



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 08:12 pm GMT

PDB ID : 1J3K
Title : Quadruple mutant (N51I+C59R+S108N+I164L) Plasmodium falciparum dihydrofolate reductase-thymidylate synthase (PfDHFR-TS) complexed with WR99210, NADPH, and dUMP
Authors : Yuvaniyama, J.; Chitnumsub, P.; Kamchonwongpaisan, S.; Vanichtanankul, J.; Sirawaraporn, W.; Taylor, P.; Walkinshaw, M.; Yuthavong, Y.
Deposited on : 2003-02-03
Resolution : 2.10 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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
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

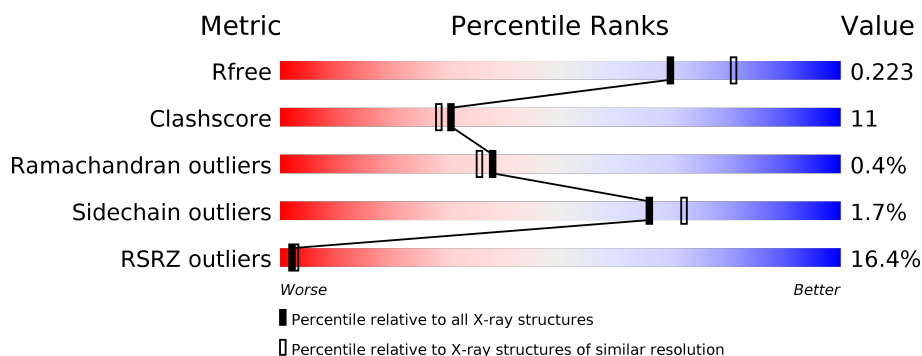
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	280	<div> <div>15%</div> <div>62%</div> <div>15%</div> <div>21%</div> </div>
1	B	280	<div> <div>34%</div> <div>48%</div> <div>29%</div> <div>21%</div> </div>
2	C	328	<div> <div>7%</div> <div>91%</div> <div>8%</div> <div>..</div> </div>
2	D	328	<div> <div>6%</div> <div>87%</div> <div>12%</div> <div>..</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10528 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 Bifunctional dihydrofolate reductase-thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1837	1190	297	338	12			
1	B	221	Total	C	N	O	S	0	0	0
			1834	1189	297	336	12			

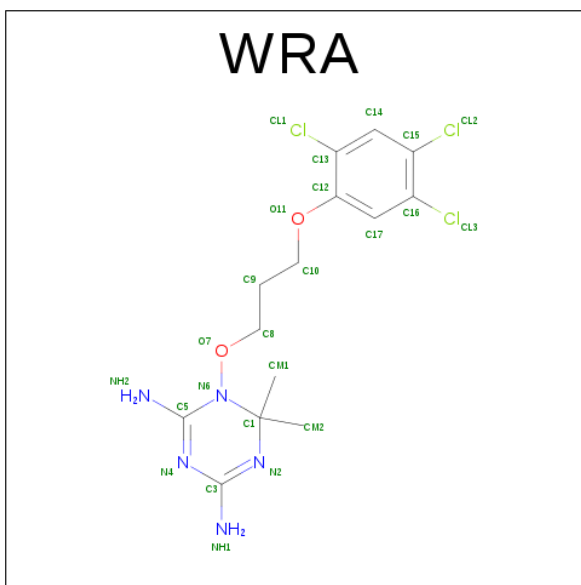
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	ILE	ASN	ENGINEERED	UNP P13922
A	59	ARG	CYS	SEE REMARK 999, ENGINEERED	UNP P13922
A	108	ASN	SER	SEE REMARK 999, ENGINEERED	UNP P13922
A	164	LEU	ILE	ENGINEERED	UNP P13922
B	51	ILE	ASN	ENGINEERED	UNP P13922
B	59	ARG	CYS	SEE REMARK 999, ENGINEERED	UNP P13922
B	108	ASN	SER	SEE REMARK 999, ENGINEERED	UNP P13922
B	164	LEU	ILE	ENGINEERED	UNP P13922

- Molecule 2 is a protein called Bifunctional dihydrofolate reductase-thymidylate synthase.

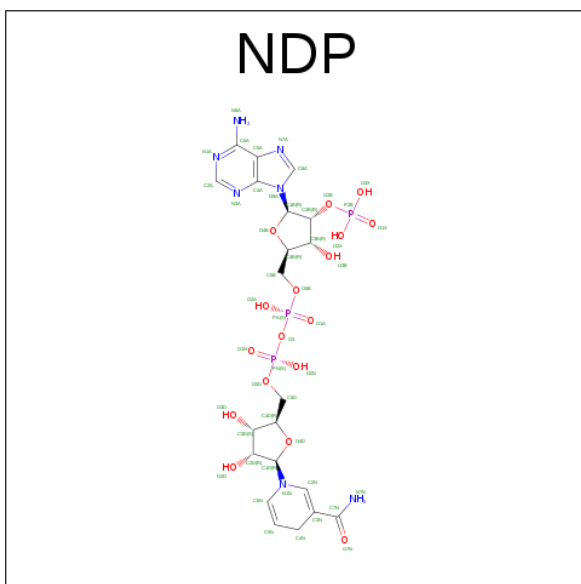
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	326	Total	C	N	O	S	0	0	0
			2713	1747	456	495	15			
2	D	326	Total	C	N	O	S	0	0	0
			2713	1747	456	495	15			

- Molecule 3 is 6,6-DIMETHYL-1-[3-(2,4,5-TRICHLOROPHENOXY)PROPOXY]-1,6-DIHYDRO-1,3,5-TRIAZINE-2,4-DIAMINE (three-letter code: WRA) (formula: C₁₄H₁₈Cl₃N₅O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 24	C 14	Cl 3	N 5	O 2	0	0
3	B	1	Total 24	C 14	Cl 3	N 5	O 2	0	0

- Molecule 4 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $\text{C}_{21}\text{H}_{30}\text{N}_7\text{O}_{17}\text{P}_3$).



