078 (0.0%)
2	D	0.31	0/129	0.72	0/173
2	E	0.31	0/129	0.72	0/173
2	F	0.31	0/129	0.72	0/173
2	P	0.69	0/27	1.93	1/36 (2.8%)
All	All	0.37	0/18306	0.89	13/24789 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	115	TYR	CB-CG-CD1	6.10	124.66	121.00
1	A	115	TYR	CB-CG-CD1	6.08	124.65	121.00
1	B	115	TYR	CB-CG-CD1	6.05	124.63	121.00
1	C	620	MET	CG-SD-CE	5.69	109.30	100.20
1	A	620	MET	CG-SD-CE	5.68	109.29	100.20
1	B	620	MET	CG-SD-CE	5.67	109.27	100.20
1	C	406	ARG	NE-CZ-NH2	5.33	122.96	120.30
1	B	406	ARG	NE-CZ-NH2	5.32	122.96	120.30
1	A	406	ARG	NE-CZ-NH2	5.28	122.94	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	1	TYR	CA-CB-CG	5.10	123.08	113.40
1	A	703	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	B	703	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	C	703	ARG	NE-CZ-NH2	-5.01	117.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	292	ALA	Mainchain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5836	0	5764	118	0
1	B	5836	0	5764	115	0
1	C	5836	0	5764	123	0
2	D	129	0	111	1	0
2	E	129	0	111	2	0
2	F	129	0	111	1	0
2	P	27	0	31	9	0
3	A	29	0	13	7	0
3	B	29	0	13	8	0
3	C	29	0	13	7	0
4	A	28	0	12	1	0
4	B	28	0	12	1	0
4	C	28	0	12	1	0
All	All	18093	0	17731	346	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 10.

All (346) 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:227:LEU:HB2	1:A:460:ALA:HB3	1.57	0.87
1:C:227:LEU:HB2	1:C:460:ALA:HB3	1.57	0.84
1:B:227:LEU:HB2	1:B:460:ALA:HB3	1.57	0.84
1:C:120:LEU:HD13	2:P:1:TYR:CG	2.13	0.83
1:C:394:LYS:HB3	1:C:397:GLU:HG3	1.63	0.81
1:B:394:LYS:HB3	1:B:397:GLU:HG3	1.63	0.81
1:A:394:LYS:HB3	1:A:397:GLU:HG3	1.63	0.80
1:B:709:VAL:HB	2:E:361:ILE:HG22	1.64	0.80
1:C:215:VAL:O	1:C:216:ARG:HB3	1.82	0.80
1:A:215:VAL:O	1:A:216:ARG:HB3	1.82	0.79
1:C:709:VAL:HB	2:F:361:ILE:HG22	1.64	0.78
1:A:621:PRO:HD3	1:A:694:SER:OG	1.84	0.78
1:B:621:PRO:HD3	1:B:694:SER:OG	1.84	0.78
1:B:215:VAL:O	1:B:216:ARG:HB3	1.82	0.78
1:C:621:PRO:HD3	1:C:694:SER:OG	1.84	0.77
1:A:709:VAL:HB	2:D:361:ILE:HG22	1.64	0.77
1:C:658:ASP:HB3	1:C:662:LEU:HD12	1.70	0.73
1:A:658:ASP:HB3	1:A:662:LEU:HD12	1.70	0.73
1:B:658:ASP:HB3	1:B:662:LEU:HD12	1.70	0.73
1:A:268:ILE:HB	1:A:273:ALA:HB3	1.71	0.72
1:B:268:ILE:HB	1:B:273:ALA:HB3	1.72	0.71
1:A:149:LYS:HG2	1:A:652:LEU:HD21	1.73	0.71
1:C:268:ILE:HB	1:C:273:ALA:HB3	1.71	0.70
1:C:320:LYS:HE2	1:C:411:ARG:HB2	1.74	0.70
1:A:320:LYS:HE2	1:A:411:ARG:HB2	1.74	0.70
1:B:320:LYS:HE2	1:B:411:ARG:HB2	1.73	0.70
1:C:149:LYS:HG2	1:C:652:LEU:HD21	1.73	0.70
1:B:149:LYS:HG2	1:B:652:LEU:HD21	1.73	0.69
1:A:279:ILE:HB	1:A:280:PRO:HD3	1.76	0.68
1:A:155:TYR:HE1	1:A:209:THR:HG23	1.59	0.67
1:B:279:ILE:HB	1:B:280:PRO:HD3	1.75	0.67
1:C:279:ILE:HB	1:C:280:PRO:HD3	1.75	0.67
1:B:155:TYR:HE1	1:B:209:THR:HG23	1.59	0.67
1:C:155:TYR:HE1	1:C:209:THR:HG23	1.59	0.67
1:B:430:ILE:HG21	1:B:570:GLU:HG2	1.76	0.66
1:C:430:ILE:HG21	1:C:570:GLU:HG2	1.76	0.66
1:A:430:ILE:HG21	1:A:570:GLU:HG2	1.76	0.65
1:A:313:VAL:HG22	1:A:317:LEU:HD22	1.79	0.65
1:A:439:CYS:HA	1:A:730:TYR:CE1	2.33	0.64
1:B:313:VAL:HG22	1:B:317:LEU:HD22	1.79	0.63
1:C:111:GLU:OE2	2:P:2:LEU:N	2.31	0.63
1:C:313:VAL:HG22	1:C:317:LEU:HD22	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:444:LEU:HD22	1:A:512:THR:HG21	1.81	0.62
1:C:439:CYS:HA	1:C:730:TYR:CE1	2.33	0.62
