



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:31 AM GMT

PDB ID : 2R1R  
Title : RIBONUCLEOTIDE REDUCTASE R1 PROTEIN WITH DTTP OCCUPY-  
ING THE SPECIFICITY SITE FROM ESCHERICHIA COLI  
Authors : Eriksson, M.; Eklund, H.  
Deposited on : 1997-07-21  
Resolution : 3.00 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 : 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

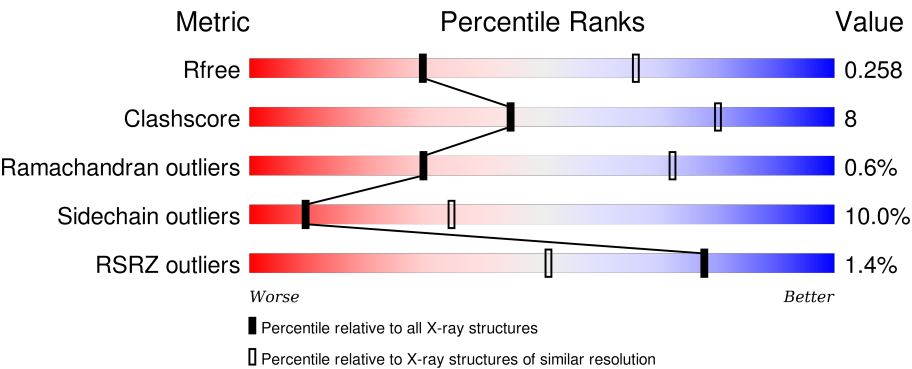
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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 <sub>free</sub>	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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	761	<div><div>%</div><div><div></div><div>71%</div><div>23%</div><div>.</div><div>.</div></div></div>
1	B	761	<div><div>%</div><div><div></div><div>71%</div><div>22%</div><div>.</div><div>.</div></div></div>
1	C	761	<div><div>%</div><div><div></div><div>71%</div><div>23%</div><div>.</div><div>.</div></div></div>
2	D	20	<div><div>5%</div><div><div></div><div>40%</div><div>20%</div><div>5%</div><div>35%</div></div></div>
2	E	20	<div><div></div><div><div></div><div>40%</div><div>20%</div><div>5%</div><div>35%</div></div></div>

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Mol	Chain	Length	Quality of chain
2	F	20	<div><div><div></div><div></div><div></div><div></div><div></div></div><div>5%40%20%5%35%</div></div>
2	P	20	<div><div><div></div><div></div><div></div><div></div><div></div></div><div>5%5%15%80%</div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17941 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.

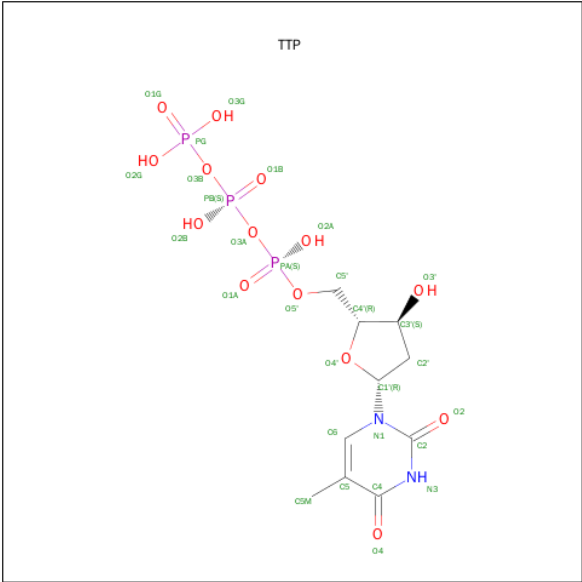
- Molecule 1 is a protein called RIBONUCLEOTIDE REDUCTASE R1 PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	733	Total	C	N	O	S	0	0	0
			5837	3708	1002	1103	24			
1	B	733	Total	C	N	O	S	0	0	0
			5837	3708	1002	1103	24			
1	C	733	Total	C	N	O	S	0	0	0
			5837	3708	1002	1103	24			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	13	Total	C	N	O	0	0	0
			104	62	15	27			
2	E	13	Total	C	N	O	0	0	0
			104	62	15	27			
2	F	13	Total	C	N	O	0	0	0
			104	62	15	27			
2	P	4	Total	C	N	O	0	0	0
			31	22	4	5			

- Molecule 3 is THYMIDINE-5'-TRIPHOSPHATE (three-letter code: TTP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>2</sub>O<sub>14</sub>P<sub>3</sub>).

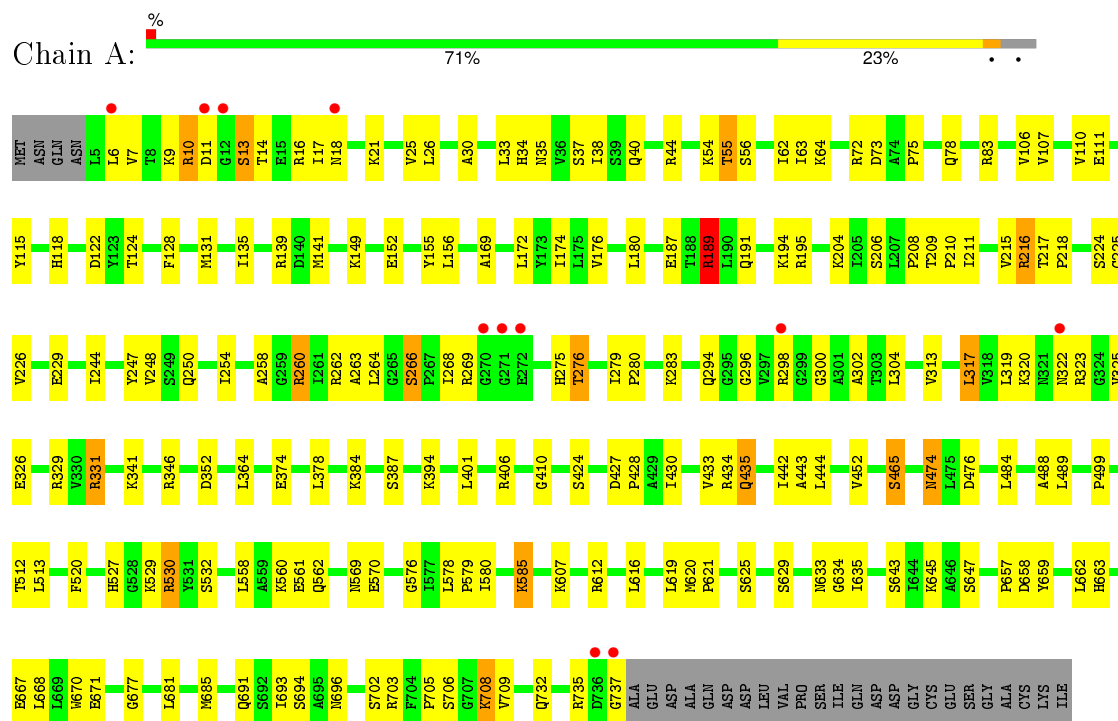


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
3	B	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
3	C	1	Total	C	N	O	P	0	0
			29	10	2	14	3		