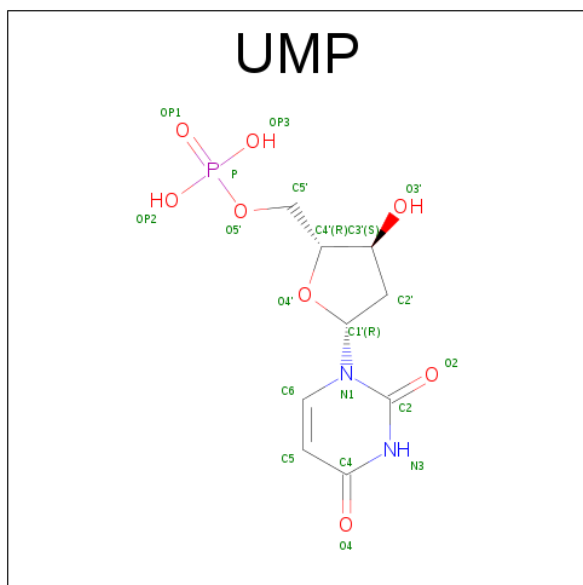
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 48	C 21	N 7	O 17	P 3	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 5 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (three-letter code: UMP) (formula: $C_9H_{13}N_2O_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
5	D	1	Total	C	N	O	P	0	0
			20	9	2	8	1		

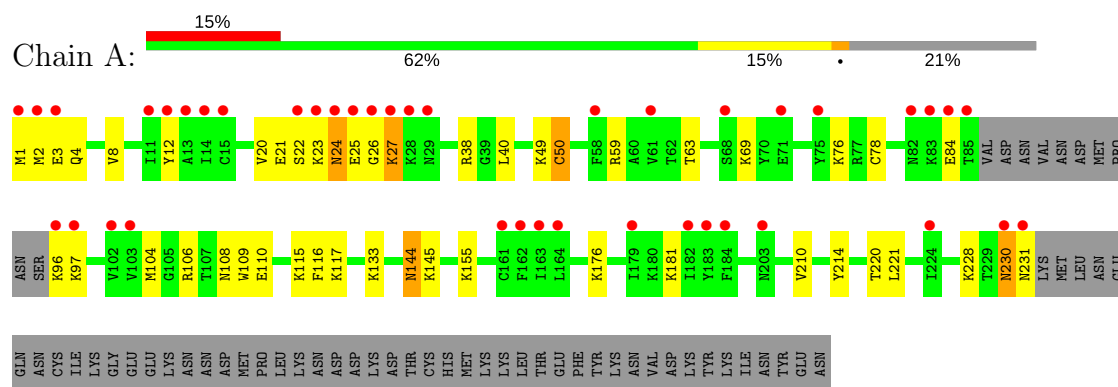
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	238	Total	O	0	0
			238	238		
6	B	102	Total	O	0	0
			102	102		
6	C	428	Total	O	0	0
			428	428		
6	D	479	Total	O	0	0
			479	479		

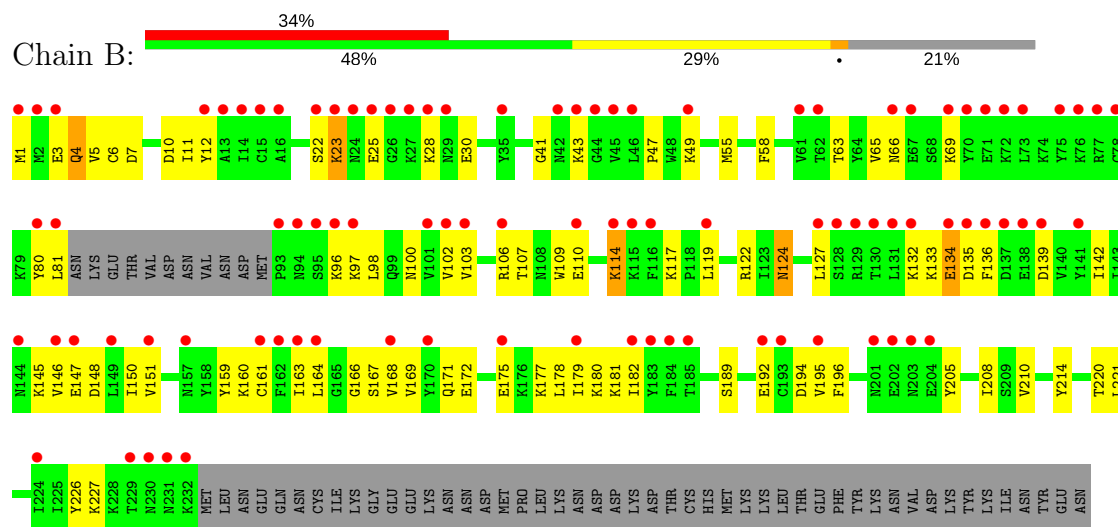
3 Residue-property plots

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.

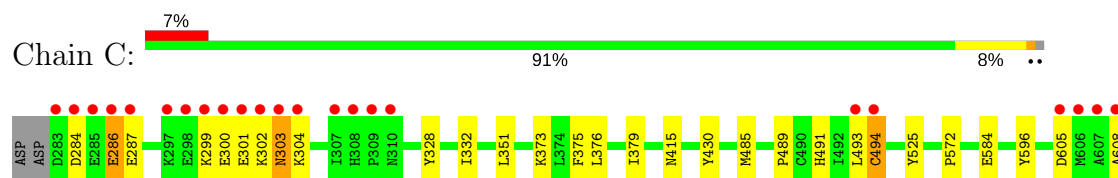
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase



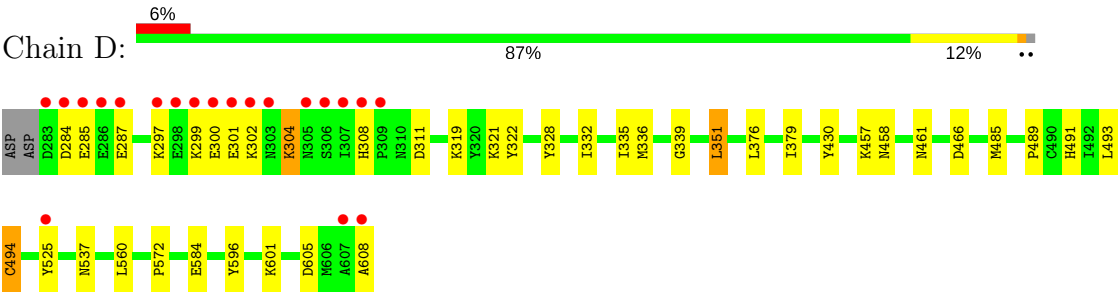
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase



- Molecule 2: Bifunctional dihydrofolate reductase-thymidylate synthase



- Molecule 2: Bifunctional dihydrofolate reductase-thymidylate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.68Å 158.09Å 165.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.98 – 2.10 28.98 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.8 (28.98-2.10) 96.9 (28.98-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.43 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.182 , 0.222 0.183 , 0.223	Depositor DCC
R_{free} test set	4520 reflections (5.03%)	DCC
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 65.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.006 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10528	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, UMP, WRA