1:B:439:CYS:HA	1:B:730:TYR:CE1	2.33	0.62
1:C:444:LEU:HD22	1:C:512:THR:HG21	1.81	0.62
1:B:444:LEU:HD22	1:B:512:THR:HG21	1.81	0.62
1:A:276:THR:HG23	1:B:293:SER:O	2.01	0.60
1:C:250:GLN:O	1:C:251:ARG:HB2	2.01	0.60
1:A:79:TYR:O	1:A:83:ARG:HG3	2.01	0.60
1:C:620:MET:HG2	1:C:621:PRO:O	2.02	0.60
1:B:79:TYR:O	1:B:83:ARG:HG3	2.01	0.60
1:A:342:LEU:HD13	1:A:376:GLU:HG3	1.83	0.60
1:A:250:GLN:O	1:A:251:ARG:HB2	2.01	0.60
1:B:250:GLN:O	1:B:251:ARG:HB2	2.01	0.60
1:A:275:HIS:CD2	3:A:762:TTP:H1'	2.36	0.60
1:C:79:TYR:O	1:C:83:ARG:HG3	2.01	0.60
1:B:275:HIS:CD2	3:B:762:TTP:H1'	2.36	0.60
1:C:342:LEU:HD13	1:C:376:GLU:HG3	1.83	0.60
1:B:342:LEU:HD13	1:B:376:GLU:HG3	1.83	0.59
1:A:620:MET:HG2	1:A:621:PRO:O	2.02	0.59
1:B:620:MET:HG2	1:B:621:PRO:O	2.02	0.59
1:C:275:HIS:CD2	3:C:762:TTP:H1'	2.36	0.59
1:A:619:LEU:HD12	1:A:693:ILE:HG12	1.85	0.59
1:A:268:ILE:HD13	3:A:762:TTP:C4	2.38	0.59
1:B:619:LEU:HD12	1:B:693:ILE:HG12	1.85	0.58
1:B:268:ILE:HG21	3:B:762:TTP:C5	2.38	0.58
1:A:268:ILE:HD11	1:A:275:HIS:HA	1.86	0.58
1:A:248:VAL:HG11	1:A:289:VAL:HA	1.86	0.58
1:C:111:GLU:HG3	2:P:2:LEU:O	2.04	0.58
1:B:248:VAL:HG11	1:B:289:VAL:HA	1.86	0.58
1:C:248:VAL:HG11	1:C:289:VAL:HA	1.86	0.58
1:C:619:LEU:HD12	1:C:693:ILE:HG12	1.85	0.58
1:A:268:ILE:HG21	3:A:762:TTP:C5	2.38	0.58
1:B:268:ILE:HD13	3:B:762:TTP:C4	2.38	0.58
1:C:268:ILE:HG21	3:C:762:TTP:C5	2.38	0.58
1:B:232:ASP:OD1	1:B:262:ARG:HG2	2.04	0.58
1:C:232:ASP:OD1	1:C:262:ARG:HG2	2.04	0.58
1:C:268:ILE:HD13	3:C:762:TTP:C4	2.38	0.58
1:A:384:LYS:NZ	1:A:392:ARG:HH22	2.02	0.57
1:B:384:LYS:NZ	1:B:392:ARG:HH22	2.02	0.57
1:C:384:LYS:NZ	1:C:392:ARG:HH22	2.02	0.57
1:A:232:ASP:OD1	1:A:262:ARG:HG2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:268:ILE:HD11	1:C:275:HIS:HA	1.86	0.57
1:B:268:ILE:HD11	1:B:275:HIS:HA	1.86	0.56
1:A:291:SER:O	1:B:276:THR:HG21	2.05	0.56
1:C:279:ILE:HD12	1:C:319:LEU:HD21	1.87	0.56
1:C:110:VAL:HG11	1:C:120:LEU:HD12	1.87	0.56
1:A:279:ILE:HD12	1:A:319:LEU:HD21	1.87	0.56
1:B:279:ILE:HD12	1:B:319:LEU:HD21	1.87	0.56
1:B:110:VAL:HG11	1:B:120:LEU:HD12	1.87	0.56
1:A:268:ILE:HG21	3:A:762:TTP:C6	2.41	0.56
1:C:555:SER:HB3	1:C:611:LEU:HD22	1.88	0.56
1:B:268:ILE:HG21	3:B:762:TTP:C6	2.41	0.55
1:B:555:SER:HB3	1:B:611:LEU:HD22	1.88	0.55
1:A:110:VAL:HG11	1:A:120:LEU:HD12	1.87	0.55
1:C:120:LEU:HD13	2:P:1:TYR:CB	2.36	0.55
1:A:276:THR:HG22	1:A:280:PRO:HG2	1.88	0.55
1:A:555:SER:HB3	1:A:611:LEU:HD22	1.88	0.55
1:A:268:ILE:HD13	3:A:762:TTP:N3	2.22	0.55
1:C:268:ILE:HG21	3:C:762:TTP:C6	2.40	0.55
1:C:276:THR:HG22	1:C:280:PRO:HG2	1.88	0.55
1:B:465:SER:HB2	1:B:489:LEU:HD11	1.89	0.54
1:A:99:PRO:HG2	1:A:137:HIS:CD2	2.42	0.54
1:B:346:ARG:HD2	1:B:352:ASP:O	2.08	0.54
1:B:268:ILE:HD13	3:B:762:TTP:N3	2.22	0.54
1:C:268:ILE:HD13	3:C:762:TTP:N3	2.22	0.54
1:B:276:THR:HG22	1:B:280:PRO:HG2	1.88	0.54
1:C:346:ARG:HD2	1:C:352:ASP:O	2.08	0.54
1:B:99:PRO:HG2	1:B:137:HIS:CD2	2.42	0.54
1:A:346:ARG:HD2	1:A:352:ASP:O	2.08	0.54
1:C:99:PRO:HG2	1:C:137:HIS:CD2	2.42	0.53
1:C:111:GLU:CG	2:P:2:LEU:HB2	2.38	0.53
1:A:465:SER:HB2	1:A:489:LEU:HD11	1.90	0.53
1:C:622:SER:O	1:C:633:ASN:HB3	2.08	0.53
1:C:555:SER:HB2	1:C:616:LEU:HD21	1.90	0.53
1:C:465:SER:HB2	1:C:489:LEU:HD11	1.89	0.53
1:A:264:LEU:HD11	1:B:294:GLN:NE2	2.24	0.53
1:B:555:SER:HB2	1:B:616:LEU:HD21	1.90	0.53
1:A:5:LEU:O	1:A:17:ILE:HB	2.09	0.53