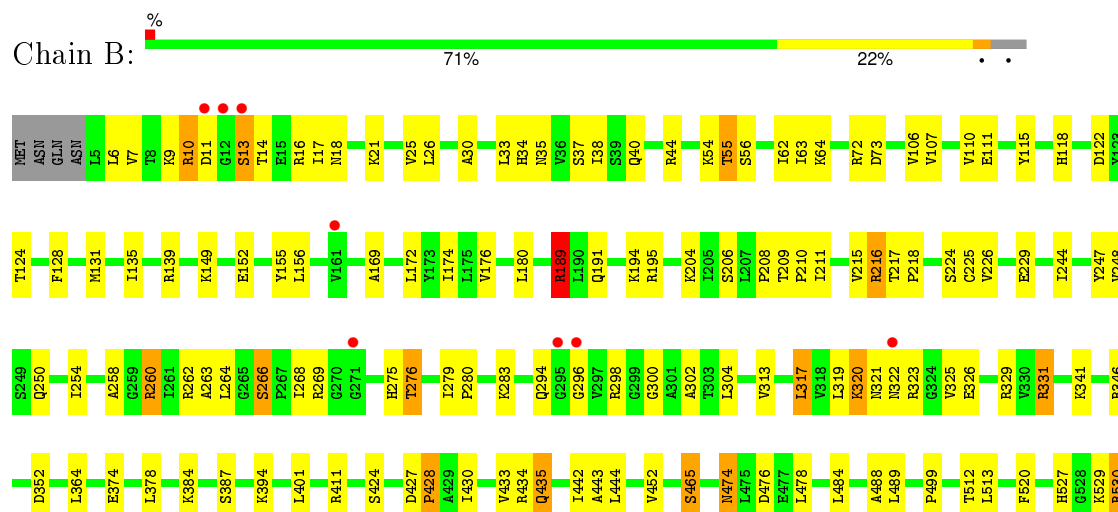
### 3 Residue-property plots

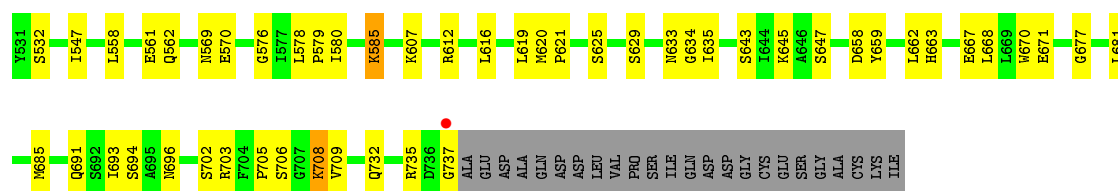
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ( $\text{RSRZ} > 2$ ). 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: RIBONUCLEOTIDE REDUCTASE R1 PROTEIN

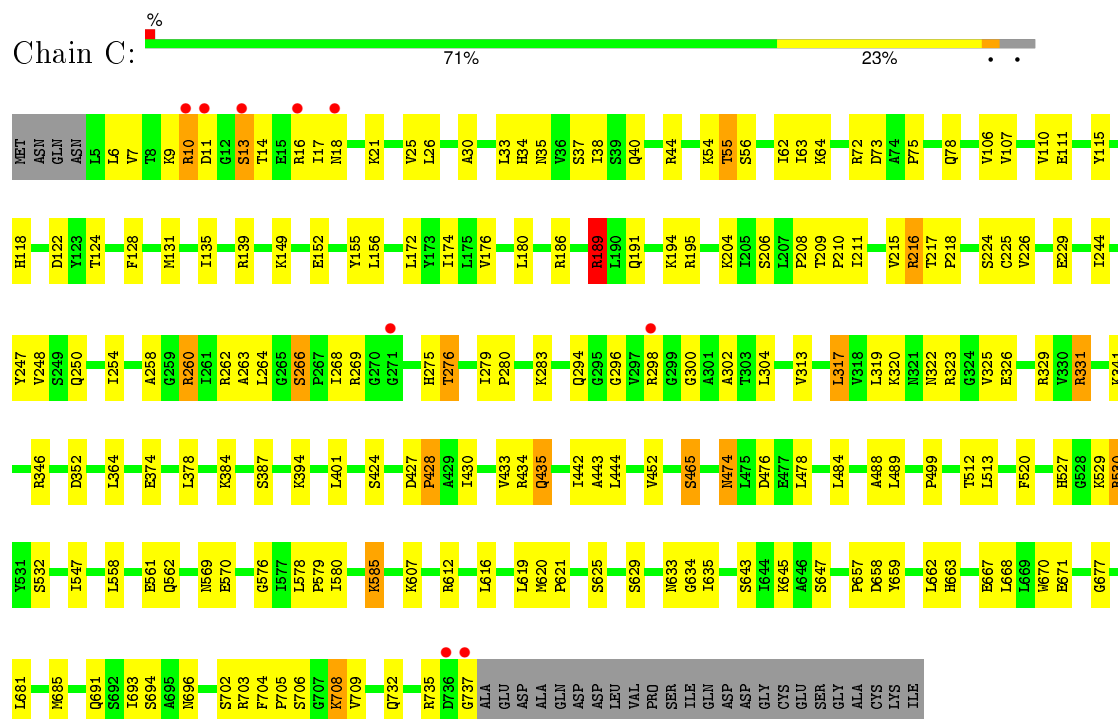


#### • Molecule 1: RIBONUCLEOTIDE REDUCTASE R1 PROTEIN

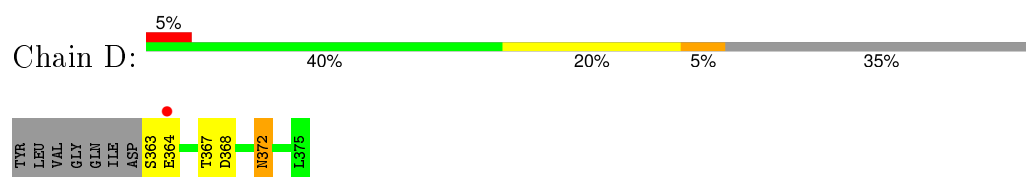




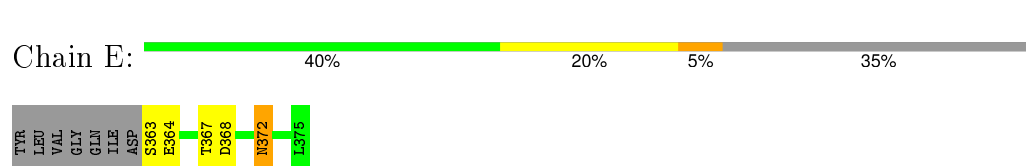
• Molecule 1: RIBONUCLEOTIDE REDUCTASE R1 PROTEIN