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	0.64	0/1871	0.88	5/2515 (0.2%)
1	B	0.46	0/1869	0.76	1/2512 (0.0%)
2	C	0.74	1/2784 (0.0%)	0.85	2/3766 (0.1%)
2	D	0.73	1/2784 (0.0%)	0.84	1/3766 (0.0%)
All	All	0.67	2/9308 (0.0%)	0.83	9/12559 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	494	CYS	CB-SG	-9.88	1.65	1.82
2	D	494	CYS	CB-SG	-7.79	1.69	1.82

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	22	SER	N-CA-C	-8.83	87.17	111.00
2	C	304	LYS	N-CA-C	6.75	129.22	111.00
2	C	351	LEU	N-CA-C	-6.23	94.19	111.00
2	D	351	LEU	N-CA-C	-6.21	94.23	111.00
1	B	30	GLU	N-CA-C	5.85	126.79	111.00
1	A	27	LYS	N-CA-C	5.49	125.83	111.00
1	A	24	ASN	N-CA-C	5.28	125.25	111.00
1	A	25	GLU	N-CA-C	5.12	124.81	111.00
1	A	3	GLU	N-CA-C	5.01	124.54	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	1837	0	1873	42	0
1	B	1834	0	1873	86	0
2	C	2713	0	2638	22	0
2	D	2713	0	2638	44	0
3	A	24	0	18	1	0
3	B	24	0	18	0	0
4	A	48	0	26	4	0
4	B	48	0	26	6	0
5	C	20	0	11	1	0
5	D	20	0	11	0	0
6	A	238	0	0	12	1
6	B	102	0	0	11	0
6	C	428	0	0	4	1
6	D	479	0	0	13	0
All	All	10528	0	9132	194	1

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 11.

