



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 08:14 pm GMT

PDB ID : 1J3J
Title : Double mutant (C59R+S108N) Plasmodium falciparum dihydrofolate reductase-thymidylate synthase (PfDHFR-TS) complexed with pyrimethamine, 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 : 2.30 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

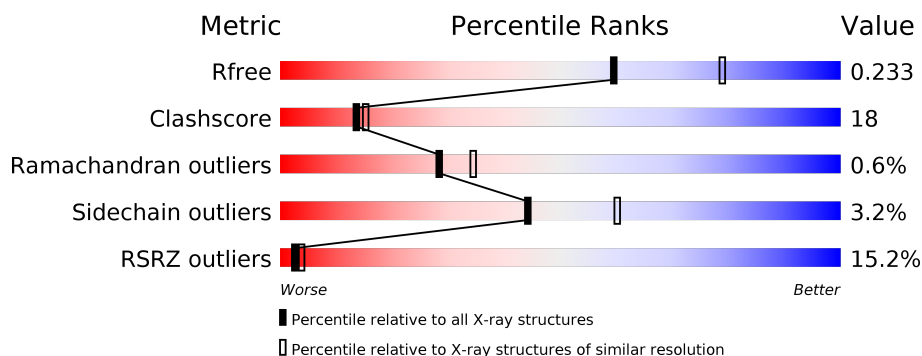
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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>10%</div> <div> <div>57%</div> <div>19%</div> <div>••</div> <div>21%</div> </div> </div>
1	B	280	<div> <div>33%</div> <div> <div>41%</div> <div>31%</div> <div>5%</div> <div>23%</div> </div> </div>
2	C	328	<div> <div>8%</div> <div> <div>73%</div> <div>24%</div> <div>••</div> </div> </div>
2	D	328	<div> <div>7%</div> <div> <div>81%</div> <div>17%</div> <div>•••</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	UMP	C	611	-	-	-	X
5	UMP	D	711	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9961 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	1188	298	339	12			
1	B	216	Total	C	N	O	S	0	0	0
			1795	1163	290	330	12			

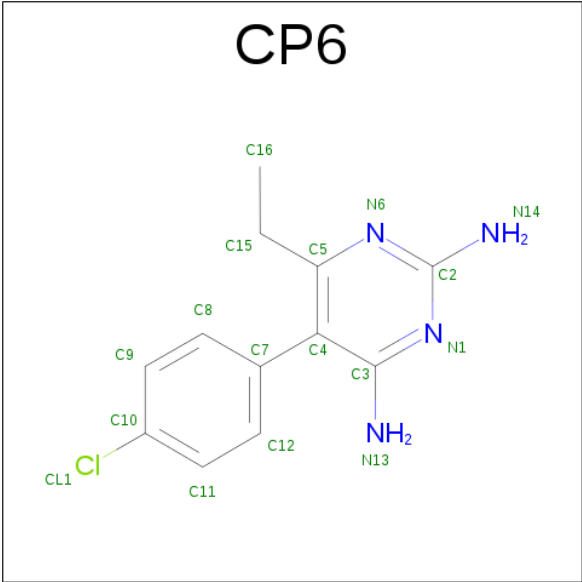
There are 4 discrepancies between the modelled and reference sequences:

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

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

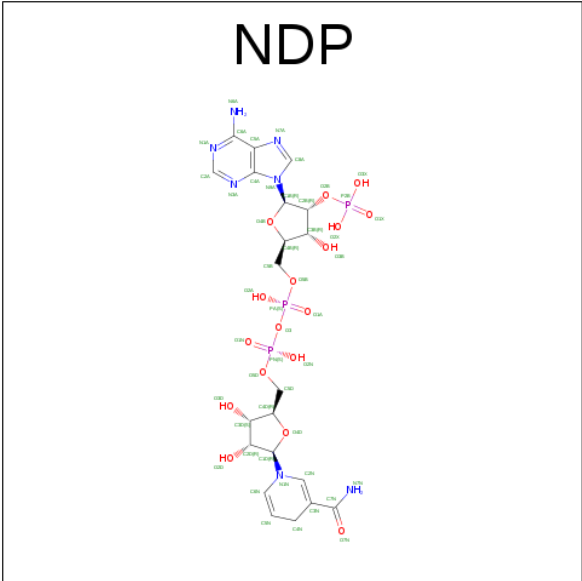
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	326	Total	C	N	O	S	0	0	0
			2713	1747	456	495	15			
2	D	326	Total	C	N	O	S	0	0	0
			2713	1747	456	495	15			

- Molecule 3 is 5-(4-CHLORO-PHENYL)-6-ETHYL-PYRIMIDINE-2,4-DIAMINE (three-letter code: CP6) (formula: C₁₂H₁₃ClN₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	0	0
			17	12	1	4		
3	B	1	Total	C	Cl	N	0	0
			17	12	1	4		

- Molecule 4 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



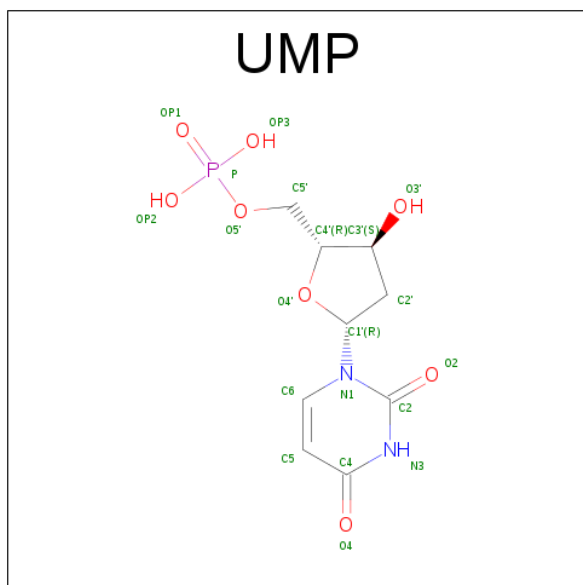
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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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		

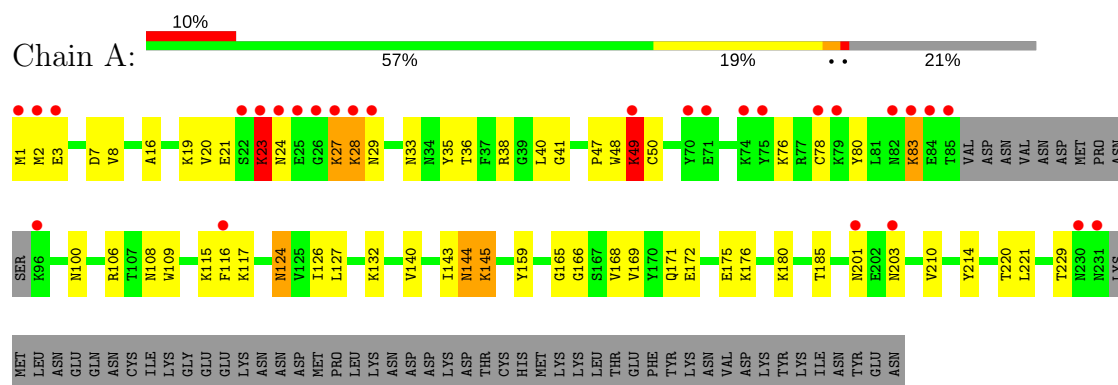
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	125	Total	O	0	0
			125	125		
6	B	60	Total	O	0	0
			60	60		
6	C	265	Total	O	0	0
			265	265		
6	D	283	Total	O	0	0
			283	283		