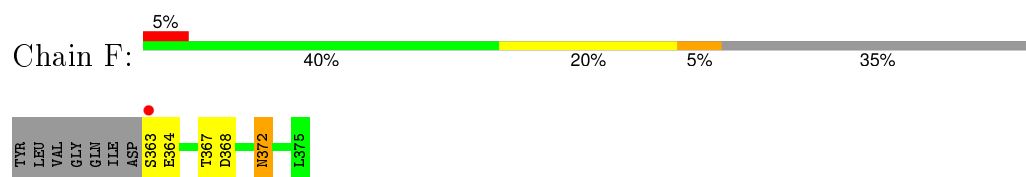
• Molecule 2: RIBONUCLEOTIDE REDUCTASE R2 PROTEIN



• Molecule 2: RIBONUCLEOTIDE REDUCTASE R2 PROTEIN



• 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, $\alpha$ , $\beta$ , $\gamma$	227.82Å 227.82Å 343.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.00 20.00 – 3.02	Depositor EDS
% Data completeness (in resolution range)	83.0 (20.00-3.00) 85.1 (20.00-3.02)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.82 (at 3.04Å)	Xtriage
Refinement program	REFMAC, TNT	Depositor
R, $R_{free}$	0.238 , 0.280 0.254 , 0.258	Depositor DCC
$R_{free}$ test set	573 reflections (1.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.8	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , -2.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.41$ , $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	0 of 56656 reflections	Xtriage
$F_o, F_c$ correlation	0.82	EDS
Total number of atoms	17941	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	5.0	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: 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	0.36	0/5965	0.97	17/8079 (0.2%)
1	B	0.36	0/5965	0.97	17/8079 (0.2%)
1	C	0.36	0/5965	0.97	17/8079 (0.2%)
2	D	0.50	0/104	1.11	0/139
2	E	0.50	0/104	1.11	0/139
2	F	0.51	0/104	1.11	0/139
2	P	0.68	0/31	1.87	2/41 (4.9%)
All	All	0.36	0/18238	0.97	53/24695 (0.2%)

There are no bond length outliers.

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	298	ARG	NE-CZ-NH1	12.79	126.70	120.30
1	B	298	ARG	NE-CZ-NH1	12.77	126.69	120.30
1	C	298	ARG	NE-CZ-NH1	12.76	126.68	120.30
1	A	16	ARG	NE-CZ-NH1	8.85	124.72	120.30
1	C	16	ARG	NE-CZ-NH1	8.82	124.71	120.30
1	B	16	ARG	NE-CZ-NH1	8.81	124.71	120.30
1	B	11	ASP	CB-CG-OD1	7.40	124.96	118.30
1	C	11	ASP	CB-CG-OD1	7.39	124.95	118.30
1	A	11	ASP	CB-CG-OD1	7.38	124.94	118.30
1	C	323	ARG	NE-CZ-NH1	6.92	123.76	120.30
1	A	323	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	C	139	ARG	NE-CZ-NH1	6.73	123.67	120.30
1	B	323	ARG	NE-CZ-NH1	6.67	123.63	120.30
1	B	298	ARG	NH1-CZ-NH2	-6.66	112.08	119.40
1	A	139	ARG	NE-CZ-NH1	6.65	123.62	120.30
1	A	298	ARG	NH1-CZ-NH2	-6.64	112.09	119.40
1	C	298	ARG	NH1-CZ-NH2	-6.64	112.09	119.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	139	ARG	NE-CZ-NH1	6.62	123.61	120.30
1	B	10	ARG	NE-CZ-NH1	6.51	123.55	120.30
1	A	10	ARG	NE-CZ-NH1	6.46	123.53	120.30
1	C	10	ARG	NE-CZ-NH1	6.45	123.53	120.30
1	C	115	TYR	CB-CG-CD1	6.31	124.78	121.00
1	A	115	TYR	CB-CG-CD1	6.29	124.77	121.00
1	B	115	TYR	CB-CG-CD1	6.26	124.75	121.00
1	A	331	ARG	NE-CZ-NH1	6.19	123.40	120.30
1	B	331	ARG	NE-CZ-NH1	6.17	123.39	120.30
1	C	10	ARG	NE-CZ-NH2	-6.12	117.24	120.30
1	B	10	ARG	NE-CZ-NH2	-6.11	117.24	120.30
1	A	10	ARG	NE-CZ-NH2	-6.08	117.26	120.30
1	C	331	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	B	737	GLY	N-CA-C	-5.83	98.52	113.10
1	C	737	GLY	N-CA-C	-5.83	98.53	113.10
1	A	737	GLY	N-CA-C	-5.83	98.54	113.10
1	C	115	TYR	CB-CG-CD2	-5.82	117.51	121.00
1	A	115	TYR	CB-CG-CD2	-5.80	117.52	121.00
1	B	115	TYR	CB-CG-CD2	-5.76	117.55	121.00
1	B	13	SER	CA-C-O	5.71	132.08	120.10
1	A	13	SER	CA-C-O	5.70	132.07	120.10
1	C	13	SER	CA-C-O	5.68	132.02	120.10
1	C	16	ARG	NH1-CZ-NH2	-5.62	113.22	119.40
1	B	16	ARG	NH1-CZ-NH2	-5.60	113.24	119.40
1	A	16	ARG	NH1-CZ-NH2	-5.57	113.28	119.40
2	P	2	LEU	CA-CB-CG	5.54	128.03	115.30
1	C	13	SER	CA-C-N	-5.39	105.34	117.20
1	A	13	SER	CA-C-N	-5.39	105.35	117.20
1	B	13	SER	CA-C-N	-5.37	105.38	117.20
1	C	703	ARG	NE-CZ-NH1	5.27	122.93	120.30
1	A	703	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	B	703	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	C	11	ASP	N-CA-CB	5.16	119.89	110.60
1	A	11	ASP	N-CA-CB	5.15	119.86	110.60
1	B	11	ASP	N-CA-CB	5.14	119.86	110.60
2	P	3	VAL	N-CA-C	5.04	124.59	111.00

There are no chirality outliers.

There are no planarity outliers.