1:A:622:SER:O	1:A:633:ASN:HB3	2.08	0.52
1:A:555:SER:HB2	1:A:616:LEU:HD21	1.90	0.52
1:A:268:ILE:O	1:A:269:ARG:HB3	2.10	0.52
1:B:622:SER:O	1:B:633:ASN:HB3	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:268:ILE:O	1:B:269:ARG:HB3	2.10	0.52
1:A:249:SER:HB2	3:B:762:TTP:C4	2.45	0.52
1:B:5:LEU:O	1:B:17:ILE:HB	2.09	0.52
1:A:187:GLU:OE1	1:C:186:ARG:HG3	2.10	0.52
1:C:135:ILE:HD11	1:C:174:ILE:HG21	1.92	0.52
1:A:529:LYS:HD2	1:A:535:SER:O	2.10	0.52
1:B:37:SER:OG	1:B:40:GLN:HB2	2.10	0.52
1:A:135:ILE:HD11	1:A:174:ILE:HG21	1.92	0.52
1:B:135:ILE:HD11	1:B:174:ILE:HG21	1.92	0.52
1:C:5:LEU:O	1:C:17:ILE:HB	2.09	0.52
1:A:37:SER:OG	1:A:40:GLN:HB2	2.10	0.51
1:B:561:GLU:HG2	1:B:562:GLN:HG3	1.92	0.51
1:C:120:LEU:HD13	2:P:1:TYR:CD2	2.45	0.51
1:C:37:SER:OG	1:C:40:GLN:HB2	2.10	0.51
1:B:529:LYS:HD2	1:B:535:SER:O	2.10	0.51
1:A:369:PHE:CG	1:A:434:ARG:HG2	2.46	0.51
1:C:268:ILE:O	1:C:269:ARG:HB3	2.10	0.51
1:C:668:LEU:HB2	1:C:671:GLU:HG3	1.93	0.51
1:B:668:LEU:HB2	1:B:671:GLU:HG3	1.93	0.51
3:A:762:TTP:C4	1:B:249:SER:HB2	2.46	0.50
1:C:369:PHE:CG	1:C:434:ARG:HG2	2.45	0.50
1:C:529:LYS:HD2	1:C:535:SER:O	2.10	0.50
1:B:369:PHE:CG	1:B:434:ARG:HG2	2.45	0.50
1:B:167:GLU:OE2	1:B:216:ARG:NH1	2.45	0.50
1:A:561:GLU:HG2	1:A:562:GLN:HG3	1.92	0.50
1:B:510:ARG:NH2	1:B:570:GLU:OE1	2.45	0.50
1:C:670:TRP:CE2	1:C:735:ARG:HG3	2.47	0.50
1:A:610:GLY:HA3	2:P:2:LEU:CD2	2.42	0.50
1:A:670:TRP:CE2	1:A:735:ARG:HG3	2.47	0.50
1:B:670:TRP:CE2	1:B:735:ARG:HG3	2.47	0.50
1:A:668:LEU:HB2	1:A:671:GLU:HG3	1.93	0.50
1:C:561:GLU:HG2	1:C:562:GLN:HG3	1.92	0.50
1:C:167:GLU:OE2	1:C:216:ARG:NH1	2.45	0.49
1:C:510:ARG:NH2	1:C:570:GLU:OE1	2.45	0.49
1:A:207:LEU:HD23	1:A:465:SER:OG	2.13	0.49
1:A:217:THR:OG1	1:A:219:THR:HG22	2.12	0.49
1:C:312:GLU:O	1:C:316:LEU:HG	2.13	0.49
1:C:207:LEU:HD23	1:C:465:SER:OG	2.13	0.49
1:A:276:THR:CG2	1:A:280:PRO:HG2	2.43	0.49
1:A:209:THR:N	1:A:210:PRO:HD2	2.28	0.49
1:A:510:ARG:NH2	1:A:570:GLU:OE1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:ALA:HA	1:A:33:LEU:HD12	1.94	0.49
1:C:217:THR:OG1	1:C:219:THR:HG22	2.12	0.49
1:A:433:VAL:HG11	1:A:443:ALA:HB1	1.94	0.49
1:B:207:LEU:HD23	1:B:465:SER:OG	2.13	0.49
1:A:187:GLU:CD	1:C:186:ARG:NH1	2.66	0.49
1:B:217:THR:OG1	1:B:219:THR:HG22	2.12	0.49
1:B:312:GLU:O	1:B:316:LEU:HG	2.13	0.49
1:B:209:THR:N	1:B:210:PRO:HD2	2.28	0.49
1:C:30:ALA:HA	1:C:33:LEU:HD12	1.94	0.49
1:C:433:VAL:HG11	1:C:443:ALA:HB1	1.94	0.48
1:A:167:GLU:OE2	1:A:216:ARG:NH1	2.45	0.48
1:B:30:ALA:HA	1:B:33:LEU:HD12	1.94	0.48
1:A:187:GLU:OE2	1:C:186:ARG:NH1	2.46	0.48
1:C:461:LEU:HD11	1:C:503:ALA:HB1	1.96	0.48
1:C:285:PHE:O	1:C:289:VAL:HG23	2.14	0.48
1:A:312:GLU:O	1:A:316:LEU:HG	2.13	0.48
1:B:285:PHE:O	1:B:289:VAL:HG23	2.14	0.48
1:B:583:TYR:CD2	1:B:687:LYS:HD2	2.48	0.48
1:C:583:TYR:CD2	1:C:687:LYS:HD2	2.48	0.48
1:C:209:THR:N	1:C:210:PRO:HD2	2.28	0.48
1:A:285:PHE:O	1:A:289:VAL:HG23	2.14	0.48
1:B:433:VAL:HG11	1:B:443:ALA:HB1	1.95	0.48
1:B:276:THR:CG2	1:B:280:PRO:HG2	2.43	0.48
1:A:17:ILE:HD13	1:A:18:ASN:N	2.29	0.48
1:A:583:TYR:CD2	1:A:687:LYS:HD2	2.48	0.48
1:C:217:THR:HB	1:C:218:PRO:HD2	1.96	0.48
1:B:224:SER:O	1:B:253:GLY:N	2.41	0.47
1:A:212:MET:O	1:A:216:ARG:NH2	2.47	0.47
1:B:552:LEU:HD23	1:B:616:LEU:HD13	1.96	0.47
1:B:217:THR:HB	1:B:218:PRO:HD2	1.96	0.47
1:C:212:MET:O	1:C:216:ARG:NH2	2.47	0.47