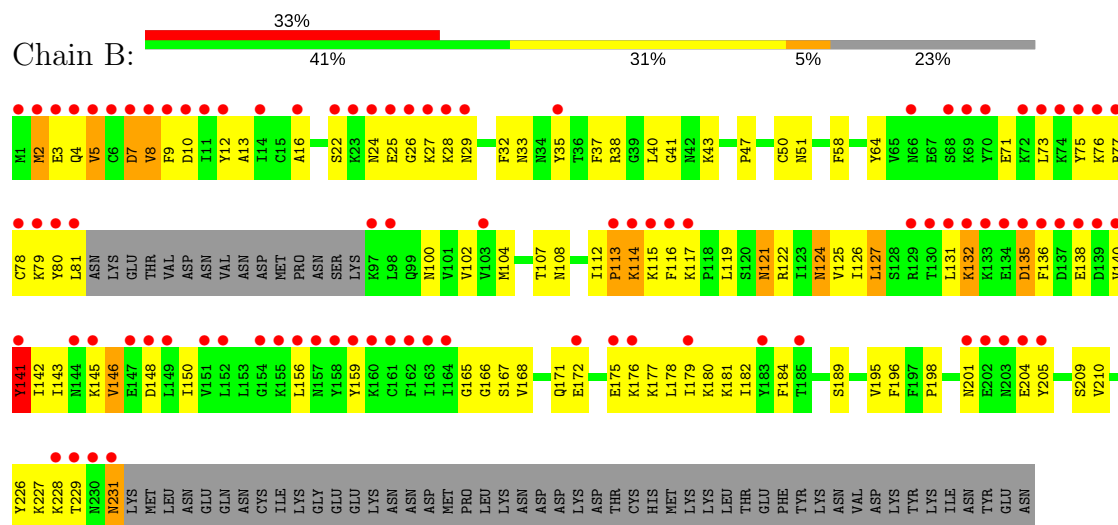
3 Residue-property plots [i](#)

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

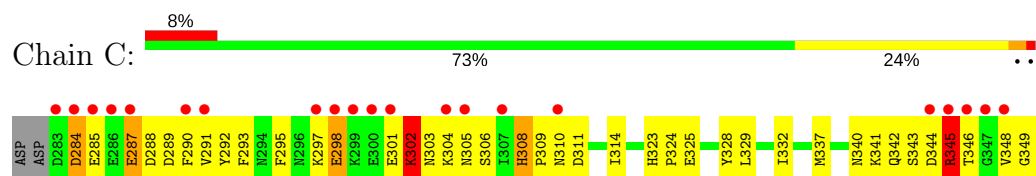
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

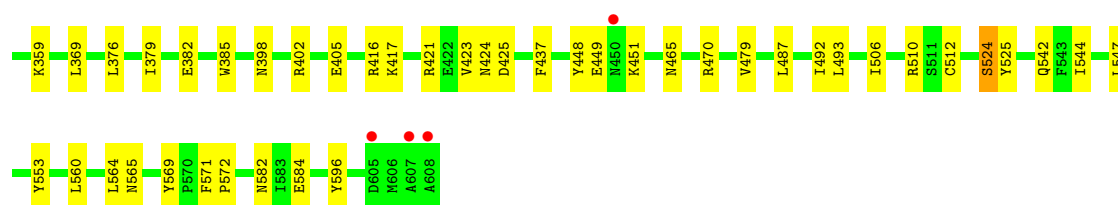


- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

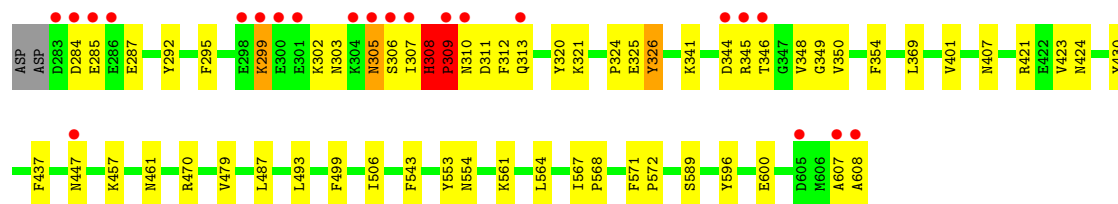
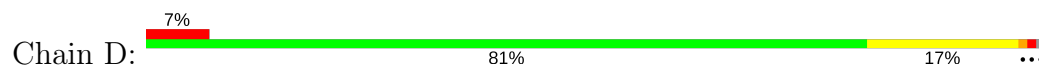


- Molecule 2: Bifunctional dihydrofolate reductase-thymidylate synthase





• 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	56.34Å 155.00Å 164.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.83 – 2.30 23.83 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.3 (23.83-2.30) 94.4 (23.83-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.31Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.198 , 0.231 0.198 , 0.233	Depositor DCC
R_{free} test set	3087 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	28.5	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9961	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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, CP6

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	0.57	0/1871	0.82	2/2515 (0.1%)
1	B	0.59	1/1829 (0.1%)	0.86	3/2460 (0.1%)
2	C	0.59	1/2784 (0.0%)	0.86	6/3766 (0.2%)
2	D	0.57	0/2784	0.84	4/3766 (0.1%)
All	All	0.58	2/9268 (0.0%)	0.85	15/12507 (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
2	C	0	1
2	D	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	8	VAL	CB-CG2	-5.82	1.40	1.52
2	C	310	ASN	CB-CG	5.52	1.63	1.51

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	2	MET	N-CA-C	9.10	135.56	111.00
2	C	298	GLU	N-CA-C	-8.74	87.40	111.00
1	A	23	LYS	N-CA-C	-7.23	91.49	111.00
2	C	298	GLU	N-CA-CB	-7.04	97.92	110.60
2	C	345	ARG	N-CA-C	-6.72	92.85	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	135	ASP	N-CA-C	5.95	127.06	111.00
2	D	308	HIS	N-CA-C	5.94	127.04	111.00
2	D	543	PHE	N-CA-C	-5.85	95.22	111.00
1	B	141	TYR	N-CA-C	5.75	126.52	111.00
2	D	401	VAL	N-CA-C	-5.48	96.20	111.00
2	C	351	LEU	N-CA-C	-5.39	96.44	111.00
2	D	309	PRO	N-CA-C	5.31	125.91	112.10
2	C	302	LYS	N-CA-C	5.20	125.03	111.00
1	A	229	THR	N-CA-C	5.19	125.00	111.00
2	C	425	ASP	N-CA-C	-5.10	97.23	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	525	TYR	Sidechain
2	D	326	TYR	Sidechain

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	1868	61	0
1	B	1795	0	1823	133	0
2	C	2713	0	2638	80	0
2	D	2713	0	2638	64	0
3	A	17	0	13	0	0
3	B	17	0	13	2	0
4	A	48	0	26	14	0
4	B	48	0	26	12	0
5	C	20	0	11	0	0
5	D	20	0	11	0	0
6	A	125	0	0	5	0
6	B	60	0	0	37	0
6	C	265	0	0	13	0
6	D	283	0	0	23	0
All	All	9961	0	9067	327	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 18.