## 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	5837	0	5762	90	0
1	B	5837	0	5762	94	0
1	C	5837	0	5762	92	0
2	D	104	0	88	2	0
2	E	104	0	88	2	0
2	F	104	0	88	2	0
2	P	31	0	34	1	0
3	A	29	0	13	2	0
3	B	29	0	13	2	0
3	C	29	0	13	2	0
All	All	17941	0	17623	281	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (281) 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:B:558:LEU:HD23	1:B:612:ARG:HG2	1.56	0.85
1:A:558:LEU:HD23	1:A:612:ARG:HG2	1.56	0.85
1:C:558:LEU:HD23	1:C:612:ARG:HG2	1.56	0.84
1:B:279:ILE:HB	1:B:280:PRO:HD3	1.60	0.84
1:C:279:ILE:HB	1:C:280:PRO:HD3	1.60	0.83
1:A:279:ILE:HB	1:A:280:PRO:HD3	1.59	0.82
1:C:7:VAL:HG23	1:C:17:ILE:HG12	1.63	0.81
1:B:7:VAL:HG23	1:B:17:ILE:HG12	1.63	0.81
1:B:619:LEU:HD12	1:B:693:ILE:HG12	1.65	0.79
1:A:619:LEU:HD12	1:A:693:ILE:HG12	1.65	0.79
1:A:7:VAL:HG23	1:A:17:ILE:HG12	1.63	0.78
1:C:619:LEU:HD12	1:C:693:ILE:HG12	1.65	0.77
1:A:465:SER:HB2	1:A:489:LEU:HD11	1.69	0.74
1:A:561:GLU:HG2	1:A:562:GLN:HG3	1.70	0.74
1:C:561:GLU:HG2	1:C:562:GLN:HG3	1.70	0.73
1:C:465:SER:HB2	1:C:489:LEU:HD11	1.69	0.73
1:B:465:SER:HB2	1:B:489:LEU:HD11	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:561:GLU:HG2	1:B:562:GLN:HG3	1.70	0.71
1:A:268:ILE:HD11	1:A:275:HIS:HA	1.74	0.69
1:A:322:ASN:HA	1:A:331:ARG:HE	1.57	0.69
1:B:322:ASN:HA	1:B:331:ARG:HE	1.57	0.69
1:C:322:ASN:HA	1:C:331:ARG:HE	1.57	0.69
1:B:208:PRO:HG2	1:B:211:ILE:HD12	1.76	0.68
1:C:208:PRO:HG2	1:C:211:ILE:HD12	1.76	0.68
1:B:268:ILE:HD11	1:B:275:HIS:HA	1.74	0.68
1:B:215:VAL:O	1:B:216:ARG:HB3	1.94	0.67
1:C:268:ILE:HD11	1:C:275:HIS:HA	1.74	0.67
1:A:215:VAL:O	1:A:216:ARG:HB3	1.94	0.67
1:A:208:PRO:HG2	1:A:211:ILE:HD12	1.76	0.67
1:C:215:VAL:O	1:C:216:ARG:HB3	1.94	0.67
1:C:578:LEU:HB3	1:C:579:PRO:HD2	1.77	0.66
2:E:372:ASN:H	2:E:372:ASN:ND2	1.93	0.66
1:A:578:LEU:HB3	1:A:579:PRO:HD2	1.77	0.65
2:F:372:ASN:ND2	2:F:372:ASN:H	1.93	0.65
1:B:578:LEU:HB3	1:B:579:PRO:HD2	1.77	0.64
2:D:372:ASN:ND2	2:D:372:ASN:H	1.93	0.64
1:A:217:THR:HB	1:A:218:PRO:HD2	1.81	0.62
1:C:317:LEU:HD23	1:C:401:LEU:HD23	1.83	0.61
1:B:317:LEU:HD23	1:B:401:LEU:HD23	1.82	0.61
1:C:217:THR:HB	1:C:218:PRO:HD2	1.81	0.61
1:B:209:THR:N	1:B:210:PRO:HD2	2.16	0.61
1:B:217:THR:HB	1:B:218:PRO:HD2	1.81	0.61
1:C:444:LEU:HD22	1:C:512:THR:HG21	1.83	0.61
1:B:18:ASN:HB2	1:B:21:LYS:HE3	1.83	0.61
1:A:18:ASN:HB2	1:A:21:LYS:HE3	1.83	0.61
1:C:209:THR:N	1:C:210:PRO:HD2	2.16	0.60
1:B:444:LEU:HD22	1:B:512:THR:HG21	1.83	0.60
1:A:317:LEU:HD23	1:A:401:LEU:HD23	1.82	0.60
1:A:444:LEU:HD22	1:A:512:THR:HG21	1.83	0.60
1:C:18:ASN:HB2	1:C:21:LYS:HE3	1.83	0.60
1:A:209:THR:N	1:A:210:PRO:HD2	2.16	0.60
1:B:128:PHE:HA	1:B:131:MET:HE3	1.84	0.59
1:B:427:ASP:HB3	1:B:430:ILE:HD12	1.84	0.59
1:C:260:ARG:HH22	1:C:434:ARG:NH2	2.01	0.59
1:A:26:LEU:HB3	1:A:38:ILE:HD12	1.84	0.59
1:B:26:LEU:HB3	1:B:38:ILE:HD12	1.84	0.59
1:A:427:ASP:HB3	1:A:430:ILE:HD12	1.84	0.59
1:C:427:ASP:HB3	1:C:430:ILE:HD12	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:LEU:HB3	1:C:38:ILE:HD12	1.84	0.58
1:A:258:ALA:HB3	1:A:304:LEU:HD21	1.85	0.58
1:A:576:GLY:HA3	1:A:607:LYS:HE2	1.86	0.58
1:B:258:ALA:HB3	1:B:304:LEU:HD21	1.85	0.58
1:A:260:ARG:HH22	1:A:434:ARG:NH2	2.01	0.58
1:B:260:ARG:HH22	1:B:434:ARG:NH2	2.01	0.58
1:C:258:ALA:HB3	1:C:304:LEU:HD21	1.85	0.57
1:C:576:GLY:HA3	1:C:607:LYS:HE2	1.86	0.57
1:A:260:ARG:HH22	1:A:434:ARG:HH21	1.53	0.57
1:B:576:GLY:HA3	1:B:607:LYS:HE2	1.86	0.57
1:B:275:HIS:CE1	3:B:762:TTP:H1'	2.40	0.57
1:C:275:HIS:CE1	3:C:762:TTP:H1'	2.40	0.57
1:C:530:ARG:HH11	1:C:667:GLU:HB2	1.70	0.56
1:B:585:LYS:H	1:B:585:LYS:HD3	1.69	0.56
1:A:530:ARG:HH11	1:A:667:GLU:HB2	1.70	0.56
1:A:275:HIS:CE1	3:A:762:TTP:H1'	2.40	0.56
1:B:530:ARG:HH11	1:B:667:GLU:HB2	1.70	0.56
1:A:7:VAL:CG2	1:A:17:ILE:HG12	2.35	0.56
1:A:585:LYS:H	1:A:585:LYS:HD3	1.69	0.56
1:C:260:ARG:HH22	1:C:434:ARG:HH21	1.53	0.56
1:B:34:HIS:O	1:B:35:ASN:HB2	2.05	0.56
1:C:585:LYS:HD3	1:C:585:LYS:H	1.69	0.56
1:C:34:HIS:O	1:C:35:ASN:HB2	2.05	0.55
1:A:34:HIS:O	1:A:35:ASN:HB2	2.05	0.55
1:B:276:THR:HG23	1:B:280:PRO:HG2	1.87	0.55
1:A:276:THR:HG23	1:A:280:PRO:HG2	1.87	0.55
1:B:260:ARG:HH22	1:B:434:ARG:HH21	1.53	0.55
1:A:128:PHE:HA	1:A:131:MET:HE3	1.89	0.55
1:A:180:LEU:HD13	1:A:488:ALA:HB1	1.89	0.55
1:C:276:THR:HG23	1:C:280:PRO:HG2	1.88	0.55
1:B:180:LEU:HD13	1:B:488:ALA:HB1	1.89	0.54
1:C:180:LEU:HD13	1:C:488:ALA:HB1	1.89	0.54
