



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:40 PM GMT

PDB ID : 3UKK  
Title : Crystal structure of R182K-UDP-galactopuranose mutase from *Aspergillus fumigatus* in complex with UDPgalp  
Authors : Van Straaten, K.E.; Sanders, D.A.R.  
Deposited on : 2011-11-09  
Resolution : 2.75 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

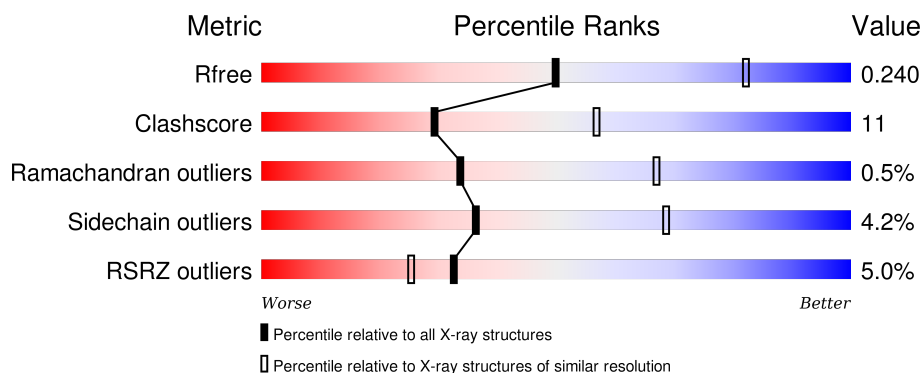
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	3340 (2.80-2.72)
Clashscore	102246	3829 (2.80-2.72)
Ramachandran outliers	100387	3767 (2.80-2.72)
Sidechain outliers	100360	3770 (2.80-2.72)
RSRZ outliers	91569	3352 (2.80-2.72)

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	517	<div> <div>4%</div> <div>78% 21% .</div> </div>
1	B	517	<div> <div>3%</div> <div>74% 23% ..</div> </div>
1	C	517	<div> <div>8%</div> <div>72% 26% .</div> </div>
1	D	517	<div> <div>5%</div> <div>73% 24% ..</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16649 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 UDP-galactopyranose mutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	517	Total	C	N	O	S	0	0	0
			4071	2581	704	765	21			
1	B	510	Total	C	N	O	S	0	0	0
			4002	2540	685	756	21			
1	C	516	Total	C	N	O	S	0	0	0
			4061	2575	701	764	21			
1	D	513	Total	C	N	O	S	0	0	0
			4031	2557	692	761	21			

There are 36 discrepancies between the modelled and reference sequences:

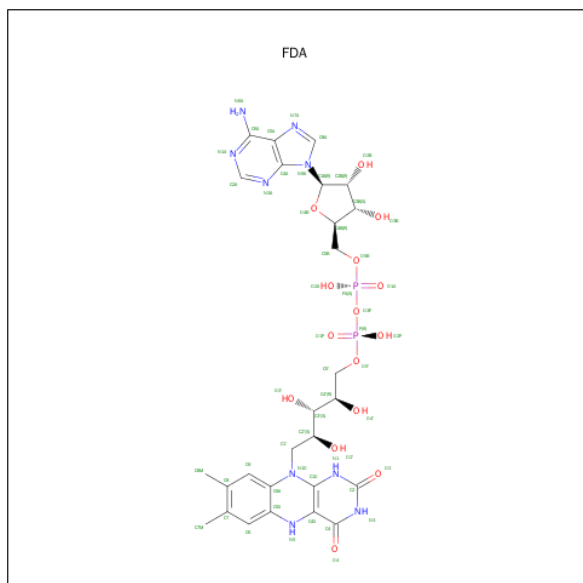
Chain	Residue	Modelled	Actual	Comment	Reference
A	182	LYS	ARG	ENGINEERED MUTATION	UNP Q4W1X2
A	511	LEU	-	EXPRESSION TAG	UNP Q4W1X2
A	512	GLU	-	EXPRESSION TAG	UNP Q4W1X2
A	513	HIS	-	EXPRESSION TAG	UNP Q4W1X2
A	514	HIS	-	EXPRESSION TAG	UNP Q4W1X2
A	515	HIS	-	EXPRESSION TAG	UNP Q4W1X2
A	516	HIS	-	EXPRESSION TAG	UNP Q4W1X2
A	517	HIS	-	EXPRESSION TAG	UNP Q4W1X2
A	518	HIS	-	EXPRESSION TAG	UNP Q4W1X2
B	182	LYS	ARG	ENGINEERED MUTATION	UNP Q4W1X2
B	511	LEU	-	EXPRESSION TAG	UNP Q4W1X2
B	512	GLU	-	EXPRESSION TAG	UNP Q4W1X2
B	513	HIS	-	EXPRESSION TAG	UNP Q4W1X2
B	514	HIS	-	EXPRESSION TAG	UNP Q4W1X2
B	515	HIS	-	EXPRESSION TAG	UNP Q4W1X2
B	516	HIS	-	EXPRESSION TAG	UNP Q4W1X2
B	517	HIS	-	EXPRESSION TAG	UNP Q4W1X2
B	518	HIS	-	EXPRESSION TAG	UNP Q4W1X2
C	182	LYS	ARG	ENGINEERED MUTATION	UNP Q4W1X2
C	511	LEU	-	EXPRESSION TAG	UNP Q4W1X2
C	512	GLU	-	EXPRESSION TAG	UNP Q4W1X2