All (194) 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:1:MET:HG3	1:A:2:MET:H	0.97	1.11
1:A:1:MET:HG3	1:A:2:MET:N	1.78	0.98
2:D:300:GLU:HG3	2:D:304:LYS:NZ	1.78	0.98
2:D:605:ASP:HB3	2:D:608:ALA:HB2	1.46	0.98
1:B:210:VAL:HB	6:B:2028:HOH:O	1.64	0.95
1:A:210:VAL:HB	6:A:2086:HOH:O	1.66	0.95
2:D:461:ASN:HB3	6:D:1537:HOH:O	1.68	0.93
1:B:114:LYS:H	1:B:114:LYS:HD2	1.37	0.89
1:A:1:MET:CG	1:A:2:MET:H	1.84	0.88
2:C:415:ASN:HB2	6:C:1911:HOH:O	1.73	0.88
1:B:142:ILE:HG22	6:B:1389:HOH:O	1.75	0.87
1:A:50:CYS:SG	6:A:1300:HOH:O	2.33	0.85
2:D:376:LEU:HD22	2:D:379:ILE:HD11	1.57	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:LYS:HE3	1:B:147:GLU:HB2	1.58	0.83
2:D:584:GLU:HB2	6:D:1723:HOH:O	1.79	0.81
1:B:171:GLN:O	1:B:175:GLU:HG3	1.81	0.80
1:A:133:LYS:HE3	6:A:1232:HOH:O	1.82	0.79
2:C:286:GLU:HG2	2:D:319:LYS:HG2	1.65	0.78
1:B:106:ARG:HB3	4:B:710:NDP:O3B	1.85	0.77
2:D:300:GLU:HG2	2:D:300:GLU:O	1.87	0.75
2:D:302:LYS:HE3	6:D:1790:HOH:O	1.86	0.75
2:D:300:GLU:HG3	2:D:304:LYS:HZ1	1.49	0.73
1:B:41:GLY:HA2	1:B:47:PRO:HD3	1.69	0.73
2:C:375:PHE:HD1	6:C:1945:HOH:O	1.70	0.73
2:C:605:ASP:HB3	2:C:608:ALA:HB2	1.71	0.73
1:A:96:LYS:HE2	6:A:1129:HOH:O	1.89	0.72
2:D:300:GLU:HG3	2:D:304:LYS:HZ2	1.54	0.70
2:D:605:ASP:HB3	2:D:608:ALA:CB	2.21	0.69
1:B:25:GLU:OE1	1:B:25:GLU:HA	1.93	0.69
1:B:124:ASN:N	1:B:124:ASN:HD22	1.89	0.68
1:B:145:LYS:HG2	1:B:146:VAL:N	2.08	0.68
1:A:78:CYS:SG	6:A:1201:HOH:O	2.51	0.68
1:B:23:LYS:HA	1:B:23:LYS:CE	2.22	0.68
1:B:114:LYS:H	1:B:114:LYS:CD	1.99	0.67
1:B:134:GLU:C	1:B:136:PHE:H	1.99	0.65
2:D:458:ASN:HB3	6:D:1541:HOH:O	1.94	0.65
1:B:161:CYS:SG	6:B:2219:HOH:O	2.54	0.65
2:D:301:GLU:HA	2:D:301:GLU:OE1	1.96	0.64
1:B:11:ILE:HG12	6:B:2219:HOH:O	1.97	0.64
2:C:605:ASP:HB3	2:C:608:ALA:CB	2.27	0.64
1:B:103:VAL:HB	1:B:163:ILE:HD13	1.80	0.64
1:B:11:ILE:HG23	6:B:2219:HOH:O	1.97	0.63
1:B:23:LYS:HA	1:B:23:LYS:HE3	1.81	0.63
1:A:96:LYS:HG3	1:A:97:LYS:N	2.15	0.62
1:B:127:LEU:HB3	4:B:710:NDP:N3A	2.15	0.62
1:B:3:GLU:HG3	1:B:80:TYR:HE1	1.66	0.61
1:A:230:ASN:O	1:A:230:ASN:CG	2.38	0.61
1:B:161:CYS:HB3	6:B:2219:HOH:O	2.01	0.61
2:D:322:TYR:OH	6:D:1347:HOH:O	2.16	0.61
1:A:21:GLU:CD	1:A:23:LYS:HE2	2.21	0.60
1:A:69:LYS:HE2	2:D:284:ASP:OD2	2.01	0.60
2:D:457:LYS:NZ	6:D:1696:HOH:O	2.35	0.60
1:B:97:LYS:HB3	1:B:97:LYS:NZ	2.18	0.59
1:B:124:ASN:HD22	1:B:124:ASN:H	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:GLU:HG2	1:A:23:LYS:HE2	1.84	0.58
2:D:300:GLU:C	2:D:302:LYS:N	2.55	0.58
1:A:96:LYS:HG3	1:A:97:LYS:H	1.70	0.57
1:B:107:THR:OG1	4:B:710:NDP:H51A	2.03	0.56
1:B:97:LYS:HD2	6:B:1383:HOH:O	2.05	0.56
1:A:115:LYS:HE3	1:A:116:PHE:CZ	2.39	0.56
1:B:80:TYR:O	1:B:81:LEU:C	2.44	0.56
2:C:494:CYS:SG	2:C:525:TYR:CE2	2.99	0.56
1:B:1:MET:O	1:B:1:MET:HG3	2.06	0.55
1:A:176:LYS:HD3	6:A:1165:HOH:O	2.06	0.55
2:C:584:GLU:HB2	6:C:2237:HOH:O	2.07	0.55
2:C:491:HIS:ND1	6:C:2176:HOH:O	2.24	0.55
2:D:537:ASN:HB3	6:D:2230:HOH:O	2.07	0.55
2:D:321:LYS:HE3	6:D:1342:HOH:O	2.05	0.55
1:B:12:TYR:HE2	1:B:160:LYS:HD3	1.72	0.54
1:B:168:VAL:O	1:B:172:GLU:HG2	2.07	0.54
2:D:332:ILE:HD13	2:D:560:LEU:HD22	1.89	0.54
1:B:132:LYS:NZ	1:B:135:ASP:OD2	2.41	0.54
1:B:58:PHE:HZ	1:B:164:LEU:HD13	1.73	0.54
2:D:493:LEU:C	2:D:493:LEU:HD12	2.27	0.54
1:B:22:SER:O	1:B:23:LYS:HB2	2.07	0.53
2:D:300:GLU:C	2:D:302:LYS:H	2.11	0.53
1:B:109:TRP:CZ2	1:B:117:LYS:HD2	2.43	0.53
1:B:133:LYS:O	1:B:136:PHE:HB2	2.09	0.53
1:B:106:ARG:NH1	1:B:110:GLU:OE1	2.42	0.52
1:B:145:LYS:HE3	1:B:147:GLU:CB	2.34	0.52
1:A:20:VAL:HG21	1:A:38:ARG:NH2	2.24	0.52
1:B:3:GLU:CG	1:B:80:TYR:HE1	2.21	0.52
1:A:21:GLU:CG	1:A:23:LYS:HE2	2.39	0.51
1:B:124:ASN:N	1:B:124:ASN:ND2	2.59	0.51
2:D:491:HIS:ND1	6:D:1876:HOH:O	2.29	0.51
1:B:11:ILE:HB	1:B:178:LEU:O	2.10	0.51
1:A:214:TYR:O	1:A:220:THR:HA	2.11	0.50
2:D:601:LYS:HG2	6:D:1429:HOH:O	2.11	0.50
4:A:610:NDP:H8A	4:A:610:NDP:H52A	1.94	0.50
1:B:196:PHE:CD1	1:B:196:PHE:N	2.79	0.50
2:C:299:LYS:HE3	2:C:302:LYS:HB2	1.93	0.50
1:B:41:GLY:N	1:B:195:VAL:HG23	2.27	0.50
2:C:376:LEU:HD22	2:C:379:ILE:HD11	1.93	0.50
1:A:50:CYS:HB2	6:A:2115:HOH:O	2.11	0.50
2:C:493:LEU:C	2:C:493:LEU:HD12	2.31	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:SER:HB3	4:B:710:NDP:O2N	2.12	0.50