1:B:7:VAL:CG2	1:B:17:ILE:HG12	2.35	0.53
1:C:7:VAL:CG2	1:C:17:ILE:HG12	2.35	0.53
1:C:128:PHE:HA	1:C:131:MET:HE3	1.91	0.53
1:B:263:ALA:O	1:B:266:SER:HB2	2.09	0.53
1:A:263:ALA:O	1:A:266:SER:HB2	2.09	0.53
1:C:152:GLU:HA	1:C:156:LEU:HD12	1.92	0.52
1:C:263:ALA:O	1:C:266:SER:HB2	2.09	0.52
1:B:152:GLU:HA	1:B:156:LEU:HD12	1.92	0.52
1:C:37:SER:HB3	1:C:40:GLN:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:SER:OG	1:C:40:GLN:HG2	2.10	0.51
1:A:37:SER:HB3	1:A:40:GLN:HG2	1.93	0.51
1:B:37:SER:OG	1:B:40:GLN:HG2	2.10	0.51
1:A:152:GLU:HA	1:A:156:LEU:HD12	1.92	0.51
1:A:215:VAL:O	1:A:216:ARG:CB	2.59	0.51
1:A:37:SER:OG	1:A:40:GLN:HG2	2.10	0.51
1:A:172:LEU:O	1:A:176:VAL:HG23	2.11	0.51
1:C:215:VAL:O	1:C:216:ARG:CB	2.59	0.51
1:B:37:SER:HB3	1:B:40:GLN:HG2	1.93	0.51
1:C:172:LEU:O	1:C:176:VAL:HG23	2.11	0.51
1:B:37:SER:CB	1:B:40:GLN:HG2	2.41	0.51
1:B:172:LEU:O	1:B:176:VAL:HG23	2.11	0.51
1:A:244:ILE:O	1:A:248:VAL:HG22	2.11	0.51
1:C:37:SER:CB	1:C:40:GLN:HG2	2.41	0.51
1:A:279:ILE:HB	1:A:280:PRO:CD	2.37	0.50
1:A:260:ARG:NH2	1:A:434:ARG:HH21	2.09	0.50
1:B:215:VAL:O	1:B:216:ARG:CB	2.59	0.50
1:A:37:SER:CB	1:A:40:GLN:HG2	2.41	0.50
1:C:260:ARG:NH2	1:C:434:ARG:HH21	2.09	0.50
1:C:244:ILE:O	1:C:248:VAL:HG22	2.11	0.50
1:C:250:GLN:HE22	1:C:499:PRO:HG3	1.77	0.50
1:B:244:ILE:O	1:B:248:VAL:HG22	2.11	0.49
1:B:250:GLN:HE22	1:B:499:PRO:HG3	1.77	0.49
1:A:433:VAL:HG11	1:A:443:ALA:HB1	1.94	0.49
1:B:260:ARG:NH2	1:B:434:ARG:HH21	2.09	0.49
1:A:520:PHE:HB3	1:A:635:ILE:HA	1.95	0.49
1:B:433:VAL:HG11	1:B:443:ALA:HB1	1.94	0.48
1:B:527:HIS:O	1:B:529:LYS:HE2	2.14	0.48
1:C:670:TRP:CH2	1:C:735:ARG:HB2	2.49	0.48
1:A:527:HIS:O	1:A:529:LYS:HE2	2.14	0.48
1:C:527:HIS:O	1:C:529:LYS:HE2	2.14	0.48
1:C:433:VAL:HG11	1:C:443:ALA:HB1	1.94	0.48
1:B:670:TRP:CH2	1:B:735:ARG:HB2	2.48	0.48
1:A:250:GLN:HE22	1:A:499:PRO:HG3	1.77	0.48
1:A:670:TRP:CH2	1:A:735:ARG:HB2	2.48	0.48
1:B:155:TYR:HE1	1:B:209:THR:HG23	1.78	0.48
1:C:520:PHE:HB3	1:C:635:ILE:HA	1.95	0.48
1:A:18:ASN:CB	1:A:21:LYS:HE3	2.44	0.48
1:A:279:ILE:HD12	1:A:319:LEU:HD21	1.96	0.47
1:B:520:PHE:HB3	1:B:635:ILE:HA	1.95	0.47
1:C:155:TYR:CE1	1:C:209:THR:HG23	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:670:TRP:CZ2	1:B:735:ARG:HB2	2.49	0.47
1:A:155:TYR:CE1	1:A:209:THR:HG23	2.50	0.47
1:A:229:GLU:OE2	1:A:260:ARG:NH1	2.48	0.47
1:C:670:TRP:CZ2	1:C:735:ARG:HB2	2.50	0.47
1:A:670:TRP:CZ2	1:A:735:ARG:HB2	2.49	0.47
1:A:560:LYS:HA	2:P:1:TYR:N	2.29	0.47
1:A:346:ARG:HD2	1:A:352:ASP:O	2.15	0.47
1:A:155:TYR:HE1	1:A:209:THR:HG23	1.78	0.47
1:B:18:ASN:CB	1:B:21:LYS:HE3	2.44	0.46
1:B:30:ALA:HA	1:B:33:LEU:HD12	1.96	0.46
1:C:279:ILE:HB	1:C:280:PRO:CD	2.37	0.46
1:C:30:ALA:HA	1:C:33:LEU:HD12	1.96	0.46
1:B:705:PRO:O	1:B:706:SER:HB2	2.15	0.46
1:C:705:PRO:O	1:C:706:SER:HB2	2.15	0.46
1:A:705:PRO:O	1:A:706:SER:HB2	2.15	0.46
1:C:155:TYR:HE1	1:C:209:THR:HG23	1.79	0.46
1:C:30:ALA:HB2	1:C:38:ILE:HD11	1.97	0.46
1:C:474:ASN:OD1	1:C:476:ASP:HB2	2.15	0.46
1:B:279:ILE:HD12	1:B:319:LEU:HD21	1.96	0.46
1:C:18:ASN:CB	1:C:21:LYS:HE3	2.44	0.46
1:A:474:ASN:OD1	1:A:476:ASP:HB2	2.15	0.46
1:A:254:ILE:O	1:A:302:ALA:HA	2.16	0.46
1:C:229:GLU:OE2	1:C:260:ARG:NH1	2.48	0.46
1:B:30:ALA:HB2	1:B:38:ILE:HD11	1.97	0.46
1:B:346:ARG:HD2	1:B:352:ASP:O	2.15	0.46
1:B:279:ILE:HB	1:B:280:PRO:CD	2.37	0.46
1:C:279:ILE:HD12	1:C:319:LEU:HD21	1.96	0.46
1:A:434:ARG:O	1:A:435:GLN:HB3	2.16	0.46
1:B:254:ILE:O	1:B:302:ALA:HA	2.16	0.46
1:A:21:LYS:O	1:A:25:VAL:HG23	2.16	0.46
1:C:434:ARG:O	1:C:435:GLN:HB3	2.16	0.46
1:B:229:GLU:OE2	1:B:260:ARG:NH1	2.48	0.46
1:B:155:TYR:CE1	1:B:209:THR:HG23	2.50	0.46
1:A:30:ALA:HA	1:A:33:LEU:HD12	1.96	0.46
1:C:135:ILE:HD11	1:C:174:ILE:HG21	1.97	0.46
1:C:21:LYS:O	1:C:25:VAL:HG23	2.16	0.46
1:A:30:ALA:HB2	1:A:38:ILE:HD11	1.97	0.46
1:B:658:ASP:HB3	1:B:662:LEU:HD12	1.97	0.46
1:A:135:ILE:HD11	1:A:174:ILE:HG21	1.97	0.46
1:B:442:ILE:HA	1:B:691:GLN:OE1	2.16	0.45
1:A:658:ASP:HB3	1:A:662:LEU:HD12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:658:ASP:HB3	1:C:662:LEU:HD12	1.98	0.45
1:A:633:ASN:O	1:A:634:GLY:C	2.55	0.45
1:B:135:ILE:HD11	1:B:174:ILE:HG21	1.97	0.45
1:C:254:ILE:O	1:C:302:ALA:HA	2.16	0.45
1:B:633:ASN:O	1:B:634:GLY:C	2.55	0.45
1:B:474:ASN:OD1	1:B:476:ASP:HB2	2.15	0.45
1:A:442:ILE:HA	1:A:691:GLN:OE1	2.16	0.45
1:B:434:ARG:O	1:B:435:GLN:HB3	2.16	0.45
1:A:275:HIS:ND1	3:A:762:TTP:H1'	2.31	0.45
1:C:346:ARG:HD2	1:C:352:ASP:O	2.15	0.45