1:C:276:THR:CG2	1:C:280:PRO:HG2	2.43	0.47
1:B:461:LEU:HD11	1:B:503:ALA:HB1	1.96	0.47
1:A:134:PHE:CG	1:A:194:LYS:HG3	2.50	0.47
1:A:552:LEU:HD23	1:A:616:LEU:HD13	1.96	0.47
1:A:268:ILE:HD12	1:A:273:ALA:HB1	1.96	0.47
1:B:268:ILE:HD12	1:B:273:ALA:HB1	1.96	0.47
1:B:5:LEU:HD22	1:B:17:ILE:HG13	1.97	0.47
1:C:17:ILE:HD13	1:C:18:ASN:N	2.29	0.47
1:C:5:LEU:HD22	1:C:17:ILE:HG13	1.97	0.47
1:B:134:PHE:CG	1:B:194:LYS:HG3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:134:PHE:CG	1:C:194:LYS:HG3	2.50	0.47
1:B:17:ILE:HD13	1:B:18:ASN:N	2.29	0.47
1:A:461:LEU:HD11	1:A:503:ALA:HB1	1.96	0.47
1:C:224:SER:O	1:C:253:GLY:N	2.40	0.47
1:B:181:PHE:O	1:B:189:ARG:HD2	2.15	0.46
1:B:212:MET:O	1:B:216:ARG:NH2	2.47	0.46
1:A:29:ALA:O	1:A:83:ARG:HD2	2.15	0.46
1:A:181:PHE:O	1:A:189:ARG:HD2	2.15	0.46
1:C:181:PHE:O	1:C:189:ARG:HD2	2.15	0.46
1:A:610:GLY:HA3	2:P:2:LEU:HD23	1.97	0.46
1:B:29:ALA:O	1:B:83:ARG:HD2	2.15	0.46
1:C:29:ALA:O	1:C:83:ARG:HD2	2.15	0.46
1:C:552:LEU:HD23	1:C:616:LEU:HD13	1.96	0.46
1:C:268:ILE:HD12	1:C:273:ALA:HB1	1.96	0.46
1:A:5:LEU:HD22	1:A:17:ILE:HG13	1.97	0.46
1:A:217:THR:HB	1:A:218:PRO:HD2	1.96	0.46
1:A:208:PRO:HB2	1:A:210:PRO:HD2	1.98	0.45
1:A:171:PHE:HA	1:A:174:ILE:HG22	1.98	0.45
1:C:171:PHE:HA	1:C:174:ILE:HG22	1.98	0.45
1:A:276:THR:HG21	1:B:293:SER:H	1.82	0.45
1:C:660:GLU:HB3	1:C:661:HIS:HD2	1.82	0.45
1:B:660:GLU:HB3	1:B:661:HIS:HD2	1.82	0.45
1:C:208:PRO:HB2	1:C:210:PRO:HD2	1.98	0.45
1:B:226:VAL:HA	1:B:460:ALA:O	2.17	0.44
1:B:262:ARG:HG3	1:B:275:HIS:CD2	2.52	0.44
1:C:18:ASN:ND2	1:C:21:LYS:HG3	2.32	0.44
1:B:180:LEU:CD1	1:B:488:ALA:HB1	2.48	0.44
1:A:660:GLU:HB3	1:A:661:HIS:HD2	1.82	0.44
1:B:208:PRO:HB2	1:B:210:PRO:HD2	1.98	0.44
1:C:262:ARG:HG3	1:C:275:HIS:CD2	2.52	0.44
1:A:440:LEU:HD12	1:A:728:THR:HB	1.98	0.44
1:C:19:LEU:HD22	1:C:46:HIS:CE1	2.53	0.44
1:B:440:LEU:HD12	1:B:728:THR:HB	1.98	0.44
1:B:19:LEU:HD22	1:B:46:HIS:CE1	2.53	0.44
1:C:226:VAL:HA	1:C:460:ALA:O	2.18	0.44
1:A:18:ASN:ND2	1:A:21:LYS:HG3	2.32	0.44
1:B:301:ALA:HB3	1:B:438:LEU:CD2	2.48	0.44
1:C:623:GLU:O	1:C:627:GLN:HG3	2.17	0.44
1:A:301:ALA:HB3	1:A:438:LEU:CD2	2.48	0.44
1:A:275:HIS:HE2	3:A:762:TTP:H2'1	1.83	0.44
1:A:145:TYR:CZ	1:A:149:LYS:HD3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:275:HIS:HE2	3:C:762:TTP:H2'1	1.83	0.44
1:C:145:TYR:CZ	1:C:149:LYS:HD3	2.53	0.44
1:C:301:ALA:HB3	1:C:438:LEU:CD2	2.48	0.44
1:C:440:LEU:HD12	1:C:728:THR:HB	1.98	0.44
1:A:238:ASN:HB3	1:B:242:SER:OG	2.17	0.44
1:B:275:HIS:HE2	3:B:762:TTP:H2'1	1.83	0.44
1:A:262:ARG:HG3	1:A:275:HIS:CD2	2.52	0.44
1:B:18:ASN:ND2	1:B:21:LYS:HG3	2.32	0.44
1:A:623:GLU:O	1:A:627:GLN:HG3	2.18	0.44
1:B:171:PHE:HA	1:B:174:ILE:HG22	1.98	0.43
1:C:180:LEU:CD1	1:C:488:ALA:HB1	2.48	0.43
1:B:208:PRO:HD2	1:B:211:ILE:HD12	2.00	0.43
1:C:328:ASN:HA	1:C:328:ASN:HD22	1.64	0.43
1:B:145:TYR:CZ	1:B:149:LYS:HD3	2.52	0.43
1:A:180:LEU:CD1	1:A:488:ALA:HB1	2.48	0.43
1:B:623:GLU:O	1:B:627:GLN:HG3	2.18	0.43
1:C:672:MET:HA	1:C:673:PRO:HD3	1.80	0.43
1:C:208:PRO:HD2	1:C:211:ILE:HD12	2.00	0.43
1:A:226:VAL:HA	1:A:460:ALA:O	2.17	0.43
1:B:339:ILE:HG22	1:B:340:ASN:N	2.34	0.43
1:A:221:GLN:OE1	1:A:250:GLN:HG2	2.19	0.43
1:B:584:LYS:NZ	2:E:375:LEU:O	2.46	0.43
1:A:447:LYS:HA	1:A:448:PRO:HD3	1.90	0.43
1:A:19:LEU:HD22	1:A:46:HIS:CE1	2.53	0.43