2:C:494:CYS:SG	2:C:525:TYR:HE2	2.35	0.50
1:B:192:GLU:HG3	6:B:1449:HOH:O	2.11	0.50
1:B:55:MET:HE2	6:B:2031:HOH:O	2.11	0.50
2:D:494:CYS:SG	2:D:525:TYR:CE2	3.05	0.50
1:B:12:TYR:CE2	1:B:160:LYS:HD3	2.47	0.49
1:A:109:TRP:CE2	1:A:117:LYS:HD2	2.48	0.49
2:C:373:LYS:HE2	2:C:375:PHE:CE2	2.47	0.49
2:C:300:GLU:HG3	2:C:301:GLU:HG3	1.95	0.49
1:A:230:ASN:OD1	1:A:230:ASN:O	2.30	0.49
2:D:494:CYS:SG	2:D:525:TYR:HE2	2.36	0.49
2:D:336:MET:HE1	2:D:560:LEU:HB2	1.93	0.49
2:D:308:HIS:O	2:D:311:ASP:HB2	2.12	0.49
1:A:4:GLN:NE2	1:A:228:LYS:NZ	2.61	0.49
1:B:134:GLU:C	1:B:136:PHE:N	2.65	0.48
1:B:80:TYR:HA	6:B:2213:HOH:O	2.14	0.48
1:B:114:LYS:N	1:B:114:LYS:HD2	2.16	0.48
1:A:20:VAL:CG2	1:A:38:ARG:NH2	2.77	0.48
1:B:66:ASN:ND2	1:B:69:LYS:HD2	2.29	0.48
1:B:119:LEU:HB3	1:B:122:ARG:CZ	2.44	0.48
1:A:109:TRP:CZ2	1:A:117:LYS:HD2	2.49	0.48
1:A:230:ASN:O	1:A:231:ASN:ND2	2.46	0.47
2:C:373:LYS:HE2	2:C:375:PHE:CZ	2.49	0.47
2:D:466:ASP:OD2	6:D:1534:HOH:O	2.20	0.47
2:D:572:PRO:HB3	2:D:596:TYR:HA	1.96	0.47
1:B:7:ASP:OD1	1:B:180:LYS:HE3	2.15	0.47
1:B:43:LYS:N	1:B:194:ASP:OD2	2.36	0.47
2:C:572:PRO:HB3	2:C:596:TYR:HA	1.95	0.47
1:B:3:GLU:HG3	1:B:80:TYR:CE1	2.48	0.47
2:C:328:TYR:CZ	2:C:332:ILE:HD11	2.50	0.47
1:B:136:PHE:CD2	1:B:142:ILE:HD11	2.50	0.47
2:C:299:LYS:CE	2:C:302:LYS:HB2	2.44	0.47
2:D:584:GLU:HG2	6:D:1724:HOH:O	2.14	0.47
1:B:106:ARG:O	1:B:110:GLU:HG3	2.15	0.46
1:B:182:ILE:HB	1:B:226:TYR:HB2	1.97	0.46
1:A:40:LEU:O	4:A:610:NDP:H2N	2.16	0.46
2:D:297:LYS:HA	2:D:297:LYS:HD3	1.59	0.46
2:D:328:TYR:CZ	2:D:332:ILE:HD11	2.50	0.46
2:D:284:ASP:O	2:D:287:GLU:HB2	2.16	0.46
1:A:144:ASN:HD22	1:A:144:ASN:H	1.63	0.46
1:A:96:LYS:HA	6:A:1209:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:GLN:OE1	1:B:5:VAL:HG23	2.14	0.45
1:B:12:TYR:CD1	1:B:181:LYS:HB2	2.52	0.45
1:A:84:GLU:HB3	6:A:1199:HOH:O	2.16	0.45
1:B:214:TYR:O	1:B:220:THR:HA	2.16	0.45
1:A:8:VAL:HA	1:A:76:LYS:HD3	1.99	0.45
1:B:145:LYS:HB3	1:B:145:LYS:HE2	1.51	0.45
4:A:610:NDP:H3B	6:A:1171:HOH:O	2.17	0.45
2:C:491:HIS:CE1	5:C:611:UMP:O4	2.69	0.45
1:B:102:VAL:HG23	1:B:102:VAL:O	2.16	0.44
1:B:23:LYS:HE3	1:B:23:LYS:CA	2.45	0.44
1:A:106:ARG:HE	4:A:610:NDP:P2B	2.41	0.44
1:B:139:ASP:OD1	1:B:139:ASP:O	2.36	0.44
1:B:171:GLN:HG3	1:B:175:GLU:OE2	2.18	0.44
1:B:221:LEU:HD23	1:B:221:LEU:N	2.33	0.44
1:B:107:THR:HB	4:B:710:NDP:O2A	2.18	0.44
2:C:284:ASP:O	2:C:287:GLU:HB2	2.18	0.44
1:A:96:LYS:CG	1:A:97:LYS:H	2.29	0.43
1:B:145:LYS:CG	1:B:146:VAL:N	2.78	0.43
1:B:41:GLY:HA2	1:B:47:PRO:CD	2.43	0.43
1:B:179:ILE:HB	1:B:205:TYR:OH	2.18	0.43
2:D:332:ILE:HG23	2:D:336:MET:HE2	2.01	0.43
1:B:166:GLY:O	1:B:169:VAL:HB	2.19	0.43
1:B:65:VAL:HG11	1:B:98:LEU:HG	2.00	0.43
1:A:228:LYS:HE3	6:A:1190:HOH:O	2.18	0.43
1:B:166:GLY:N	4:B:710:NDP:O1A	2.51	0.43
1:A:108:ASN:HD21	3:A:609:WRA:H91	1.83	0.43
2:D:332:ILE:CG2	2:D:336:MET:HE2	2.49	0.43
1:A:221:LEU:HD23	1:A:221:LEU:N	2.33	0.42
2:C:300:GLU:O	2:C:303:ASN:HB2	2.19	0.42
1:B:63:THR:HG22	1:B:122:ARG:NE	2.34	0.42
1:B:161:CYS:CB	6:B:2219:HOH:O	2.61	0.42
2:D:351:LEU:HA	2:D:351:LEU:HD23	1.92	0.42
2:D:321:LYS:CE	6:D:1342:HOH:O	2.65	0.42
1:B:100:ASN:OD1	1:B:159:TYR:HB3	2.18	0.42
1:B:175:GLU:C	1:B:177:LYS:H	2.23	0.42
1:A:59:ARG:O	1:A:63:THR:HG23	2.19	0.42
1:B:3:GLU:O	1:B:3:GLU:CG	2.68	0.42
1:B:58:PHE:HE1	1:B:164:LEU:HD22	1.84	0.42
1:B:41:GLY:H	1:B:195:VAL:HG23	1.83	0.41
2:D:284:ASP:N	2:D:284:ASP:OD1	2.53	0.41
1:B:148:ASP:O	1:B:151:VAL:HB	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:LEU:HD12	1:B:127:LEU:N	2.35	0.41
2:D:299:LYS:HG2	2:D:301:GLU:HB2	2.02	0.41
1:B:1:MET:O	1:B:1:MET:CG	2.68	0.41
1:A:155:LYS:NZ	6:A:1153:HOH:O	2.50	0.41
1:B:6:CYS:O	1:B:10:ASP:HA	2.20	0.41
2:D:335:ILE:O	2:D:339:GLY:N	2.50	0.41
2:D:376:LEU:HD22	2:D:379:ILE:CD1	2.39	0.41
1:A:106:ARG:NH1	1:A:110:GLU:OE1	2.54	0.41
1:B:208:ILE:HD13	1:B:227:LYS:HB2	2.02	0.41
1:A:144:ASN:ND2	1:A:145:LYS:HG3	2.36	0.41
1:B:96:LYS:HD3	1:B:96:LYS:HA	1.84	0.41
2:C:485:MET:SD	2:C:489:PRO:HD3	2.60	0.41
1:A:12:TYR:CD1	1:A:181:LYS:HB2	2.56	0.40
1:B:5:VAL:HG11	1:B:150:ILE:HD12	2.03	0.40
1:A:21:GLU:HG2	1:A:23:LYS:HG2	2.04	0.40
2:D:284:ASP:O	2:D:285:GLU:C	2.60	0.40
2:D:485:MET:SD	2:D:489:PRO:HD3	2.61	0.40