1:B:489:LEU:HB3	1:B:513:LEU:HD22	1.98	0.45
1:B:329:ARG:HG3	1:B:331:ARG:NH2	2.32	0.45
1:C:442:ILE:HA	1:C:691:GLN:OE1	2.16	0.45
1:C:489:LEU:HB3	1:C:513:LEU:HD22	1.98	0.45
1:C:275:HIS:ND1	3:C:762:TTP:H1'	2.31	0.45
1:A:489:LEU:HB3	1:A:513:LEU:HD22	1.98	0.45
1:B:21:LYS:O	1:B:25:VAL:HG23	2.16	0.45
1:B:191:GLN:O	1:B:195:ARG:HG3	2.17	0.45
1:C:633:ASN:O	1:C:634:GLY:C	2.55	0.45
1:C:191:GLN:O	1:C:195:ARG:HG3	2.17	0.45
1:A:191:GLN:O	1:A:195:ARG:HG3	2.16	0.44
1:A:659:TYR:CE1	1:A:663:HIS:HB3	2.52	0.44
1:B:275:HIS:ND1	3:B:762:TTP:H1'	2.31	0.44
1:C:659:TYR:CE1	1:C:663:HIS:HB3	2.52	0.44
1:C:329:ARG:HG3	1:C:331:ARG:NH2	2.32	0.44
1:B:9:LYS:HA	1:B:55:THR:OG1	2.17	0.44
1:A:9:LYS:HA	1:A:55:THR:OG1	2.17	0.44
1:A:329:ARG:HG3	1:A:331:ARG:NH2	2.32	0.44
1:B:668:LEU:HB2	1:B:671:GLU:HG3	2.00	0.44
1:A:187:GLU:OE2	1:C:186:ARG:HD2	2.18	0.44
1:A:681:LEU:O	1:A:685:MET:HG3	2.18	0.44
1:C:668:LEU:HB2	1:C:671:GLU:HG3	2.00	0.44
1:C:681:LEU:O	1:C:685:MET:HG3	2.18	0.44
1:C:374:GLU:HG3	1:C:378:LEU:HD11	2.00	0.44
1:B:659:TYR:CE1	1:B:663:HIS:HB3	2.52	0.43
1:C:9:LYS:HA	1:C:55:THR:OG1	2.17	0.43
1:B:558:LEU:HD23	1:B:612:ARG:CG	2.38	0.43
1:A:374:GLU:HG3	1:A:378:LEU:HD11	2.00	0.43
1:A:532:SER:HA	1:A:677:GLY:HA3	2.00	0.43
1:A:668:LEU:HB2	1:A:671:GLU:HG3	2.00	0.43
1:A:558:LEU:HD23	1:A:612:ARG:CG	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:681:LEU:O	1:B:685:MET:HG3	2.18	0.43
2:F:368:ASP:O	2:F:372:ASN:ND2	2.51	0.43
1:C:621:PRO:HD3	1:C:694:SER:OG	2.19	0.43
1:A:621:PRO:HD3	1:A:694:SER:OG	2.19	0.43
1:B:374:GLU:HG3	1:B:378:LEU:HD11	2.00	0.43
1:C:558:LEU:HD23	1:C:612:ARG:CG	2.38	0.43
1:A:708:LYS:HE3	1:A:708:LYS:HB3	1.90	0.42
1:B:106:VAL:O	1:B:110:VAL:HG23	2.19	0.42
1:C:106:VAL:O	1:C:110:VAL:HG23	2.19	0.42
1:B:122:ASP:O	1:B:189:ARG:NH2	2.52	0.42
1:B:621:PRO:HD3	1:B:694:SER:OG	2.19	0.42
1:B:532:SER:HA	1:B:677:GLY:HA3	2.00	0.42
1:C:122:ASP:O	1:C:189:ARG:NH2	2.52	0.42
2:E:368:ASP:O	2:E:372:ASN:ND2	2.51	0.42
1:B:578:LEU:HB3	1:B:579:PRO:CD	2.48	0.42
1:C:578:LEU:HB3	1:C:579:PRO:CD	2.48	0.42
1:A:122:ASP:O	1:A:189:ARG:NH2	2.53	0.42
1:A:106:VAL:O	1:A:110:VAL:HG23	2.19	0.42
1:C:569:ASN:ND2	1:C:569:ASN:H	2.18	0.42
1:B:226:VAL:HG21	1:B:247:TYR:CD1	2.55	0.42
1:C:532:SER:HA	1:C:677:GLY:HA3	2.01	0.42
1:C:708:LYS:HB3	1:C:708:LYS:HE3	1.90	0.42
1:C:427:ASP:HA	1:C:428:PRO:HD2	1.93	0.42
1:A:226:VAL:HG21	1:A:247:TYR:CD1	2.55	0.42
2:D:368:ASP:O	2:D:372:ASN:ND2	2.51	0.42
1:C:269:ARG:O	1:C:269:ARG:HG3	2.20	0.41
1:B:569:ASN:ND2	1:B:569:ASN:H	2.18	0.41
1:A:313:VAL:HG22	1:A:317:LEU:HD22	2.02	0.41
1:B:169:ALA:O	1:B:172:LEU:HB3	2.21	0.41
1:C:226:VAL:HG21	1:C:247:TYR:CD1	2.55	0.41
1:B:427:ASP:HA	1:B:428:PRO:HD2	1.93	0.41
1:B:260:ARG:NH2	1:B:434:ARG:NH2	2.68	0.41
1:A:107:VAL:O	1:A:111:GLU:HG3	2.20	0.41
1:C:313:VAL:HG22	1:C:317:LEU:HD22	2.02	0.41
1:B:269:ARG:HG3	1:B:269:ARG:O	2.21	0.41
1:A:62:ILE:HG13	1:A:63:ILE:N	2.36	0.41
1:B:62:ILE:HG13	1:B:63:ILE:N	2.36	0.41
1:A:169:ALA:O	1:A:172:LEU:HB3	2.21	0.41
1:C:62:ILE:HG13	1:C:63:ILE:N	2.36	0.41
1:B:411:ARG:HD3	1:B:411:ARG:HH11	1.68	0.41
1:C:7:VAL:HG23	1:C:17:ILE:CG1	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:217:THR:HB	1:B:218:PRO:CD	2.50	0.41
1:A:269:ARG:O	1:A:269:ARG:HG3	2.20	0.41
1:A:569:ASN:H	1:A:569:ASN:ND2	2.18	0.41
1:C:260:ARG:NH2	1:C:434:ARG:NH2	2.68	0.41
1:B:107:VAL:O	1:B:111:GLU:HG3	2.21	0.41
1:C:75:PRO:O	1:C:78:GLN:HB2	2.21	0.41
1:B:708:LYS:HB3	1:B:708:LYS:HE3	1.90	0.40
1:B:313:VAL:HG22	1:B:317:LEU:HD22	2.02	0.40
1:C:704:PHE:HA	1:C:705:PRO:HD3	1.94	0.40
1:B:320:LYS:HE3	1:B:411:ARG:HB2	2.03	0.40
1:C:478:LEU:HD13	1:C:547:ILE:HG13	2.04	0.40
1:A:75:PRO:O	1:A:78:GLN:HB2	2.21	0.40
1:B:321:ASN:O	1:B:329:ARG:NE	2.46	0.40
1:A:406:ARG:O	1:A:410:GLY:N	2.48	0.40
1:B:478:LEU:HD13	1:B:547:ILE:HG13	2.04	0.40
1:C:107:VAL:O	1:C:111:GLU:HG3	2.21	0.40
1:B:7:VAL:HG23	1:B:17:ILE:CG1	2.43	0.40
1:A:83:ARG:HG2	1:A:141:MET:HG3	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%)	669 (92%)	58 (8%)	4 (0%)	34	76
1	B	731/761 (96%)	669 (92%)	58 (8%)	4 (0%)	34	76
1	C	731/761 (96%)	669 (92%)	58 (8%)	4 (0%)	34	76
2	D	11/20 (55%)	10 (91%)	1 (9%)	0	100	100
2	E	11/20 (55%)	10 (91%)	1 (9%)	0	100	100
2	F	11/20 (55%)	10 (91%)	1 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	P	2/20 (10%)	0	1 (50%)	1 (50%)	0 0
All	All	2228/2363 (94%)	2037 (91%)	178 (8%)	13 (1%)	30 72