All (327) 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:78:CYS:HA	6:B:1635:HOH:O	1.40	1.20
1:B:178:LEU:HG	6:B:1639:HOH:O	1.43	1.19
2:C:346:THR:HA	6:C:1377:HOH:O	1.48	1.12
1:A:165:GLY:HA3	4:A:610:NDP:H5N	1.31	1.11
2:D:309:PRO:HA	6:D:1684:HOH:O	1.49	1.09
1:A:140:VAL:HB	6:A:1679:HOH:O	1.55	1.06
1:B:131:LEU:HB3	6:B:1628:HOH:O	1.56	1.05
1:B:4:GLN:O	1:B:8:VAL:HG23	1.57	1.03
1:B:114:LYS:H	1:B:114:LYS:HD2	1.24	0.98
1:B:179:ILE:HG23	6:B:1640:HOH:O	1.68	0.94
1:B:140:VAL:HG12	1:B:140:VAL:O	1.67	0.93
1:B:4:GLN:HG3	1:B:7:ASP:OD2	1.69	0.93
1:B:210:VAL:HB	6:B:1645:HOH:O	1.69	0.91
1:B:24:ASN:HB3	6:B:1001:HOH:O	1.69	0.91
1:A:3:GLU:OE1	1:A:80:TYR:HD1	1.51	0.91
2:C:344:ASP:HB2	2:D:470:ARG:NH1	1.87	0.88
1:B:12:TYR:HA	6:B:1640:HOH:O	1.73	0.88
2:C:344:ASP:HB2	2:D:470:ARG:HH12	1.39	0.88
1:B:136:PHE:CE2	6:B:1628:HOH:O	2.28	0.86
1:B:138:GLU:O	1:B:141:TYR:CE1	2.30	0.84
2:C:345:ARG:HE	2:C:348:VAL:HG21	1.41	0.83
1:B:136:PHE:HE2	6:B:1628:HOH:O	1.60	0.83
1:B:176:LYS:C	6:B:1639:HOH:O	2.17	0.82
1:B:2:MET:HE2	1:B:2:MET:HA	1.62	0.82
2:C:332:ILE:HD13	2:C:560:LEU:HD22	1.60	0.82
2:D:348:VAL:HA	6:D:1314:HOH:O	1.79	0.81
1:B:2:MET:HA	1:B:2:MET:CE	2.10	0.81
1:B:165:GLY:HA3	4:B:710:NDP:H5N	1.61	0.81
2:C:376:LEU:HD22	2:C:379:ILE:HD11	1.63	0.80
1:B:81:LEU:HD12	6:B:1635:HOH:O	1.80	0.80
1:A:78:CYS:HB3	1:A:83:LYS:O	1.84	0.78
4:B:710:NDP:H52N	6:B:1627:HOH:O	1.82	0.77
2:C:303:ASN:HB3	2:C:306:SER:OG	1.85	0.76
1:B:124:ASN:H	1:B:124:ASN:HD22	1.30	0.76
1:B:124:ASN:N	1:B:124:ASN:HD22	1.84	0.75
1:B:29:ASN:HB2	1:B:32:PHE:CE1	2.22	0.75
1:B:177:LYS:HD3	6:B:1638:HOH:O	1.87	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:610:NDP:H8A	4:A:610:NDP:H52A	1.71	0.73
1:A:126:ILE:HG13	6:A:1679:HOH:O	1.90	0.72
1:B:41:GLY:HA2	1:B:47:PRO:HD3	1.73	0.71
1:B:182:ILE:HB	1:B:226:TYR:HB2	1.72	0.71
1:B:107:THR:HB	4:B:710:NDP:O2A	1.91	0.71
1:B:9:PHE:HE2	1:B:80:TYR:HE2	1.38	0.71
1:B:8:VAL:HG22	6:B:1636:HOH:O	1.90	0.70
1:B:81:LEU:CD1	6:B:1635:HOH:O	2.38	0.70
2:C:285:GLU:C	2:C:287:GLU:H	1.94	0.69
1:B:112:ILE:HB	1:B:117:LYS:HD3	1.74	0.69
2:D:457:LYS:HE2	6:D:1229:HOH:O	1.93	0.69
1:A:171:GLN:HG3	1:A:175:GLU:OE2	1.93	0.68
1:B:3:GLU:HG2	1:B:80:TYR:HE1	1.59	0.68
2:C:284:ASP:O	2:C:287:GLU:HB3	1.93	0.68
1:B:4:GLN:C	1:B:8:VAL:HG23	2.14	0.68
1:A:210:VAL:HG12	6:A:1665:HOH:O	1.93	0.68
2:D:447:ASN:HA	6:D:1220:HOH:O	1.94	0.68
2:D:308:HIS:O	2:D:311:ASP:HB2	1.94	0.68
1:B:171:GLN:HG3	1:B:175:GLU:OE2	1.95	0.67
1:B:40:LEU:O	4:B:710:NDP:H2N	1.94	0.67
1:B:71:GLU:O	1:B:75:TYR:HB2	1.95	0.67
1:A:48:TRP:O	1:A:49:LYS:HB2	1.95	0.67
1:B:171:GLN:O	1:B:175:GLU:HG3	1.95	0.67
1:A:24:ASN:HB2	1:A:28:LYS:HE2	1.77	0.66
2:C:376:LEU:HD22	2:C:379:ILE:CD1	2.26	0.66
2:C:309:PRO:C	2:C:311:ASP:N	2.49	0.65
4:B:710:NDP:H6N	6:B:1627:HOH:O	1.95	0.65
1:B:140:VAL:CG1	1:B:140:VAL:O	2.42	0.65
2:C:344:ASP:OD1	2:C:345:ARG:N	2.31	0.64
1:B:114:LYS:H	1:B:114:LYS:CD	1.99	0.64
2:C:309:PRO:C	2:C:311:ASP:H	2.00	0.64
1:B:13:ALA:N	6:B:1640:HOH:O	2.31	0.63
1:A:106:ARG:HE	4:A:610:NDP:P2B	2.22	0.63
2:C:344:ASP:O	6:C:1185:HOH:O	2.15	0.63
1:B:176:LYS:O	6:B:1639:HOH:O	2.15	0.62
2:D:421:ARG:NE	6:D:1206:HOH:O	2.20	0.62
1:B:121:ASN:N	1:B:121:ASN:HD22	1.97	0.62
1:B:76:LYS:HA	1:B:79:LYS:HB3	1.81	0.62
2:C:285:GLU:C	2:C:287:GLU:N	2.51	0.62
2:C:341:LYS:HE3	6:C:1362:HOH:O	2.00	0.62
1:A:127:LEU:HD23	1:A:143:ILE:HG13	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:MET:HB2	1:B:108:ASN:HD22	1.65	0.61
1:A:41:GLY:HA2	1:A:47:PRO:HD3	1.81	0.61
1:B:127:LEU:HD12	1:B:143:ILE:HD11	1.81	0.61
1:B:9:PHE:CE2	1:B:80:TYR:HE2	2.18	0.61
2:D:310:ASN:O	2:D:313:GLN:HB2	2.00	0.61
1:A:27:LYS:O	1:A:27:LYS:HD2	2.01	0.60
2:C:344:ASP:CG	2:C:345:ARG:HG2	2.22	0.60
1:A:108:ASN:OD1	4:A:610:NDP:H2D	2.01	0.60
1:B:8:VAL:CG2	6:B:1636:HOH:O	2.47	0.60
2:C:287:GLU:O	2:C:290:PHE:HB3	2.02	0.60
2:D:421:ARG:NH2	6:D:1206:HOH:O	2.22	0.60
1:B:229:THR:C	1:B:231:ASN:N	2.52	0.60
1:B:29:ASN:HD22	1:B:32:PHE:HE1	1.49	0.59
2:C:542:GLN:NE2	6:C:1046:HOH:O	2.30	0.59
2:C:493:LEU:C	2:C:493:LEU:HD12	2.22	0.59
1:A:2:MET:HG3	1:A:2:MET:O	2.03	0.59
1:A:210:VAL:CG1	6:A:1665:HOH:O	2.49	0.59
1:B:166:GLY:HA2	4:B:710:NDP:C5N	2.33	0.59
1:B:9:PHE:HE2	1:B:80:TYR:CE2	2.19	0.59
1:B:171:GLN:HE21	1:B:175:GLU:CG	2.16	0.58
2:C:301:GLU:O	2:C:304:LYS:HG3	2.02	0.58
2:D:457:LYS:HG2	6:D:1229:HOH:O	2.03	0.58
1:B:25:GLU:HA	1:B:25:GLU:OE1	2.03	0.58
1:B:9:PHE:HZ	1:B:81:LEU:HD23	1.69	0.58
2:C:344:ASP:OD2	2:C:345:ARG:HG2	2.04	0.58
2:D:303:ASN:HB3	2:D:306:SER:OG	2.04	0.58
1:B:121:ASN:N	1:B:121:ASN:ND2	2.52	0.58
1:A:40:LEU:O	4:A:610:NDP:H2N	2.02	0.58
1:B:5:VAL:HA	1:B:8:VAL:HB	1.86	0.58
1:A:109:TRP:CE2	1:A:117:LYS:HD2	2.39	0.58
1:B:3:GLU:N	6:B:1636:HOH:O	2.37	0.57
2:C:301:GLU:OE1	2:C:337:MET:CE	2.52	0.57
2:D:346:THR:CG2	2:D:348:VAL:HG23	2.34	0.57