All (1) 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)
6:A:1592:HOH:O	6:C:1593:HOH:O[3_645]	2.18	0.02

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	217/280 (78%)	208 (96%)	8 (4%)	1 (0%)	32	28
1	B	217/280 (78%)	198 (91%)	18 (8%)	1 (0%)	32	28
2	C	324/328 (99%)	312 (96%)	11 (3%)	1 (0%)	44	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	324/328 (99%)	307 (95%)	16 (5%)	1 (0%)	44	44
All	All	1082/1216 (89%)	1025 (95%)	53 (5%)	4 (0%)	38	35

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	430	TYR
1	A	26	GLY
1	B	28	LYS
2	D	430	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	210/268 (78%)	203 (97%)	7 (3%)	43	45
1	B	210/268 (78%)	203 (97%)	7 (3%)	43	45
2	C	300/302 (99%)	298 (99%)	2 (1%)	87	91
2	D	300/302 (99%)	299 (100%)	1 (0%)	94	96
All	All	1020/1140 (90%)	1003 (98%)	17 (2%)	66	72

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	27	LYS
1	A	49	LYS
1	A	50	CYS
1	A	104	MET
1	A	144	ASN
1	A	230	ASN
1	B	4	GLN
1	B	23	LYS
1	B	49	LYS

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Mol	Chain	Res	Type
1	B	114	LYS
1	B	124	ASN
1	B	134	GLU
1	B	189	SER
2	C	286	GLU
2	C	303	ASN
2	D	304	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	99	GLN
1	A	144	ASN
1	A	171	GLN
1	A	231	ASN
1	B	99	GLN
1	B	157	ASN
1	B	171	GLN
1	B	231	ASN
2	C	303	ASN
2	C	394	ASN
2	C	424	ASN
2	D	394	ASN
2	D	424	ASN
2	D	450	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

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	WRA	A	609	-	21,25,25	2.88	13 (61%)	24,36,36	1.51	5 (20%)
4	NDP	A	610	-	43,52,52	2.63	18 (41%)	49,80,80	2.05	14 (28%)
3	WRA	B	709	-	21,25,25	3.09	12 (57%)	24,36,36	1.33	4 (16%)
4	NDP	B	710	-	43,52,52	2.68	21 (48%)	49,80,80	1.96	13 (26%)
5	UMP	C	611	-	17,21,21	1.85	4 (23%)	23,31,31	3.34	9 (39%)
5	UMP	D	711	-	17,21,21	1.91	4 (23%)	23,31,31	3.72	9 (39%)

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	WRA	A	609	-	-	0/7/27/27	0/2/2/2
4	NDP	A	610	-	-	0/30/77/77	0/5/5/5
3	WRA	B	709	-	-	0/7/27/27	0/2/2/2
4	NDP	B	710	-	-	0/30/77/77	0/5/5/5
5	UMP	C	611	-	-	0/6/22/22	0/2/2/2
5	UMP	D	711	-	-	0/6/22/22	0/2/2/2

All (72) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	710	NDP	C3B-C2B	-4.57	1.42	1.53
4	B	710	NDP	C3B-C4B	-3.81	1.43	1.53
4	B	710	NDP	PA-O2A	-3.77	1.36	1.55
4	B	710	NDP	C4N-C5N	-3.66	1.41	1.49
4	B	710	NDP	O4B-C1B	-3.61	1.36	1.41
4	A	610	NDP	C2D-C3D	-3.34	1.44	1.53
4	A	610	NDP	P2B-O2X	-3.30	1.41	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	711	UMP	P-O5'	-3.13	1.50	1.60
4	B	710	NDP	C2D-C3D	-3.04	1.45	1.53
4	B	710	NDP	PA-O1A	-2.90	1.40	1.50
4	A	610	NDP	C8A-N7A	-2.90	1.29	1.34
4	A	610	NDP	C4N-C5N	-2.89	1.42	1.49
4	A	610	NDP	P2B-O2B	-2.26	1.55	1.59
4	B	710	NDP	C8A-N7A	-2.10	1.30	1.34
4	B	710	NDP	PN-O2N	-2.10	1.44	1.55
5	C	611	UMP	P-O5'	-2.03	1.53	1.60
4	B	710	NDP	O3D-C3D	2.10	1.47	1.43
4	A	610	NDP	O3B-C3B	2.14	1.47	1.43
3	A	609	WRA	C15-CL2	2.27	1.79	1.73
4	B	710	NDP	C2D-C1D	2.29	1.60	1.53
4	B	710	NDP	C2A-N1A	2.31	1.38	1.33
5	D	711	UMP	O3'-C3'	2.32	1.48	1.43
4	A	610	NDP	C6N-N1N	2.37	1.44	1.37
3	B	709	WRA	C5-N4	2.37	1.38	1.34
4	A	610	NDP	O3D-C3D	2.44	1.48	1.43
3	A	609	WRA	C5-N4	2.46	1.39	1.34
3	A	609	WRA	C9-C10	2.48	1.61	1.51
3	B	709	WRA	O7-C8	2.49	1.49	1.45
5	C	611	UMP	O3'-C3'	2.54	1.48	1.43
4	B	710	NDP	C2A-N3A	2.57	1.36	1.32
4	A	610	NDP	C2A-N1A	2.58	1.38	1.33
4	A	610	NDP	C2A-N3A	2.58	1.36	1.32
3	A	609	WRA	C16-CL3	2.60	1.79	1.73
3	A	609	WRA	C16-C15	2.62	1.45	1.39
5	C	611	UMP	O4'-C1'	2.76	1.48	1.42
3	B	709	WRA	C15-CL2	2.80	1.80	1.73
3	A	609	WRA	O11-C10	2.81	1.53	1.43
3	B	709	WRA	C9-C10	2.86	1.63	1.51
4	A	610	NDP	C2N-C3N	2.97	1.43	1.34
3	B	709	WRA	C14-C13	3.14	1.43	1.38
3	B	709	WRA	O11-C10	3.20	1.54	1.43
4	A	610	NDP	C5D-C4D	3.23	1.61	1.51
4	A	610	NDP	PA-O5B	3.24	1.72	1.59
3	A	609	WRA	C12-C13	3.27	1.45	1.39
5	D	711	UMP	O4'-C1'	3.41	1.50	1.42
3	A	609	WRA	C17-C12	3.45	1.45	1.38
3	A	609	WRA	O11-C12	3.54	1.44	1.37
3	A	609	WRA	C17-C16	3.60	1.44	1.38
3	B	709	WRA	O11-C12	3.82	1.45	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	710	NDP	C6N-N1N	3.84	1.48	1.37
4	A	610	NDP	O4D-C1D	3.98	1.51	1.42
3	B	709	WRA	C14-C15	4.00	1.45	1.38
4	B	710	NDP	PN-O1N	4.14	1.66	1.50
4	B	710	NDP	C6N-C5N	4.18	1.41	1.33
5	D	711	UMP	C4-N3	4.24	1.40	1.33
4	B	710	NDP	O4D-C1D	4.30	1.52	1.42
4	B	710	NDP	C2N-C3N	4.54	1.47	1.34
4	A	610	NDP	C6N-C5N	4.64	1.41	1.33
4	B	710	NDP	C4A-N3A	4.74	1.42	1.35
3	B	709	WRA	C12-C13	4.74	1.48	1.39
3	B	709	WRA	C16-C15	4.81	1.50	1.39
5	C	611	UMP	C4-N3	4.89	1.41	1.33
4	A	610	NDP	O4B-C4B	4.96	1.56	1.45
3	A	609	WRA	C14-C13	5.04	1.47	1.38
3	A	609	WRA	C14-C15	5.11	1.47	1.38
4	B	710	NDP	O3B-C3B	5.18	1.54	1.43
3	B	709	WRA	C17-C16	5.23	1.47	1.38
4	A	610	NDP	C4A-N3A	5.58	1.43	1.35
3	A	609	WRA	O7-C8	5.65	1.54	1.45
4	B	710	NDP	C5D-C4D	5.75	1.69	1.51
3	B	709	WRA	C17-C12	5.98	1.49	1.38
4	A	610	NDP	O4B-C1B	8.94	1.53	1.41