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	216	ARG
1	B	216	ARG
1	C	216	ARG
1	A	296	GLY
1	B	296	GLY
1	C	296	GLY
1	A	189	ARG
1	B	189	ARG
1	C	189	ARG
1	A	300	GLY
1	B	300	GLY
1	C	300	GLY
2	P	3	VAL

### 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	628/651 (96%)	568 (90%)	60 (10%)	10 38
1	B	628/651 (96%)	569 (91%)	59 (9%)	11 39
1	C	628/651 (96%)	568 (90%)	60 (10%)	10 38
2	D	13/19 (68%)	9 (69%)	4 (31%)	0 2
2	E	13/19 (68%)	9 (69%)	4 (31%)	0 2
2	F	13/19 (68%)	9 (69%)	4 (31%)	0 2
2	P	3/19 (16%)	1 (33%)	2 (67%)	0 0
All	All	1926/2029 (95%)	1733 (90%)	193 (10%)	9 34

All (193) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	10	ARG
1	A	13	SER
1	A	14	THR
1	A	44	ARG
1	A	54	LYS
1	A	55	THR
1	A	56	SER
1	A	64	LYS
1	A	72	ARG
1	A	73	ASP
1	A	118	HIS
1	A	124	THR
1	A	149	LYS
1	A	189	ARG
1	A	194	LYS
1	A	204	LYS
1	A	206	SER
1	A	224	SER
1	A	225	CYS
1	A	260	ARG
1	A	262	ARG
1	A	264	LEU
1	A	266	SER
1	A	276	THR
1	A	283	LYS
1	A	294	GLN
1	A	317	LEU
1	A	320	LYS
1	A	325	VAL
1	A	326	GLU
1	A	341	LYS
1	A	364	LEU
1	A	384	LYS
1	A	387	SER
1	A	394	LYS
1	A	424	SER
1	A	428	PRO
1	A	435	GLN
1	A	452	VAL
1	A	465	SER
1	A	474	ASN

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Mol	Chain	Res	Type
1	A	484	LEU
1	A	530	ARG
1	A	570	GLU
1	A	580	ILE
1	A	585	LYS
1	A	616	LEU
1	A	620	MET
1	A	625	SER
1	A	629	SER
1	A	643	SER
1	A	645	LYS
1	A	647	SER
1	A	657	PRO
1	A	696	ASN
1	A	702	SER
1	A	708	LYS
1	A	709	VAL
1	A	732	GLN
2	D	363	SER
2	D	364	GLU
2	D	367	THR
2	D	372	ASN
1	B	6	LEU
1	B	10	ARG
1	B	13	SER
1	B	14	THR
1	B	44	ARG
1	B	54	LYS
1	B	55	THR
1	B	56	SER
1	B	64	LYS
1	B	72	ARG
1	B	73	ASP
1	B	118	HIS
1	B	124	THR
1	B	149	LYS
1	B	189	ARG
1	B	194	LYS
1	B	204	LYS
1	B	206	SER
1	B	224	SER
1	B	225	CYS

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Mol	Chain	Res	Type
1	B	260	ARG
1	B	262	ARG
1	B	264	LEU
1	B	266	SER
1	B	276	THR
1	B	283	LYS
1	B	294	GLN
1	B	317	LEU
1	B	320	LYS
1	B	325	VAL
1	B	326	GLU
1	B	341	LYS
1	B	364	LEU
1	B	384	LYS
1	B	387	SER
1	B	394	LYS
1	B	424	SER
1	B	428	PRO
1	B	435	GLN
1	B	452	VAL
1	B	465	SER
1	B	474	ASN
1	B	484	LEU
1	B	530	ARG
1	B	570	GLU
1	B	580	ILE
1	B	585	LYS
1	B	616	LEU
1	B	620	MET
1	B	625	SER
1	B	629	SER
1	B	643	SER
1	B	645	LYS
1	B	647	SER
1	B	696	ASN
1	B	702	SER
1	B	708	LYS
1	B	709	VAL
1	B	732	GLN
2	E	363	SER
2	E	364	GLU
2	E	367	THR