1:A:426:PHE:O	1:A:428:PRO:HD3	2.19	0.43
1:B:426:PHE:O	1:B:428:PRO:HD3	2.19	0.43
1:A:208:PRO:HD2	1:A:211:ILE:HD12	2.00	0.43
1:C:111:GLU:CD	2:P:2:LEU:HB2	2.39	0.43
1:C:369:PHE:CD1	1:C:434:ARG:HA	2.54	0.43
1:B:369:PHE:CD1	1:B:434:ARG:HA	2.54	0.43
1:C:86:ILE:HG21	1:C:140:ASP:HB3	2.01	0.43
1:A:283:LYS:CG	1:A:330:VAL:HG22	2.49	0.43
1:B:86:ILE:HG21	1:B:140:ASP:HB3	2.01	0.43
1:A:369:PHE:CD1	1:A:434:ARG:HA	2.54	0.42
1:C:339:ILE:HG22	1:C:340:ASN:N	2.34	0.42
1:C:320:LYS:HE2	1:C:411:ARG:CB	2.47	0.42
1:B:320:LYS:HE2	1:B:411:ARG:CB	2.47	0.42
1:A:94:TYR:CG	1:A:100:PRO:HD3	2.54	0.42
1:C:283:LYS:CG	1:C:330:VAL:HG22	2.49	0.42
1:A:89:LEU:CD2	1:A:165:ILE:HD13	2.50	0.42
1:C:221:GLN:OE1	1:C:250:GLN:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:94:TYR:CG	1:C:100:PRO:HD3	2.54	0.42
1:B:221:GLN:OE1	1:B:250:GLN:HG2	2.19	0.42
1:A:584:LYS:NZ	1:A:586:ASP:OD1	2.52	0.42
1:C:286:GLN:HG3	1:C:333:MET:HG3	2.02	0.42
1:A:320:LYS:HE2	1:A:411:ARG:CB	2.47	0.42
1:B:545:GLU:HG3	1:B:595:LEU:HD23	2.02	0.42
1:A:545:GLU:HG3	1:A:595:LEU:HD23	2.02	0.42
1:B:286:GLN:HG3	1:B:333:MET:HG3	2.01	0.42
1:B:439:CYS:SG	4:B:763:GDP:H3'	2.60	0.42
1:A:286:GLN:HG3	1:A:333:MET:HG3	2.01	0.42
1:A:578:LEU:HB3	1:A:579:PRO:HD2	2.02	0.42
1:B:283:LYS:CG	1:B:330:VAL:HG22	2.49	0.42
1:A:439:CYS:SG	4:A:763:GDP:H3'	2.60	0.41
1:C:426:PHE:O	1:C:428:PRO:HD3	2.19	0.41
1:A:86:ILE:HG21	1:A:140:ASP:HB3	2.01	0.41
1:A:339:ILE:HG22	1:A:340:ASN:N	2.34	0.41
1:C:545:GLU:HG3	1:C:595:LEU:HD23	2.02	0.41
1:C:89:LEU:CD2	1:C:165:ILE:HD13	2.50	0.41
1:B:94:TYR:CD1	1:B:100:PRO:HD3	2.55	0.41
1:B:94:TYR:CG	1:B:100:PRO:HD3	2.54	0.41
1:C:136:ASP:HB3	1:C:139:ARG:HG3	2.02	0.41
1:A:444:LEU:HA	1:A:445:PRO:HD3	1.92	0.41
1:C:439:CYS:SG	4:C:763:GDP:H3'	2.60	0.41
1:C:94:TYR:CD1	1:C:100:PRO:HD3	2.56	0.41
1:B:578:LEU:HB3	1:B:579:PRO:HD2	2.02	0.41
1:C:282:TYR:CE2	1:C:316:LEU:HD22	2.56	0.41
1:B:282:TYR:CE2	1:B:316:LEU:HD22	2.56	0.41
1:B:89:LEU:CD2	1:B:165:ILE:HD13	2.50	0.41
1:C:578:LEU:HB3	1:C:579:PRO:HD2	2.02	0.41
1:B:305:PHE:CZ	1:B:436:SER:HB3	2.56	0.41
1:B:136:ASP:HB3	1:B:139:ARG:HG3	2.02	0.41
1:A:242:SER:OG	1:B:238:ASN:HB3	2.20	0.41
1:A:681:LEU:O	1:A:685:MET:HG3	2.20	0.41
1:C:305:PHE:CZ	1:C:436:SER:HB3	2.56	0.41
1:A:94:TYR:CD1	1:A:100:PRO:HD3	2.56	0.41
1:C:681:LEU:O	1:C:685:MET:HG3	2.20	0.41
1:A:305:PHE:CZ	1:A:436:SER:HB3	2.56	0.41
1:C:215:VAL:O	1:C:216:ARG:CB	2.59	0.41
1:B:248:VAL:HG21	1:B:288:ALA:O	2.21	0.41
1:C:248:VAL:HG21	1:C:288:ALA:O	2.21	0.41
1:A:283:LYS:HG3	1:A:330:VAL:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:269:ARG:HG3	1:B:269:ARG:O	2.21	0.41
1:B:681:LEU:O	1:B:685:MET:HG3	2.20	0.41
1:C:275:HIS:NE2	3:C:762:TTP:H2'1	2.37	0.40
1:C:269:ARG:O	1:C:269:ARG:HG3	2.22	0.40
1:A:264:LEU:HD11	1:B:294:GLN:HE22	1.87	0.40
1:C:621:PRO:HD3	1:C:694:SER:CB	2.52	0.40
1:C:155:TYR:CE1	1:C:209:THR:HG23	2.49	0.40
1:C:278:CYS:HB3	1:C:282:TYR:CE1	2.56	0.40
1:C:283:LYS:HG3	1:C:330:VAL:HG22	2.03	0.40
1:A:269:ARG:O	1:A:269:ARG:HG3	2.21	0.40
1:A:209:THR:N	1:A:210:PRO:CD	2.85	0.40
1:C:583:TYR:CG	1:C:687:LYS:HD2	2.56	0.40
1:B:275:HIS:NE2	3:B:762:TTP:H2'1	2.37	0.40
1:C:384:LYS:HZ2	1:C:392:ARG:HH22	1.68	0.40
1:B:278:CYS:HB3	1:B:282:TYR:CE1	2.56	0.40
1:A:282:TYR:CE2	1:A:316:LEU:HD22	2.56	0.40
1:B:283:LYS:HG3	1:B:330:VAL:HG22	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	731/761 (96%)	694 (95%)	33 (4%)	4 (0%)	34	78