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	610	NDP	C4B-O4B-C1B	-5.27	104.16	109.77
4	A	610	NDP	C1D-N1N-C2N	-5.08	112.47	121.09
4	B	710	NDP	N3A-C2A-N1A	-4.18	125.22	128.86
4	B	710	NDP	O3X-P2B-O1X	-4.10	94.44	110.50
4	B	710	NDP	C3N-C2N-N1N	-4.04	117.22	123.08
4	B	710	NDP	C1D-N1N-C2N	-4.03	114.25	121.09
4	A	610	NDP	N3A-C2A-N1A	-3.66	125.67	128.86
4	A	610	NDP	C3N-C2N-N1N	-3.57	117.90	123.08
3	A	609	WRA	N4-C3-N2	-3.55	120.75	126.46
3	B	709	WRA	N4-C3-N2	-3.28	121.18	126.46
4	A	610	NDP	O4B-C4B-C5B	-3.18	98.67	109.40
5	D	711	UMP	C5-C4-N3	-3.10	115.72	123.12
4	A	610	NDP	O5D-C5D-C4D	-3.04	98.23	109.00
4	A	610	NDP	O3X-P2B-O1X	-2.91	99.11	110.50
5	C	611	UMP	C5-C4-N3	-2.88	116.24	123.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	710	NDP	O5B-PA-O1A	-2.84	97.79	109.25
4	B	710	NDP	O7N-C7N-N7N	-2.56	116.71	122.92
4	B	710	NDP	C2D-C1D-N1N	-2.51	106.87	113.32
5	D	711	UMP	O4'-C4'-C3'	-2.48	99.74	105.68
4	A	610	NDP	O5B-C5B-C4B	-2.45	100.32	109.00
4	A	610	NDP	O3B-C3B-C4B	-2.42	104.03	111.09
4	A	610	NDP	O7N-C7N-N7N	-2.33	117.26	122.92
5	D	711	UMP	O4'-C1'-C2'	-2.31	101.81	106.25
4	B	710	NDP	O3D-C3D-C4D	-2.24	104.53	111.09
4	A	610	NDP	O3D-C3D-C4D	-2.24	104.54	111.09
5	C	611	UMP	O4'-C1'-C2'	-2.18	102.07	106.25
4	A	610	NDP	O3X-P2B-O2B	-2.15	96.23	106.00
3	A	609	WRA	CM2-C1-CM1	-2.13	107.75	110.90
5	C	611	UMP	C6-N1-C2	2.04	124.59	121.28
5	C	611	UMP	C2'-C3'-C4'	2.07	107.14	102.73
3	B	709	WRA	NH1-C3-N4	2.18	119.44	116.54
4	B	710	NDP	O4D-C1D-N1N	2.27	112.65	108.07
3	A	609	WRA	NH1-C3-N4	2.30	119.60	116.54
5	D	711	UMP	C2'-C1'-N1	2.35	119.78	114.23
5	D	711	UMP	C2'-C3'-C4'	2.39	107.82	102.73
3	B	709	WRA	C5-N4-C3	2.45	121.02	116.17
5	C	611	UMP	C4'-O4'-C1'	2.47	115.46	109.42
5	C	611	UMP	C2'-C1'-N1	2.47	120.08	114.23
3	B	709	WRA	O11-C12-C13	2.48	119.44	116.38
5	D	711	UMP	P-O5'-C5'	2.48	125.14	118.30
4	A	610	NDP	C2D-C3D-C4D	2.62	107.72	102.62
3	A	609	WRA	O11-C12-C13	2.81	119.84	116.38
5	C	611	UMP	P-O5'-C5'	2.82	126.05	118.30
5	D	711	UMP	C4'-O4'-C1'	2.84	116.37	109.42
3	A	609	WRA	C5-N4-C3	3.12	122.32	116.17
4	B	710	NDP	O2A-PA-O1A	3.22	128.97	112.28
5	D	711	UMP	O4'-C1'-N1	3.24	113.23	107.78
4	B	710	NDP	C2D-C3D-C4D	3.34	109.12	102.62
5	C	611	UMP	O4'-C1'-N1	3.51	113.69	107.78
4	B	710	NDP	C2B-C3B-C4B	3.81	110.62	101.95
4	A	610	NDP	O2X-P2B-O1X	4.08	126.46	110.50
4	B	710	NDP	O2X-P2B-O1X	4.67	128.76	110.50
5	C	611	UMP	C4-N3-C2	13.94	126.11	114.13
5	D	711	UMP	C4-N3-C2	15.85	127.75	114.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	609	WRA	1	0
4	A	610	NDP	4	0
4	B	710	NDP	6	0
5	C	611	UMP	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, 95th 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 ²)	Q<0.9
1	A	221/280 (78%)	0.91	41 (18%) 1 2	23, 41, 87, 95	0
1	B	221/280 (78%)	2.22	95 (42%) 0 0	29, 73, 95, 95	0
2	C	326/328 (99%)	0.17	23 (7%) 17 21	21, 31, 90, 95	0
2	D	326/328 (99%)	0.09	20 (6%) 22 27	19, 32, 86, 95	0
All	All	1094/1216 (89%)	0.71	179 (16%) 2 3	19, 37, 94, 95	0

All (179) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	11.7
1	A	2	MET	10.6
1	B	75	TYR	9.7
1	A	23	LYS	9.4
1	A	26	GLY	9.4
1	B	1	MET	8.9
1	A	24	ASN	8.8
1	B	93	PRO	8.6
1	A	230	ASN	8.5
1	B	27	LYS	8.4
1	A	231	ASN	8.2
1	B	81	LEU	8.1
1	B	14	ILE	7.9
1	B	94	ASN	7.9
2	C	607	ALA	7.9
2	D	301	GLU	7.8
2	C	303	ASN	7.6
1	B	232	LYS	7.6
2	C	300	GLU	7.5
1	B	95	SER	7.5
1	B	96	LYS	7.2