1:A:109:TRP:CZ2	1:A:117:LYS:HD2	2.39	0.57
1:B:210:VAL:O	1:B:210:VAL:HG23	2.05	0.57
2:C:301:GLU:OE1	2:C:337:MET:HE3	2.05	0.57
2:C:465:ASN:O	2:D:345:ARG:NH2	2.38	0.57
1:B:229:THR:C	1:B:231:ASN:H	2.08	0.56
1:B:2:MET:CA	1:B:2:MET:CE	2.80	0.56
2:C:284:ASP:N	2:C:284:ASP:OD1	2.38	0.56
1:A:3:GLU:OE1	1:A:80:TYR:CD1	2.44	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:LEU:HD22	6:B:1628:HOH:O	2.04	0.56
2:C:344:ASP:OD2	2:C:553:TYR:HE1	1.88	0.55
2:D:421:ARG:CZ	6:D:1206:HOH:O	2.53	0.55
2:D:493:LEU:C	2:D:493:LEU:HD12	2.27	0.55
1:A:124:ASN:N	1:A:124:ASN:HD22	2.05	0.55
1:B:168:VAL:HG11	4:B:710:NDP:H8A	1.88	0.55
2:C:301:GLU:CG	2:C:304:LYS:HE2	2.37	0.55
1:A:172:GLU:OE2	4:A:610:NDP:N7A	2.40	0.54
1:B:9:PHE:CE2	1:B:80:TYR:CE2	2.95	0.54
2:C:340:ASN:HB3	2:D:499:PHE:CE1	2.42	0.54
1:A:24:ASN:HB2	1:A:28:LYS:CE	2.38	0.54
1:A:169:VAL:HG23	4:A:610:NDP:O1A	2.08	0.54
1:A:27:LYS:C	1:A:29:ASN:H	2.11	0.54
2:C:344:ASP:CB	2:D:470:ARG:HH12	2.18	0.54
1:B:142:ILE:HG22	1:B:143:ILE:N	2.23	0.54
1:B:9:PHE:CZ	1:B:81:LEU:HD23	2.42	0.54
2:C:350:VAL:HG12	2:C:553:TYR:CD1	2.43	0.54
1:B:12:TYR:CD1	1:B:181:LYS:HB2	2.43	0.53
1:B:167:SER:HB3	4:B:710:NDP:O2N	2.08	0.53
1:A:166:GLY:HA2	4:A:610:NDP:C5N	2.39	0.53
1:B:5:VAL:HG11	1:B:150:ILE:HD12	1.91	0.53
2:D:309:PRO:N	6:D:1683:HOH:O	2.41	0.53
1:B:12:TYR:CE1	1:B:180:LYS:HD3	2.44	0.53
1:B:131:LEU:HD13	6:B:1628:HOH:O	2.07	0.53
1:B:12:TYR:CA	6:B:1640:HOH:O	2.45	0.53
1:A:127:LEU:O	4:A:610:NDP:H1B	2.09	0.53
2:C:288:ASP:HA	2:C:291:VAL:HG23	1.91	0.53
2:C:402:ARG:HG2	2:C:402:ARG:HH11	1.73	0.53
2:D:344:ASP:HA	6:D:1328:HOH:O	2.07	0.53
2:D:572:PRO:HB3	2:D:596:TYR:HA	1.90	0.53
1:B:119:LEU:HB3	1:B:122:ARG:CZ	2.39	0.53
1:B:3:GLU:HG2	1:B:80:TYR:CE1	2.42	0.53
2:C:448:TYR:O	2:C:451:LYS:HB2	2.09	0.52
2:D:607:ALA:O	2:D:608:ALA:CB	2.56	0.52
1:B:124:ASN:N	1:B:124:ASN:ND2	2.51	0.52
1:B:9:PHE:HZ	1:B:81:LEU:CD2	2.23	0.52
1:A:8:VAL:HA	1:A:76:LYS:HD3	1.90	0.52
2:C:572:PRO:HB3	2:C:596:TYR:HA	1.91	0.52
1:B:76:LYS:O	1:B:80:TYR:N	2.43	0.52
1:B:113:PRO:O	1:B:117:LYS:HG3	2.09	0.52
1:A:20:VAL:HG12	1:A:21:GLU:N	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:710:NDP:H2D	6:B:1627:HOH:O	2.10	0.51
1:B:132:LYS:HE2	1:B:135:ASP:OD2	2.10	0.51
2:C:421:ARG:NH2	6:C:1119:HOH:O	2.40	0.51
1:B:115:LYS:C	6:B:1631:HOH:O	2.49	0.51
1:B:131:LEU:CB	6:B:1628:HOH:O	2.32	0.51
2:C:421:ARG:NE	6:C:1119:HOH:O	2.25	0.51
2:D:346:THR:HB	2:D:348:VAL:HG23	1.93	0.51
1:A:166:GLY:HA2	4:A:610:NDP:C6N	2.41	0.51
2:C:343:SER:CB	6:C:1378:HOH:O	2.58	0.51
2:C:398:ASN:ND2	6:C:1517:HOH:O	2.22	0.50
2:D:344:ASP:C	2:D:346:THR:H	2.13	0.50
1:B:29:ASN:HB2	1:B:32:PHE:CZ	2.46	0.50
1:A:100:ASN:OD1	1:A:159:TYR:HB3	2.12	0.50
2:C:301:GLU:HG3	2:C:304:LYS:HE2	1.92	0.50
2:C:584:GLU:HB2	6:C:1061:HOH:O	2.10	0.50
1:B:166:GLY:HA2	4:B:710:NDP:H5N	1.94	0.50
2:C:353:LYS:NZ	6:C:1358:HOH:O	2.45	0.50
1:A:168:VAL:HB	4:A:610:NDP:H51A	1.94	0.49
2:C:329:LEU:HD22	2:C:564:LEU:HD12	1.94	0.49
1:B:29:ASN:ND2	1:B:32:PHE:CE1	2.78	0.49
2:C:290:PHE:HB2	2:D:320:TYR:OH	2.12	0.49
2:C:342:GLN:O	2:C:349:GLY:HA2	2.11	0.49
1:B:145:LYS:O	1:B:148:ASP:HB2	2.12	0.49
1:B:171:GLN:HE21	1:B:175:GLU:HG3	1.77	0.49
2:D:461:ASN:ND2	6:D:1229:HOH:O	2.44	0.49
2:D:321:LYS:HB3	2:D:326:TYR:CD2	2.48	0.49
2:D:312:PHE:HE1	2:D:561:LYS:HA	1.77	0.49
2:C:292:TYR:O	2:C:295:PHE:HB3	2.13	0.49
2:C:512:CYS:SG	2:C:547:LEU:HD22	2.53	0.49
2:C:382:GLU:O	2:C:385:TRP:HB3	2.12	0.49
1:B:35:TYR:CZ	1:B:38:ARG:HD3	2.48	0.48
1:B:125:VAL:HG12	1:B:126:ILE:N	2.28	0.48
2:C:302:LYS:HB2	6:C:1359:HOH:O	2.13	0.48
1:A:35:TYR:CZ	1:A:38:ARG:HD3	2.48	0.48
1:B:4:GLN:N	6:B:1636:HOH:O	2.24	0.48
2:C:359:LYS:HG2	2:C:544:ILE:HG12	1.95	0.48
1:A:24:ASN:CB	1:A:28:LYS:NZ	2.76	0.48
1:B:210:VAL:HG21	2:D:326:TYR:HE2	1.76	0.48
2:C:305:ASN:O	2:C:308:HIS:NE2	2.47	0.48
2:C:402:ARG:HD3	2:C:405:GLU:OE1	2.14	0.48
1:B:131:LEU:CG	6:B:1628:HOH:O	2.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:309:PRO:C	2:D:311:ASP:N	2.62	0.48
1:B:41:GLY:H	1:B:195:VAL:HG23	1.79	0.48
1:B:4:GLN:C	1:B:8:VAL:CG2	2.82	0.48
2:C:344:ASP:OD2	2:C:553:TYR:CE1	2.67	0.48
2:C:416:ARG:O	2:C:417:LYS:HB2	2.13	0.47
2:D:302:LYS:O	2:D:305:ASN:ND2	2.46	0.47
1:B:75:TYR:O	1:B:79:LYS:HB2	2.15	0.47
1:A:20:VAL:CG1	1:A:21:GLU:N	2.77	0.47
1:B:176:LYS:CB	6:B:1639:HOH:O	2.63	0.47
1:B:205:TYR:HA	1:B:227:LYS:O	2.14	0.47
1:B:166:GLY:N	4:B:710:NDP:O1A	2.41	0.47
1:B:77:ARG:O	1:B:81:LEU:HG	2.15	0.47
2:C:324:PRO:HB2	2:C:571:PHE:HE2	1.79	0.47
1:A:214:TYR:O	1:A:220:THR:HA	2.15	0.47
1:B:168:VAL:O	1:B:172:GLU:HG2	2.15	0.47
1:B:29:ASN:ND2	1:B:32:PHE:HE1	2.12	0.47
1:A:115:LYS:HE3	1:A:116:PHE:CE2	2.49	0.47
2:D:303:ASN:O	2:D:307:ILE:HG12	2.15	0.47
2:C:524:SER:OG	6:C:1523:HOH:O	2.20	0.47
1:A:3:GLU:HG3	1:A:3:GLU:H	1.42	0.46
1:A:24:ASN:HB2	1:A:28:LYS:NZ	2.31	0.46
1:B:10:ASP:OD2	1:B:73:LEU:HD22	2.15	0.46