1	B	731/761 (96%)	694 (95%)	33 (4%)	4 (0%)	34	78
1	C	731/761 (96%)	694 (95%)	33 (4%)	4 (0%)	34	78
2	D	14/20 (70%)	13 (93%)	1 (7%)	0	100	100
2	E	14/20 (70%)	13 (93%)	1 (7%)	0	100	100
2	F	14/20 (70%)	13 (93%)	1 (7%)	0	100	100
2	P	1/20 (5%)	1 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2236/2363 (95%)	2122 (95%)	102 (5%)	12 (0%)	34	78

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	275	HIS
1	B	275	HIS
1	C	275	HIS
1	A	216	ARG
1	B	216	ARG
1	C	216	ARG
1	A	300	GLY
1	B	300	GLY
1	C	300	GLY
1	A	731	TYR
1	B	731	TYR
1	C	731	TYR

### 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	627/650 (96%)	570 (91%)	57 (9%)	12	42
1	B	627/650 (96%)	570 (91%)	57 (9%)	12	42
1	C	627/650 (96%)	570 (91%)	57 (9%)	12	42
2	D	16/19 (84%)	13 (81%)	3 (19%)	2	10
2	E	16/19 (84%)	13 (81%)	3 (19%)	2	10
2	F	16/19 (84%)	13 (81%)	3 (19%)	2	10
2	P	3/19 (16%)	2 (67%)	1 (33%)	0	0
All	All	1932/2026 (95%)	1751 (91%)	181 (9%)	11	41

All (181) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	9	LYS
1	A	13	SER
1	A	14	THR
1	A	16	ARG
1	A	17	ILE
1	A	24	ARG
1	A	39	SER
1	A	40	GLN
1	A	45	SER
1	A	51	ASP
1	A	54	LYS
1	A	72	ARG
1	A	91	LYS
1	A	111	GLU
1	A	118	HIS
1	A	130	GLN
1	A	139	ARG
1	A	149	LYS
1	A	182	SER
1	A	183	ASN
1	A	189	ARG
1	A	206	SER
1	A	209	THR
1	A	216	ARG
1	A	225	CYS
1	A	226	VAL
1	A	266	SER
1	A	276	THR
1	A	291	SER
1	A	298	ARG
1	A	315	SER
1	A	317	LEU
1	A	320	LYS
1	A	361	VAL
1	A	364	LEU
1	A	384	LYS
1	A	387	SER
1	A	394	LYS
1	A	424	SER
1	A	447	LYS
1	A	452	VAL
1	A	465	SER

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Mol	Chain	Res	Type
1	A	484	LEU
1	A	555	SER
1	A	616	LEU
1	A	620	MET
1	A	625	SER
1	A	626	SER
1	A	629	SER
1	A	630	ASN
1	A	643	SER
1	A	648	LYS
1	A	696	ASN
1	A	698	ASN
1	A	708	LYS
1	A	736	ASP
2	D	360	GLN
2	D	361	ILE
2	D	367	THR
1	B	5	LEU
1	B	9	LYS
1	B	13	SER
1	B	14	THR
1	B	16	ARG
1	B	17	ILE
1	B	24	ARG
1	B	39	SER
1	B	40	GLN
1	B	45	SER
1	B	51	ASP
1	B	54	LYS
1	B	72	ARG
1	B	91	LYS
1	B	111	GLU
1	B	118	HIS
1	B	130	GLN
1	B	139	ARG
1	B	149	LYS
1	B	182	SER
1	B	183	ASN
1	B	189	ARG
1	B	206	SER
1	B	209	THR
1	B	216	ARG

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Mol	Chain	Res	Type
1	B	225	CYS
1	B	226	VAL
1	B	266	SER
1	B	276	THR
1	B	291	SER
1	B	298	ARG
1	B	315	SER
1	B	317	LEU
1	B	320	LYS
1	B	361	VAL
1	B	364	LEU
1	B	384	LYS
1	B	387	SER
1	B	394	LYS
1	B	424	SER
1	B	447	LYS
1	B	452	VAL
1	B	465	SER
1	B	484	LEU
1	B	555	SER
1	B	616	LEU
1	B	620	MET
1	B	625	SER
1	B	626	SER
1	B	629	SER
1	B	630	ASN
1	B	643	SER
1	B	648	LYS
1	B	696	ASN
1	B	698	ASN
1	B	708	LYS
1	B	736	ASP
2	E	360	GLN
2	E	361	ILE
2	E	367	THR
1	C	5	LEU
1	C	9	LYS
1	C	13	SER
1	C	14	THR
1	C	16	ARG
1	C	17	ILE
1	C	24	ARG

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Mol	Chain	Res	Type
1	C	39	SER
1	C	40	GLN
1	C	45	SER
1	C	51	ASP
1	C	54	LYS
1	C	72	ARG
1	C	91	LYS
1	C	111	GLU
1	C	118	HIS
1	C	130	GLN
1	C	139	ARG
1	C	149	LYS
1	C	182	SER
1	C	183	ASN
1	C	189	ARG
1	C	206	SER
1	C	209	THR
1	C	216	ARG
1	C	225	CYS
1	C	226	VAL
1	C	266	SER
1	C	276	THR
1	C	291	SER
1	C	298	ARG
1	C	315	SER
1	C	317	LEU
1	C	320	LYS
1	C	361	VAL
1	C	364	LEU
1	C	384	LYS
1	C	387	SER
1	C	394	LYS
1	C	424	SER
1	C	447	LYS
1	C	452	VAL
1	C	465	SER
1	C	484	LEU
1	C	555	SER
1	C	616	LEU
1	C	620	MET