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Mol	Chain	Res	Type	RSRZ
2	D	607	ALA	7.0
1	B	130	THR	6.9
2	C	302	LYS	6.9
1	B	26	GLY	6.8
2	C	301	GLU	6.7
1	B	2	MET	6.7
1	B	116	PHE	6.7
1	B	24	ASN	6.6
2	D	300	GLU	6.5
2	C	608	ALA	6.5
2	D	303	ASN	6.3
1	B	163	ILE	6.0
2	D	283	ASP	6.0
1	B	162	PHE	5.9
1	A	75	TYR	5.9
1	B	28	LYS	5.8
1	A	25	GLU	5.7
1	B	22	SER	5.7
1	B	231	ASN	5.6
1	B	138	GLU	5.6
1	B	70	TYR	5.5
2	C	299	LYS	5.4
1	B	13	ALA	5.4
2	D	608	ALA	5.3
1	B	164	LEU	5.3
2	D	308	HIS	5.3
2	C	284	ASP	5.2
1	B	230	ASN	5.2
2	D	284	ASP	5.1
1	A	28	LYS	5.1
1	B	23	LYS	5.1
1	B	135	ASP	5.0
1	B	136	PHE	5.0
1	B	3	GLU	4.9
1	B	139	ASP	4.9
2	D	302	LYS	4.9
1	A	29	ASN	4.9
1	B	71	GLU	4.8
1	B	131	LEU	4.8
2	C	283	ASP	4.8
2	C	298	GLU	4.8
1	B	44	GLY	4.8

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Mol	Chain	Res	Type	RSRZ
1	B	182	ILE	4.8
1	B	78	CYS	4.8
1	A	85	THR	4.7
1	A	96	LYS	4.5
1	B	144	ASN	4.5
1	B	203	ASN	4.4
2	D	285	GLU	4.4
1	B	15	CYS	4.4
1	B	73	LEU	4.4
2	D	309	PRO	4.4
1	B	25	GLU	4.3
1	A	22	SER	4.1
1	B	128	SER	4.1
2	D	299	LYS	4.1
2	C	304	LYS	4.0
1	B	134	GLU	4.0
1	B	184	PHE	3.9
1	A	163	ILE	3.9
1	A	13	ALA	3.9
1	A	11	ILE	3.9
1	B	103	VAL	3.8
1	A	14	ILE	3.8
1	A	162	PHE	3.8
1	B	183	TYR	3.8
1	B	97	LYS	3.7
1	B	12	TYR	3.7
1	B	80	TYR	3.7
2	C	606	MET	3.6
2	D	298	GLU	3.5
1	B	157	ASN	3.5
1	A	182	ILE	3.5
2	D	287	GLU	3.5
1	A	3	GLU	3.5
1	B	61	VAL	3.5
1	B	204	GLU	3.5
1	B	192	GLU	3.4
1	B	115	LYS	3.3
2	C	286	GLU	3.3
1	A	161	CYS	3.3
1	B	193	CYS	3.3
1	A	102	VAL	3.3
1	B	146	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	66	ASN	3.2
1	B	102	VAL	3.2
1	A	71	GLU	3.2
1	B	129	ARG	3.1
1	B	185	THR	3.1
1	B	29	ASN	3.1
1	B	106	ARG	3.1
2	D	307	ILE	3.1
1	A	82	ASN	3.1
1	B	35	TYR	3.1
1	B	229	THR	3.0
1	A	164	LEU	3.0
1	B	195	VAL	3.0
1	A	12	TYR	3.0
2	C	285	GLU	2.9
1	B	45	VAL	2.9
1	B	132	LYS	2.9
1	B	137	ASP	2.9
2	D	306	SER	2.9
1	B	16	ALA	2.8
1	B	114	LYS	2.8
1	A	103	VAL	2.8
1	B	67	GLU	2.8
1	B	127	LEU	2.8
1	B	72	LYS	2.7
2	D	305	ASN	2.7
2	C	310	ASN	2.7
1	B	168	VAL	2.6
1	A	15	CYS	2.6
2	C	309	PRO	2.6
1	B	202	GLU	2.6
1	B	149	LEU	2.6
1	B	49	LYS	2.6
1	B	224	ILE	2.6
1	B	151	VAL	2.6
1	B	147	GLU	2.6
1	B	175	GLU	2.5
1	A	27	LYS	2.5
1	A	68	SER	2.5
2	D	525	TYR	2.5
1	B	179	ILE	2.5
1	A	184	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	203	ASN	2.5
1	B	43	LYS	2.5
1	B	69	LYS	2.5
2	C	287	GLU	2.5
1	A	83	LYS	2.5
1	A	97	LYS	2.5
1	A	183	TYR	2.4
2	C	307	ILE	2.4
1	B	46	LEU	2.4
1	A	84	GLU	2.4
1	B	110	GLU	2.3
1	A	61	VAL	2.3
1	B	141	TYR	2.3
1	B	76	LYS	2.3
2	C	308	HIS	2.3
1	B	170	TYR	2.2
1	A	58	PHE	2.2
1	B	161	CYS	2.2
1	B	101	VAL	2.2
1	B	201	ASN	2.2
1	B	77	ARG	2.2
2	C	297	LYS	2.1
1	A	224	ILE	2.1
2	C	605	ASP	2.1
2	D	286	GLU	2.1
1	B	42	ASN	2.1
1	B	62	THR	2.1
2	D	297	LYS	2.1
2	C	494	CYS	2.1
1	B	119	LEU	2.0
1	A	179	ILE	2.0
2	C	493	LEU	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, 95th 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 ²)	Q<0.9
3	WRA	A	609	24/24	0.55	0.27	1.69	29,41,47,49	0
3	WRA	B	709	24/24	0.40	0.32	0.70	57,64,65,67	0
4	NDP	B	710	48/48	0.75	0.27	0.04	76,85,95,95	0
4	NDP	A	610	48/48	0.95	0.10	-0.70	32,40,49,50	0
5	UMP	C	611	20/20	0.98	0.08	-0.95	23,27,32,32	0
5	UMP	D	711	20/20	0.98	0.08	-1.26	27,31,36,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.