1:B:26:GLY:C	1:B:27:LYS:HG2	2.36	0.46
1:B:138:GLU:C	1:B:140:VAL:H	2.19	0.46
2:C:354:PHE:CE2	2:D:506:ILE:HG13	2.51	0.46
2:D:423:VAL:O	2:D:424:ASN:HB2	2.15	0.46
1:A:201:ASN:OD1	1:A:203:ASN:HB2	2.16	0.46
2:C:582:ASN:HB3	6:C:1061:HOH:O	2.15	0.46
2:D:307:ILE:HG22	2:D:312:PHE:CE2	2.51	0.46
2:D:600:GLU:HG3	6:D:1691:HOH:O	2.16	0.46
1:A:109:TRP:CE3	1:A:126:ILE:HD11	2.51	0.45
1:B:177:LYS:CD	6:B:1638:HOH:O	2.55	0.45
1:B:58:PHE:CZ	3:B:709:CP6:H12	2.51	0.45
2:C:328:TYR:CZ	2:C:332:ILE:HD11	2.52	0.45
1:B:100:ASN:OD1	1:B:159:TYR:HB3	2.16	0.45
2:D:309:PRO:O	2:D:310:ASN:C	2.48	0.45
1:B:80:TYR:O	1:B:81:LEU:C	2.55	0.45
1:B:41:GLY:N	1:B:195:VAL:HG23	2.32	0.45
2:D:344:ASP:CA	6:D:1328:HOH:O	2.64	0.45
1:A:221:LEU:N	1:A:221:LEU:HD23	2.32	0.45
1:A:166:GLY:HA2	4:A:610:NDP:H5N	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:LYS:HG2	1:A:23:LYS:H	1.49	0.45
2:C:437:PHE:CD1	2:D:479:VAL:HB	2.51	0.45
2:D:607:ALA:O	2:D:608:ALA:HB3	2.16	0.45
1:A:35:TYR:CE2	1:A:38:ARG:HD3	2.51	0.45
2:D:292:TYR:O	2:D:295:PHE:HB3	2.16	0.45
2:C:297:LYS:HA	2:C:297:LYS:HD3	1.61	0.44
1:B:201:ASN:HB3	1:B:204:GLU:HG3	1.98	0.44
1:B:51:ASN:HB2	6:B:1008:HOH:O	2.17	0.44
2:C:305:ASN:O	2:C:308:HIS:CE1	2.71	0.44
2:D:344:ASP:N	6:D:1328:HOH:O	2.49	0.44
2:D:344:ASP:OD1	6:D:1328:HOH:O	2.21	0.44
1:A:132:LYS:HB3	6:A:1481:HOH:O	2.18	0.44
1:B:122:ARG:O	1:B:124:ASN:ND2	2.51	0.44
1:B:22:SER:HB3	6:B:1001:HOH:O	2.18	0.44
2:D:407:ASN:ND2	6:D:1569:HOH:O	2.49	0.44
1:B:64:TYR:HB3	6:B:1642:HOH:O	2.17	0.44
2:D:324:PRO:HB2	2:D:571:PHE:HE2	1.82	0.44
2:D:346:THR:HG22	2:D:348:VAL:HG23	1.99	0.44
1:A:27:LYS:O	1:A:29:ASN:N	2.44	0.44
2:C:470:ARG:HD3	6:D:1329:HOH:O	2.17	0.44
2:D:308:HIS:O	2:D:311:ASP:CB	2.65	0.44
1:B:43:LYS:N	6:B:1626:HOH:O	2.49	0.44
1:B:9:PHE:CZ	1:B:81:LEU:CD2	3.00	0.44
2:C:314:ILE:HD12	2:C:565:ASN:HB3	1.98	0.44
1:A:7:ASP:OD1	1:A:180:LYS:HE3	2.18	0.43
1:B:227:LYS:HG2	1:B:228:LYS:N	2.33	0.43
2:D:312:PHE:CE1	2:D:561:LYS:HG2	2.53	0.43
2:D:349:GLY:HA3	2:D:554:ASN:ND2	2.34	0.43
1:A:108:ASN:OD1	4:A:610:NDP:H6N	2.18	0.43
1:B:138:GLU:C	1:B:140:VAL:N	2.71	0.43
2:D:350:VAL:HG12	2:D:553:TYR:CD1	2.53	0.43
1:B:41:GLY:HA3	4:B:710:NDP:H1D	2.00	0.43
2:D:447:ASN:CG	6:D:1220:HOH:O	2.57	0.43
1:A:109:TRP:CD2	1:A:126:ILE:HD11	2.54	0.43
1:B:196:PHE:HB2	6:B:1620:HOH:O	2.18	0.43
2:C:344:ASP:CG	2:C:345:ARG:N	2.72	0.43
2:C:423:VAL:O	2:C:424:ASN:HB2	2.19	0.43
1:B:114:LYS:N	1:B:114:LYS:HD2	2.08	0.42
1:B:28:LYS:HA	6:B:1703:HOH:O	2.19	0.42
2:C:325:GLU:HG3	2:C:369:LEU:HD22	2.00	0.42
2:C:449:GLU:O	2:C:449:GLU:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:ASN:ND2	1:A:145:LYS:HG2	2.34	0.42
1:A:23:LYS:HE2	1:A:23:LYS:HB3	1.53	0.42
1:A:210:VAL:HG12	2:C:323:HIS:HB2	2.00	0.42
1:A:40:LEU:HD22	4:A:610:NDP:C3N	2.50	0.42
1:B:102:VAL:HG23	1:B:102:VAL:O	2.20	0.42
2:C:506:ILE:HG13	2:D:354:PHE:CE2	2.54	0.42
2:D:341:LYS:HE2	6:D:1316:HOH:O	2.18	0.42
2:D:457:LYS:NZ	6:D:1228:HOH:O	2.53	0.42
1:B:178:LEU:CD2	6:B:1639:HOH:O	2.60	0.42
2:C:289:ASP:HA	2:C:292:TYR:CD2	2.54	0.42
1:A:172:GLU:O	1:A:176:LYS:HG3	2.19	0.42
2:D:421:ARG:HH11	2:D:421:ARG:HG2	1.84	0.42
2:D:567:ILE:HA	2:D:568:PRO:HD3	1.90	0.42
1:B:209:SER:HB3	2:C:293:PHE:CE2	2.55	0.42
2:C:297:LYS:HB3	2:C:298:GLU:O	2.20	0.42
1:B:171:GLN:OE1	1:B:198:PRO:HB3	2.19	0.42
1:B:209:SER:HB3	2:C:293:PHE:HE2	1.85	0.42
1:A:19:LYS:HG2	1:A:36:THR:HG22	2.00	0.42
2:D:341:LYS:HG3	6:D:1316:HOH:O	2.19	0.42
1:B:8:VAL:HG11	1:B:80:TYR:CD2	2.55	0.41
2:D:589:SER:HB3	6:D:1270:HOH:O	2.20	0.41
1:B:16:ALA:HB2	3:B:709:CP6:N14	2.34	0.41
2:C:479:VAL:HB	2:D:437:PHE:CD1	2.54	0.41
1:A:16:ALA:HA	1:A:185:THR:HB	2.01	0.41
2:C:421:ARG:HG2	2:C:421:ARG:HH11	1.85	0.41
2:D:312:PHE:HB2	6:D:1684:HOH:O	2.21	0.41
1:A:171:GLN:HA	1:A:171:GLN:OE1	2.21	0.41
1:A:23:LYS:O	1:A:24:ASN:C	2.58	0.41
1:B:141:TYR:CE2	1:B:156:LEU:HD11	2.55	0.41
1:B:126:ILE:O	1:B:143:ILE:HG12	2.21	0.41
1:B:37:PHE:O	1:B:184:PHE:HZ	2.04	0.41
1:B:33:ASN:OD1	1:B:35:TYR:N	2.53	0.41
1:A:33:ASN:HA	2:C:569:TYR:OH	2.21	0.41
2:C:301:GLU:OE1	2:C:337:MET:HE2	2.21	0.41
2:C:343:SER:HA	2:C:349:GLY:HA2	2.03	0.40
1:A:27:LYS:C	1:A:29:ASN:N	2.73	0.40
1:B:145:LYS:HG2	1:B:146:VAL:N	2.35	0.40
2:D:325:GLU:HG3	2:D:369:LEU:HD22	2.03	0.40
1:B:113:PRO:HB2	1:B:116:PHE:CD2	2.56	0.40
2:D:346:THR:CB	2:D:348:VAL:HG23	2.51	0.40
2:D:284:ASP:O	2:D:287:GLU:HB3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:PRO:HB2	1:B:116:PHE:HD2	1.87	0.40
2:C:492:ILE:HD11	2:C:510:ARG:HD3	2.03	0.40
2:D:299:LYS:HD3	2:D:299:LYS:HA	1.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	217/280 (78%)	208 (96%)	8 (4%)	1 (0%)	32	39
1	B	212/280 (76%)	193 (91%)	16 (8%)	3 (1%)	13	13
2	C	324/328 (99%)	303 (94%)	20 (6%)	1 (0%)	44	55
2	D	324/328 (99%)	309 (95%)	13 (4%)	2 (1%)	28	34
All	All	1077/1216 (89%)	1013 (94%)	57 (5%)	7 (1%)	28	34