1	C	625	SER
1	C	626	SER

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Mol	Chain	Res	Type
1	C	629	SER
1	C	630	ASN
1	C	643	SER
1	C	648	LYS
1	C	696	ASN
1	C	698	ASN
1	C	708	LYS
1	C	736	ASP
2	F	360	GLN
2	F	361	ILE
2	F	367	THR
2	P	3	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	HIS
1	A	250	GLN
1	A	328	ASN
1	A	596	HIS
1	A	630	ASN
1	A	661	HIS
2	D	360	GLN
1	B	46	HIS
1	B	250	GLN
1	B	294	GLN
1	B	328	ASN
1	B	596	HIS
1	B	630	ASN
1	B	661	HIS
1	C	46	HIS
1	C	250	GLN
1	C	328	ASN
1	C	596	HIS
1	C	630	ASN
1	C	661	HIS

### 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 ⓘ

6 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$
3	TTP	A	762	-	21,30,30	1.58	4 (19%)	31,47,47	2.98	7 (22%)
4	GDP	A	763	-	23,30,30	1.41	4 (17%)	30,47,47	2.35	5 (16%)
3	TTP	B	762	-	21,30,30	1.58	4 (19%)	31,47,47	2.98	7 (22%)
4	GDP	B	763	-	23,30,30	1.41	3 (13%)	30,47,47	2.35	5 (16%)
3	TTP	C	762	-	21,30,30	1.58	4 (19%)	31,47,47	2.97	7 (22%)
4	GDP	C	763	-	23,30,30	1.41	3 (13%)	30,47,47	2.36	5 (16%)

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
3	TTP	A	762	-	-	0/18/34/34	0/2/2/2
4	GDP	A	763	-	-	0/12/32/32	0/3/3/3
3	TTP	B	762	-	-	0/18/34/34	0/2/2/2
4	GDP	B	763	-	-	0/12/32/32	0/3/3/3
3	TTP	C	762	-	-	0/18/34/34	0/2/2/2
4	GDP	C	763	-	-	0/12/32/32	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	762	TTP	PG-O3G	-3.15	1.43	1.54
3	C	762	TTP	PG-O3G	-3.15	1.43	1.54
3	B	762	TTP	PG-O3G	-3.15	1.43	1.54
4	C	763	GDP	C8-N7	-2.68	1.29	1.34
4	A	763	GDP	C8-N7	-2.67	1.29	1.34
4	B	763	GDP	C8-N7	-2.65	1.29	1.34
4	A	763	GDP	PB-O2B	-2.09	1.47	1.54
4	B	763	GDP	PB-O2B	-2.08	1.47	1.54
4	C	763	GDP	PB-O2B	-2.07	1.47	1.54
3	B	762	TTP	C6-C5	-2.05	1.34	1.40
3	A	762	TTP	C6-C5	-2.03	1.34	1.40
3	C	762	TTP	C6-C5	-2.03	1.34	1.40
4	A	763	GDP	PA-O2A	-2.00	1.46	1.54
3	B	762	TTP	C6-N1	2.17	1.38	1.35
3	A	762	TTP	C6-N1	2.21	1.38	1.35
3	C	762	TTP	C6-N1	2.22	1.38	1.35
3	C	762	TTP	C4-N3	3.62	1.39	1.33
3	A	762	TTP	C4-N3	3.63	1.39	1.33
3	B	762	TTP	C4-N3	3.63	1.39	1.33
4	A	763	GDP	C6-N1	3.92	1.40	1.33
4	C	763	GDP	C6-N1	3.92	1.40	1.33
4	B	763	GDP	C6-N1	3.94	1.40	1.33

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	762	TTP	C5-C4-N3	-9.22	114.87	125.14
3	A	762	TTP	C5-C4-N3	-9.21	114.89	125.14
3	C	762	TTP	C5-C4-N3	-9.18	114.92	125.14
4	C	763	GDP	C5-C6-N1	-8.90	111.42	123.59
4	A	763	GDP	C5-C6-N1	-8.88	111.45	123.59
4	B	763	GDP	C5-C6-N1	-8.87	111.46	123.59
4	C	763	GDP	N3-C2-N1	-2.40	123.79	127.44
4	A	763	GDP	N3-C2-N1	-2.38	123.82	127.44
4	B	763	GDP	N3-C2-N1	-2.37	123.83	127.44
4	A	763	GDP	O3A-PA-O5'	-2.10	97.35	102.94
4	C	763	GDP	O3A-PA-O5'	-2.10	97.38	102.94
4	B	763	GDP	O3A-PA-O5'	-2.09	97.38	102.94
3	B	762	TTP	O3'-C3'-C2'	2.27	118.25	110.74
3	A	762	TTP	O3'-C3'-C2'	2.28	118.30	110.74
3	C	762	TTP	O3'-C3'-C2'	2.28	118.30	110.74
3	C	762	TTP	O5'-C5'-C4'	2.46	118.20	109.12
3	A	762	TTP	O5'-C5'-C4'	2.47	118.24	109.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	762	TTP	O5'-C5'-C4'	2.48	118.27	109.12
3	C	762	TTP	C2'-C1'-N1	2.65	120.59	114.16
3	A	762	TTP	C2'-C1'-N1	2.66	120.61	114.16
3	B	762	TTP	C2'-C1'-N1	2.66	120.63	114.16
3	C	762	TTP	O2A-PA-O5'	2.67	121.91	108.46
3	B	762	TTP	O2A-PA-O5'	2.67	121.92	108.46
3	A	762	TTP	O2A-PA-O5'	2.67	121.93	108.46
4	A	763	GDP	O2B-PB-O1B	2.77	119.51	110.58