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Mol	Chain	Res	Type
2	E	372	ASN
1	C	6	LEU
1	C	10	ARG
1	C	13	SER
1	C	14	THR
1	C	44	ARG
1	C	54	LYS
1	C	55	THR
1	C	56	SER
1	C	64	LYS
1	C	72	ARG
1	C	73	ASP
1	C	118	HIS
1	C	124	THR
1	C	149	LYS
1	C	189	ARG
1	C	194	LYS
1	C	204	LYS
1	C	206	SER
1	C	224	SER
1	C	225	CYS
1	C	260	ARG
1	C	262	ARG
1	C	264	LEU
1	C	266	SER
1	C	276	THR
1	C	283	LYS
1	C	294	GLN
1	C	317	LEU
1	C	320	LYS
1	C	325	VAL
1	C	326	GLU
1	C	341	LYS
1	C	364	LEU
1	C	384	LYS
1	C	387	SER
1	C	394	LYS
1	C	424	SER
1	C	428	PRO
1	C	435	GLN
1	C	452	VAL
1	C	465	SER

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Mol	Chain	Res	Type
1	C	474	ASN
1	C	484	LEU
1	C	530	ARG
1	C	570	GLU
1	C	580	ILE
1	C	585	LYS
1	C	616	LEU
1	C	620	MET
1	C	625	SER
1	C	629	SER
1	C	643	SER
1	C	645	LYS
1	C	647	SER
1	C	657	PRO
1	C	696	ASN
1	C	702	SER
1	C	708	LYS
1	C	709	VAL
1	C	732	GLN
2	F	363	SER
2	F	364	GLU
2	F	367	THR
2	F	372	ASN
2	P	1	TYR
2	P	2	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	GLN
1	A	250	GLN
1	A	569	ASN
1	A	627	GLN
2	D	372	ASN
1	B	130	GLN
1	B	250	GLN
1	B	569	ASN
2	E	372	ASN
1	C	130	GLN
1	C	250	GLN
1	C	569	ASN
2	F	372	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 ⓘ

3 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	1.47	4 (19%)	31,47,47	2.82	4 (12%)
3	TTP	B	762	-	21,30,30	1.46	4 (19%)	31,47,47	2.82	4 (12%)
3	TTP	C	762	-	21,30,30	1.48	4 (19%)	31,47,47	2.81	4 (12%)

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
3	TTP	B	762	-	-	0/18/34/34	0/2/2/2
3	TTP	C	762	-	-	0/18/34/34	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	762	TTP	PA-O2A	-2.25	1.45	1.54
3	C	762	TTP	PA-O2A	-2.24	1.45	1.54
3	B	762	TTP	PA-O2A	-2.23	1.45	1.54
3	C	762	TTP	PG-O1G	2.29	1.58	1.51
3	A	762	TTP	PG-O1G	2.30	1.58	1.51
3	B	762	TTP	PG-O1G	2.33	1.58	1.51
3	B	762	TTP	C6-N1	2.65	1.39	1.35
3	A	762	TTP	C6-N1	2.67	1.39	1.35
3	C	762	TTP	C6-N1	2.72	1.39	1.35
3	B	762	TTP	C4-N3	3.71	1.40	1.33
3	C	762	TTP	C4-N3	3.72	1.40	1.33
3	A	762	TTP	C4-N3	3.72	1.40	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	762	TTP	C5-C4-N3	-9.53	114.53	125.14
3	B	762	TTP	C5-C4-N3	-9.52	114.54	125.14
3	C	762	TTP	C5-C4-N3	-9.48	114.58	125.14
3	A	762	TTP	PB-O3B-PG	-4.30	118.25	132.67
3	C	762	TTP	PB-O3B-PG	-4.29	118.27	132.67
3	B	762	TTP	PB-O3B-PG	-4.29	118.28	132.67
3	B	762	TTP	O3'-C3'-C4'	-2.25	100.96	110.05
3	A	762	TTP	O3'-C3'-C4'	-2.25	100.96	110.05
3	C	762	TTP	O3'-C3'-C4'	-2.24	100.98	110.05
3	C	762	TTP	C4-N3-C2	10.88	124.65	115.25
3	A	762	TTP	C4-N3-C2	10.89	124.66	115.25
3	B	762	TTP	C4-N3-C2	10.92	124.68	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	762	TTP	2	0
3	B	762	TTP	2	0
3	C	762	TTP	2	0

## 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 ⓘ

### 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%)	-0.49	11 (1%) 76 49	2, 6, 7, 9	0
1	B	733/761 (96%)	-0.46	9 (1%) 81 55	2, 6, 7, 9	0
1	C	733/761 (96%)	-0.41	9 (1%) 81 55	2, 6, 7, 9	0
2	D	13/20 (65%)	0.58	1 (7%) 16 6	4, 6, 7, 7	0
2	E	13/20 (65%)	0.37	0 100 100	4, 6, 7, 7	0
2	F	13/20 (65%)	0.35	1 (7%) 16 6	4, 6, 7, 7	0
2	P	4/20 (20%)	0.40	1 (25%) 1 1	2, 2, 2, 3	0
All	All	2242/2363 (94%)	-0.44	32 (1%) 78 51	2, 6, 7, 9	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	737	GLY	4.5
1	C	737	GLY	4.1
1	A	11	ASP	3.8
1	A	737	GLY	3.6
1	B	11	ASP	3.0
1	A	12	GLY	2.7
1	B	271	GLY	2.7
1	B	12	GLY	2.7
1	B	295	GLY	2.7
1	B	296	GLY	2.6
1	C	11	ASP	2.6
1	C	16	ARG	2.5
2	P	4	GLY	2.5
1	C	736	ASP	2.4
1	A	270	GLY	2.4
1	A	736	ASP	2.4
1	A	298	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	18	ASN	2.3
2	F	363	SER	2.3
1	A	271	GLY	2.3
1	C	298	ARG	2.3
1	A	18	ASN	2.3
1	A	6	LEU	2.3
1	B	322	ASN	2.2
2	D	364	GLU	2.2
1	C	10	ARG	2.2
1	B	13	SER	2.2
1	C	13	SER	2.1
1	C	271	GLY	2.0
1	A	322	ASN	2.0
1	B	161	VAL	2.0
1	A	272	GLU	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
3	TTP	B	762	29/29	0.93	0.20	0.11	2,2,5,6	0
3	TTP	A	762	29/29	0.94	0.18	-0.07	2,2,5,6	0
3	TTP	C	762	29/29	0.91	0.18	-0.25	2,2,5,6	0

## 6.5 Other polymers

There are no such residues in this entry.