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	5	VAL
2	C	308	HIS
2	D	430	TYR
1	A	49	LYS
2	D	308	HIS
1	B	113	PRO
1	B	146	VAL

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar

resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	210/268 (78%)	200 (95%)	10 (5%)	30	40
1	B	205/268 (76%)	195 (95%)	10 (5%)	29	39
2	C	300/302 (99%)	294 (98%)	6 (2%)	60	77
2	D	300/302 (99%)	294 (98%)	6 (2%)	60	77
All	All	1015/1140 (89%)	983 (97%)	32 (3%)	44	60

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	23	LYS
1	A	27	LYS
1	A	28	LYS
1	A	49	LYS
1	A	50	CYS
1	A	83	LYS
1	A	124	ASN
1	A	144	ASN
1	A	145	LYS
1	B	7	ASP
1	B	50	CYS
1	B	114	LYS
1	B	121	ASN
1	B	124	ASN
1	B	127	LEU
1	B	132	LYS
1	B	141	TYR
1	B	189	SER
1	B	231	ASN
2	C	284	ASP
2	C	287	GLU
2	C	302	LYS
2	C	345	ARG
2	C	487	LEU
2	C	524	SER
2	D	285	GLU
2	D	299	LYS

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Mol	Chain	Res	Type
2	D	305	ASN
2	D	309	PRO
2	D	487	LEU
2	D	564	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	99	GLN
1	A	144	ASN
1	B	99	GLN
1	B	121	ASN
1	B	171	GLN
2	C	316	ASN
2	C	394	ASN
2	C	424	ASN
2	D	394	ASN
2	D	424	ASN
2	D	554	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	CP6	A	609	-	18,18,18	2.70	11 (61%)	22,25,25	1.88	8 (36%)
4	NDP	A	610	-	43,52,52	3.04	19 (44%)	49,80,80	2.27	21 (42%)
3	CP6	B	709	-	18,18,18	2.80	10 (55%)	22,25,25	2.09	9 (40%)
4	NDP	B	710	-	43,52,52	2.25	13 (30%)	49,80,80	1.83	11 (22%)
5	UMP	C	611	-	17,21,21	2.20	5 (29%)	23,31,31	3.64	7 (30%)
5	UMP	D	711	-	17,21,21	2.35	6 (35%)	23,31,31	3.67	8 (34%)