4	B	763	GDP	O2B-PB-O1B	2.78	119.54	110.58
4	C	763	GDP	O2B-PB-O1B	2.78	119.54	110.58
3	A	762	TTP	O4'-C1'-N1	5.69	117.58	107.72
3	B	762	TTP	O4'-C1'-N1	5.70	117.58	107.72
3	C	762	TTP	O4'-C1'-N1	5.70	117.59	107.72
4	B	763	GDP	C6-N1-C2	6.65	125.17	115.94
4	A	763	GDP	C6-N1-C2	6.66	125.19	115.94
4	C	763	GDP	C6-N1-C2	6.68	125.22	115.94
3	C	762	TTP	C4-N3-C2	10.33	124.18	115.25
3	B	762	TTP	C4-N3-C2	10.34	124.19	115.25
3	A	762	TTP	C4-N3-C2	10.37	124.21	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	762	TTP	7	0
4	A	763	GDP	1	0
3	B	762	TTP	8	0
4	B	763	GDP	1	0
3	C	762	TTP	7	0
4	C	763	GDP	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

### 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	733/761 (96%)	0.42	52 (7%) 19 10	6, 21, 73, 104	0
1	B	733/761 (96%)	0.23	19 (2%) 59 45	6, 21, 73, 104	0
1	C	733/761 (96%)	0.35	14 (1%) 70 55	6, 21, 73, 104	0
2	D	16/20 (80%)	1.11	4 (25%) 1 1	43, 79, 87, 93	0
2	E	16/20 (80%)	1.21	3 (18%) 2 1	43, 79, 87, 93	0
2	F	16/20 (80%)	1.23	3 (18%) 2 1	43, 79, 87, 93	0
2	P	3/20 (15%)	0.46	0 100 100	47, 47, 52, 56	0
All	All	2250/2363 (95%)	0.35	95 (4%) 40 26	6, 22, 79, 104	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	296	GLY	9.1
1	C	296	GLY	6.6
1	B	297	VAL	5.9
1	B	273	ALA	5.7
2	E	361	ILE	5.4
1	C	273	ALA	5.0
1	A	473	ASN	4.5
1	A	296	GLY	4.3
1	B	274	PHE	4.2
1	C	272	GLU	4.1
1	A	272	GLU	4.0
1	A	11	ASP	4.0
1	B	737	GLY	3.9
1	B	11	ASP	3.9
1	B	272	GLU	3.8
1	B	55	THR	3.8
2	F	360	GLN	3.7

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Mol	Chain	Res	Type	RSRZ
2	F	361	ILE	3.6
1	B	384	LYS	3.6
1	C	270	GLY	3.6
1	A	55	THR	3.5
1	C	297	VAL	3.5
1	A	92	LYS	3.4
1	A	9	LYS	3.3
2	D	360	GLN	3.3
1	A	58	ILE	3.2
1	A	294	GLN	3.1
1	A	271	GLY	3.1
1	A	95	GLY	3.1
1	A	12	GLY	3.0
2	D	372	ASN	3.0
1	A	14	THR	3.0
1	A	10	ARG	3.0
1	C	298	ARG	3.0
2	E	372	ASN	2.9
2	D	364	GLU	2.9
1	A	737	GLY	2.9
1	A	273	ALA	2.8
1	A	62	ILE	2.8
1	B	5	LEU	2.8
1	A	160	ARG	2.8
1	A	269	ARG	2.8
1	A	297	VAL	2.8
1	A	59	HIS	2.7
1	B	294	GLN	2.7
1	A	101	ALA	2.7
1	B	17	ILE	2.7
1	B	271	GLY	2.7
1	C	737	GLY	2.7
2	D	361	ILE	2.6
1	B	52	GLY	2.6
1	A	8	THR	2.6
1	A	275	HIS	2.6
1	A	57	ASP	2.6
1	A	298	ARG	2.6
1	B	392	ARG	2.6
1	B	10	ARG	2.5
1	C	7	VAL	2.5
1	A	19	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	8	THR	2.5
1	C	294	GLN	2.4
1	A	53	ILE	2.4
1	A	13	SER	2.4
1	A	6	LEU	2.4
1	C	392	ARG	2.4
2	E	360	GLN	2.3
1	A	336	GLY	2.3
1	A	156	LEU	2.3
1	A	191	GLN	2.3
1	A	323	ARG	2.3
1	A	159	ASN	2.3
1	A	119	LEU	2.3
1	C	353	ILE	2.3
2	F	372	ASN	2.3
1	A	126	GLU	2.2
1	A	166	TYR	2.2
1	C	271	GLY	2.2
1	A	174	ILE	2.2
1	B	295	GLY	2.2
1	A	295	GLY	2.1
1	B	7	VAL	2.1
1	A	270	GLY	2.1
1	A	17	ILE	2.1
1	A	161	VAL	2.1
1	C	276	THR	2.1
1	A	65	ALA	2.1
1	A	91	LYS	2.1
1	A	54	LYS	2.1
1	A	576	GLY	2.1
1	A	299	GLY	2.0
1	A	623	GLU	2.0
1	A	100	PRO	2.0
1	C	16	ARG	2.0
1	A	630	ASN	2.0
1	A	484	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 [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
4	GDP	B	763	28/28	0.62	0.55	4.70	62,62,63,63	28
4	GDP	C	763	28/28	0.61	0.62	4.49	62,62,63,63	28
4	GDP	A	763	28/28	0.56	0.60	3.68	62,62,63,63	28
3	TTP	A	762	29/29	0.62	0.44	1.06	70,71,75,75	0
3	TTP	B	762	29/29	0.70	0.37	0.51	70,71,75,75	0
3	TTP	C	762	29/29	0.68	0.34	0.07	70,71,75,75	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.