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	CP6	A	609	-	-	0/6/6/6	0/2/2/2
4	NDP	A	610	-	-	0/30/77/77	0/5/5/5
3	CP6	B	709	-	-	0/6/6/6	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 (64) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	610	NDP	C4N-C5N	-5.27	1.37	1.49
4	B	710	NDP	C4N-C5N	-5.02	1.38	1.49
4	A	610	NDP	P2B-O2B	-4.16	1.52	1.59
4	A	610	NDP	C2D-C3D	-3.96	1.42	1.53
3	A	609	CP6	C10-CL1	-3.61	1.66	1.74
3	B	709	CP6	C10-CL1	-3.46	1.67	1.74
4	A	610	NDP	P2B-O2X	-2.99	1.42	1.54
4	B	710	NDP	PA-O1A	-2.98	1.39	1.50
3	A	609	CP6	C4-C7	-2.80	1.45	1.50
5	C	611	UMP	P-OP3	-2.42	1.44	1.54
4	A	610	NDP	PA-O1A	-2.31	1.42	1.50
5	C	611	UMP	P-OP2	-2.22	1.45	1.54
4	A	610	NDP	C8A-N7A	-2.14	1.30	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	711	UMP	P-OP3	-2.06	1.46	1.54
3	B	709	CP6	C2-N1	2.02	1.39	1.35
4	B	710	NDP	C1D-N1N	2.03	1.52	1.46
5	D	711	UMP	O3'-C3'	2.11	1.48	1.43
3	A	609	CP6	C3-N1	2.14	1.38	1.35
5	C	611	UMP	C2-N3	2.16	1.42	1.38
5	D	711	UMP	O4'-C4'	2.18	1.49	1.45
4	A	610	NDP	C3B-C4B	2.21	1.58	1.53
3	B	709	CP6	C12-C11	2.26	1.42	1.38
4	A	610	NDP	C1D-N1N	2.28	1.53	1.46
4	A	610	NDP	C6N-N1N	2.37	1.44	1.37
4	B	710	NDP	C2D-C1D	2.38	1.60	1.53
4	A	610	NDP	PA-O5B	2.44	1.69	1.59
5	D	711	UMP	C2-N3	2.47	1.43	1.38
3	A	609	CP6	C12-C11	2.50	1.43	1.38
3	A	609	CP6	C2-N1	2.56	1.40	1.35
3	B	709	CP6	C2-N6	2.66	1.40	1.35
4	B	710	NDP	C6N-N1N	2.67	1.44	1.37
4	B	710	NDP	O4B-C1B	2.73	1.45	1.41
3	A	609	CP6	C2-N6	2.76	1.40	1.35
4	A	610	NDP	C5D-C4D	2.87	1.60	1.51
3	B	709	CP6	C3-N1	3.00	1.39	1.35
4	B	710	NDP	O4D-C1D	3.11	1.49	1.42
4	B	710	NDP	C2A-N3A	3.21	1.37	1.32
4	B	710	NDP	C2A-N1A	3.24	1.40	1.33
3	A	609	CP6	C2-N14	3.27	1.40	1.34
3	B	709	CP6	C12-C7	3.27	1.46	1.39
3	B	709	CP6	C2-N14	3.45	1.41	1.34
3	A	609	CP6	C12-C7	3.56	1.46	1.39
3	A	609	CP6	C9-C10	3.72	1.45	1.38
4	A	610	NDP	C2A-N1A	3.80	1.41	1.33
3	A	609	CP6	C4-C5	4.11	1.50	1.41
3	B	709	CP6	C9-C10	4.18	1.46	1.38
4	A	610	NDP	C2A-N3A	4.34	1.39	1.32
5	D	711	UMP	O4'-C1'	4.34	1.52	1.42
4	B	710	NDP	C6N-C5N	4.37	1.41	1.33
5	C	611	UMP	O4'-C1'	4.42	1.52	1.42
4	B	710	NDP	C4A-N3A	4.54	1.42	1.35
4	B	710	NDP	C5D-C4D	4.59	1.66	1.51
4	A	610	NDP	O4D-C1D	4.75	1.53	1.42
3	B	709	CP6	C4-C5	4.88	1.52	1.41
3	A	609	CP6	C4-C3	4.95	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	610	NDP	O4B-C4B	5.09	1.56	1.45
4	A	610	NDP	C4A-N3A	5.18	1.43	1.35
3	B	709	CP6	C4-C3	5.47	1.50	1.43
5	C	611	UMP	C4-N3	5.70	1.43	1.33
4	A	610	NDP	C6N-C5N	5.77	1.44	1.33
4	B	710	NDP	C2N-C3N	5.83	1.51	1.34
4	A	610	NDP	C2N-C3N	6.02	1.52	1.34
5	D	711	UMP	C4-N3	6.20	1.44	1.33
4	A	610	NDP	O4B-C1B	9.24	1.54	1.41

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	610	NDP	O4B-C4B-C5B	-6.05	88.96	109.40
4	B	710	NDP	C4B-O4B-C1B	-5.39	104.03	109.77
4	B	710	NDP	C3N-C2N-N1N	-4.45	116.62	123.08
4	A	610	NDP	C4B-O4B-C1B	-4.40	105.09	109.77
4	A	610	NDP	C3N-C2N-N1N	-4.39	116.72	123.08
3	B	709	CP6	C4-C3-N13	-4.36	117.50	120.87
4	B	710	NDP	N3A-C2A-N1A	-4.04	125.34	128.86
3	A	609	CP6	C4-C3-N13	-3.55	118.12	120.87
4	B	710	NDP	O3X-P2B-O1X	-3.49	96.84	110.50
4	A	610	NDP	C1D-N1N-C2N	-3.45	115.23	121.09
5	D	711	UMP	O4'-C1'-C2'	-3.45	99.64	106.25
4	A	610	NDP	N3A-C2A-N1A	-3.41	125.89	128.86
5	C	611	UMP	O4'-C1'-C2'	-3.39	99.75	106.25
5	D	711	UMP	C5-C4-N3	-3.27	115.32	123.12
5	C	611	UMP	C5-C4-N3	-3.23	115.40	123.12
4	A	610	NDP	C2D-C1D-N1N	-3.20	105.09	113.32
4	A	610	NDP	O5D-C5D-C4D	-3.05	98.19	109.00
3	A	609	CP6	C4-C3-N1	-3.01	120.80	122.49
4	B	710	NDP	C1D-N1N-C2N	-3.01	115.99	121.09
5	D	711	UMP	O4'-C4'-C3'	-2.96	98.57	105.68
3	B	709	CP6	C4-C3-N1	-2.92	120.85	122.49
4	A	610	NDP	O5B-C5B-C4B	-2.78	99.14	109.00
4	A	610	NDP	O4B-C4B-C3B	-2.74	99.73	105.17
4	B	710	NDP	O3X-P2B-O2X	-2.68	96.80	107.61
4	A	610	NDP	O3X-P2B-O2X	-2.59	97.16	107.61
5	C	611	UMP	O4'-C4'-C3'	-2.56	99.53	105.68
3	A	609	CP6	C9-C10-CL1	-2.50	115.42	119.35
4	B	710	NDP	O7N-C7N-N7N	-2.49	116.88	122.92
4	A	610	NDP	O4B-C1B-C2B	-2.46	102.28	106.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	610	NDP	O3D-C3D-C4D	-2.35	104.22	111.09
4	A	610	NDP	O3X-P2B-O1X	-2.27	101.61	110.50
3	B	709	CP6	C9-C10-CL1	-2.22	115.85	119.35
4	B	710	NDP	O3X-P2B-O2B	-2.06	96.63	106.00
4	A	610	NDP	O5B-PA-O1A	-2.06	100.95	109.25
5	D	711	UMP	C2'-C3'-C4'	2.09	107.18	102.73
4	A	610	NDP	O2A-PA-O1A	2.10	123.13	112.28
4	B	710	NDP	C2D-C3D-C4D	2.14	106.79	102.62
3	A	609	CP6	C2-N1-C3	2.16	119.39	116.99
3	B	709	CP6	C2-N1-C3	2.27	119.51	116.99
3	B	709	CP6	C12-C7-C4	2.27	124.59	120.79
4	A	610	NDP	O2B-C2B-C3B	2.29	120.09	111.63
4	A	610	NDP	C2D-C3D-C4D	2.39	107.27	102.62
3	A	609	CP6	C2-N6-C5	2.40	118.16	116.31
5	C	611	UMP	C4'-O4'-C1'	2.55	115.66	109.42
3	A	609	CP6	N13-C3-N1	2.67	120.95	117.00
4	A	610	NDP	O2X-P2B-O2B	2.74	118.45	106.00
3	B	709	CP6	C11-C10-CL1	2.76	123.71	119.35
3	B	709	CP6	N13-C3-N1	2.86	121.23	117.00
4	B	710	NDP	O2X-P2B-O2B	2.88	119.09	106.00
3	A	609	CP6	C7-C4-C3	2.91	123.83	120.69
5	D	711	UMP	C4'-O4'-C1'	3.07	116.93	109.42
3	A	609	CP6	C11-C10-CL1	3.17	124.36	119.35
4	A	610	NDP	C5B-C4B-C3B	3.22	127.54	115.29
3	B	709	CP6	C7-C4-C3	3.44	124.41	120.69
5	C	611	UMP	C2'-C1'-N1	3.70	122.97	114.23
5	D	711	UMP	C2'-C1'-N1	3.71	123.00	114.23
3	B	709	CP6	C2-N6-C5	3.74	119.20	116.31
4	A	610	NDP	O4D-C1D-N1N	3.88	115.88	108.07
4	B	710	NDP	O2X-P2B-O1X	3.91	125.81	110.50
4	A	610	NDP	O2X-P2B-O1X	3.93	125.88	110.50
5	D	711	UMP	O4'-C1'-N1	4.63	115.59	107.78
5	C	611	UMP	O4'-C1'-N1	5.43	116.93	107.78
5	C	611	UMP	C4-N3-C2	14.35	126.45	114.13
5	D	711	UMP	C4-N3-C2	14.61	126.68	114.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	610	NDP	14	0
3	B	709	CP6	2	0
4	B	710	NDP	12	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%)	0.77	28 (12%) 4 6	16, 34, 86, 94	0
1	B	216/280 (77%)	2.26	91 (42%) 0 0	23, 73, 94, 94	0
2	C	326/328 (99%)	0.09	25 (7%) 14 19	14, 23, 77, 94	0
2	D	326/328 (99%)	-0.01	22 (6%) 19 25	14, 22, 71, 94	0
All	All	1089/1216 (89%)	0.63	166 (15%) 2 4	14, 28, 93, 94	0

All (166) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	85	THR	13.3
1	A	1	MET	12.7
1	B	75	TYR	11.7
1	B	26	GLY	11.5
1	B	2	MET	11.4
1	A	24	ASN	10.8
1	B	1	MET	10.0
1	B	80	TYR	9.4
1	A	2	MET	9.0
1	A	25	GLU	8.6
1	A	26	GLY	8.3
2	D	608	ALA	8.1
1	B	70	TYR	7.7
1	B	24	ASN	7.7
1	A	230	ASN	7.6
1	B	230	ASN	7.6
1	B	28	LYS	7.4
1	B	27	LYS	7.3
1	B	9	PHE	6.8
1	B	135	ASP	6.8
1	B	3	GLU	6.7

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Mol	Chain	Res	Type	RSRZ
2	C	298	GLU	6.7
2	C	299	LYS	6.5
2	D	283	ASP	6.4
1	B	151	VAL	6.4
1	A	22	SER	6.3
2	D	299	LYS	6.0
1	B	136	PHE	6.0
1	B	139	ASP	5.9
2	C	283	ASP	5.9
1	B	81	LEU	5.9
1	B	73	LEU	5.9
1	B	130	THR	5.9
1	B	137	ASP	5.9
1	B	131	LEU	5.8
2	C	344	ASP	5.7
2	C	284	ASP	5.7
1	B	134	GLU	5.7
1	B	116	PHE	5.5
1	B	74	LYS	5.5
1	B	144	ASN	5.5
2	C	346	THR	5.5
1	B	23	LYS	5.4
1	A	27	LYS	5.4
1	B	25	GLU	5.4
2	D	345	ARG	5.4
1	B	10	ASP	5.3
1	B	6	CYS	5.3
2	C	304	LYS	5.3
1	B	77	ARG	5.2
1	B	138	GLU	5.2
1	A	23	LYS	5.2
1	A	231	ASN	5.2
1	A	82	ASN	5.1
1	B	231	ASN	5.0
2	C	307	ILE	5.0
1	B	115	LYS	4.9
1	B	22	SER	4.9
2	C	345	ARG	4.9
1	A	29	ASN	4.9
2	C	347	GLY	4.8
2	D	305	ASN	4.8
1	B	76	LYS	4.6

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Mol	Chain	Res	Type	RSRZ
1	B	78	CYS	4.6
1	A	3	GLU	4.5
2	C	301	GLU	4.5
1	A	84	GLU	4.4
1	B	29	ASN	4.4
2	C	286	GLU	4.3
1	B	4	GLN	4.2
2	C	285	GLU	4.2
2	C	287	GLU	4.1
2	D	346	THR	4.1
1	A	96	LYS	4.1
1	B	129	ARG	4.0
2	D	284	ASP	4.0
1	B	79	LYS	4.0
1	A	28	LYS	4.0
2	C	300	GLU	3.8
2	D	310	ASN	3.8
1	B	12	TYR	3.7
1	B	14	ILE	3.6
1	B	141	TYR	3.6
1	B	66	ASN	3.6
2	D	300	GLU	3.6
1	B	155	LYS	3.5
1	B	97	LYS	3.5
1	B	11	ILE	3.5
1	B	154	GLY	3.5
2	D	285	GLU	3.5
1	B	140	VAL	3.4
1	B	176	LYS	3.4
1	A	71	GLU	3.4
1	A	75	TYR	3.4
2	C	310	ASN	3.4
1	B	5	VAL	3.3
2	C	348	VAL	3.3
1	A	79	LYS	3.3
2	D	307	ILE	3.3
1	B	132	LYS	3.3
1	B	157	ASN	3.2
2	D	298	GLU	3.2
1	A	78	CYS	3.2
2	C	305	ASN	3.2
1	B	72	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	114	LYS	3.2
1	B	133	LYS	3.1
1	B	161	CYS	3.0
1	B	203	ASN	3.0
1	B	159	TYR	3.0
1	B	113	PRO	3.0
1	B	162	PHE	2.9
1	B	35	TYR	2.9
2	C	607	ALA	2.9
2	D	309	PRO	2.9
1	B	179	ILE	2.8
2	C	290	PHE	2.8
2	C	297	LYS	2.8
1	B	156	LEU	2.8
1	A	116	PHE	2.8
1	B	8	VAL	2.7
1	A	201	ASN	2.7
1	B	229	THR	2.7
2	C	608	ALA	2.7
1	B	228	LYS	2.7
2	D	286	GLU	2.7
1	B	158	TYR	2.7
2	D	344	ASP	2.6
1	A	203	ASN	2.6
1	B	185	THR	2.6
1	B	205	TYR	2.6
1	B	160	LYS	2.6
1	B	148	ASP	2.5
1	B	164	ILE	2.5
1	B	175	GLU	2.5
1	B	98	LEU	2.5
2	C	291	VAL	2.5
1	B	145	LYS	2.5
1	B	149	LEU	2.5
1	B	69	LYS	2.4
1	B	201	ASN	2.4
1	B	16	ALA	2.4
1	A	83	LYS	2.4
1	B	152	LEU	2.4
2	D	313	GLN	2.4
1	B	183	TYR	2.4
1	B	204	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	103	VAL	2.3
2	D	605	ASP	2.3
1	B	68	SER	2.3
1	B	163	ILE	2.3
1	A	74	LYS	2.3
1	B	117	LYS	2.3
2	D	447	ASN	2.3
1	B	147	GLU	2.2
1	B	172	GLU	2.2
1	A	70	TYR	2.2
2	D	306	SER	2.2
2	D	301	GLU	2.1
1	A	49	LYS	2.1
2	C	450	ASN	2.1
2	D	304	LYS	2.1
1	B	202	GLU	2.1
2	D	607	ALA	2.0
2	C	605	ASP	2.0
1	B	7	ASP	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
5	UMP	D	711	20/20	0.87	0.28	12.25	49,65,74,74	0
5	UMP	C	611	20/20	0.90	0.26	8.72	42,56,66,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	NDP	A	610	48/48	0.90	0.21	1.77	48,53,68,70	0
4	NDP	B	710	48/48	0.72	0.35	0.92	93,93,93,93	0
3	CP6	A	609	17/17	0.85	0.19	0.89	5,17,19,20	0
3	CP6	B	709	17/17	0.75	0.23	0.41	44,49,50,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.