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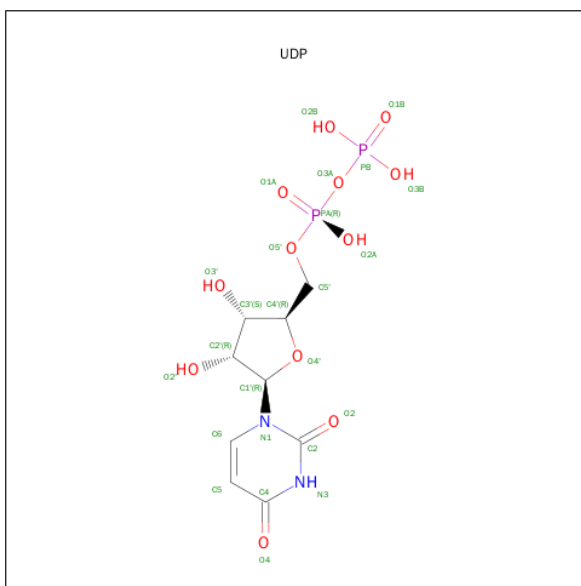
Chain	Residue	Modelled	Actual	Comment	Reference
C	513	HIS	-	EXPRESSION TAG	UNP Q4W1X2
C	514	HIS	-	EXPRESSION TAG	UNP Q4W1X2
C	515	HIS	-	EXPRESSION TAG	UNP Q4W1X2
C	516	HIS	-	EXPRESSION TAG	UNP Q4W1X2
C	517	HIS	-	EXPRESSION TAG	UNP Q4W1X2
C	518	HIS	-	EXPRESSION TAG	UNP Q4W1X2
D	182	LYS	ARG	ENGINEERED MUTATION	UNP Q4W1X2
D	511	LEU	-	EXPRESSION TAG	UNP Q4W1X2
D	512	GLU	-	EXPRESSION TAG	UNP Q4W1X2
D	513	HIS	-	EXPRESSION TAG	UNP Q4W1X2
D	514	HIS	-	EXPRESSION TAG	UNP Q4W1X2
D	515	HIS	-	EXPRESSION TAG	UNP Q4W1X2
D	516	HIS	-	EXPRESSION TAG	UNP Q4W1X2
D	517	HIS	-	EXPRESSION TAG	UNP Q4W1X2
D	518	HIS	-	EXPRESSION TAG	UNP Q4W1X2

- Molecule 2 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (three-letter code: FDA) (formula:  $C_{27}H_{35}N_9O_{15}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	B	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	D	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 3 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula:  $\text{C}_9\text{H}_{14}\text{N}_2\text{O}_{12}\text{P}_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	B	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	C	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	D	1	Total 25	C 9	N 2	O 12	P 2	0	0

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

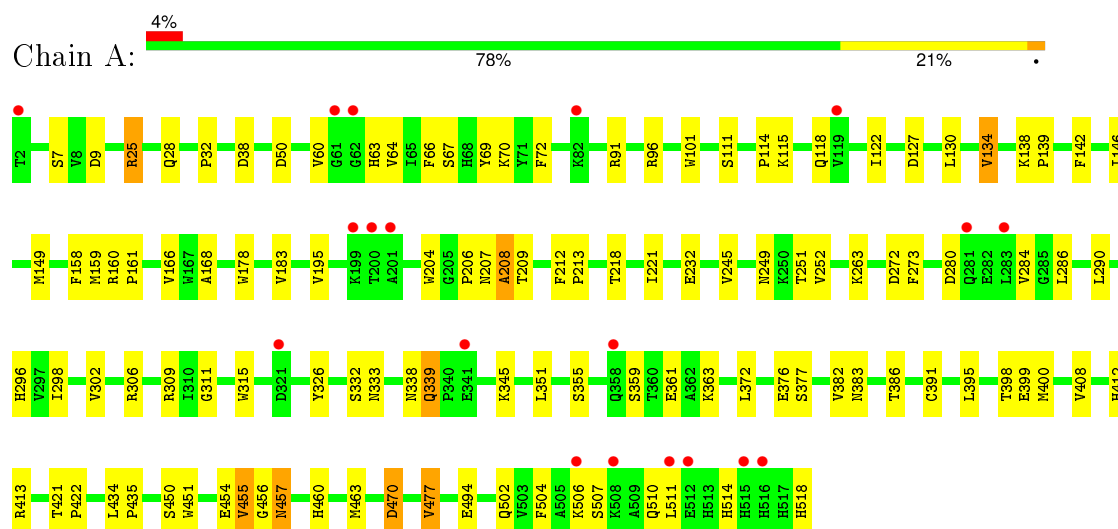
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	54	Total O	0	0
			54 54		
5	B	53	Total O	0	0
			53 53		
5	C	37	Total O	0	0
			37 37		
5	D	28	Total O	0	0
			28 28		

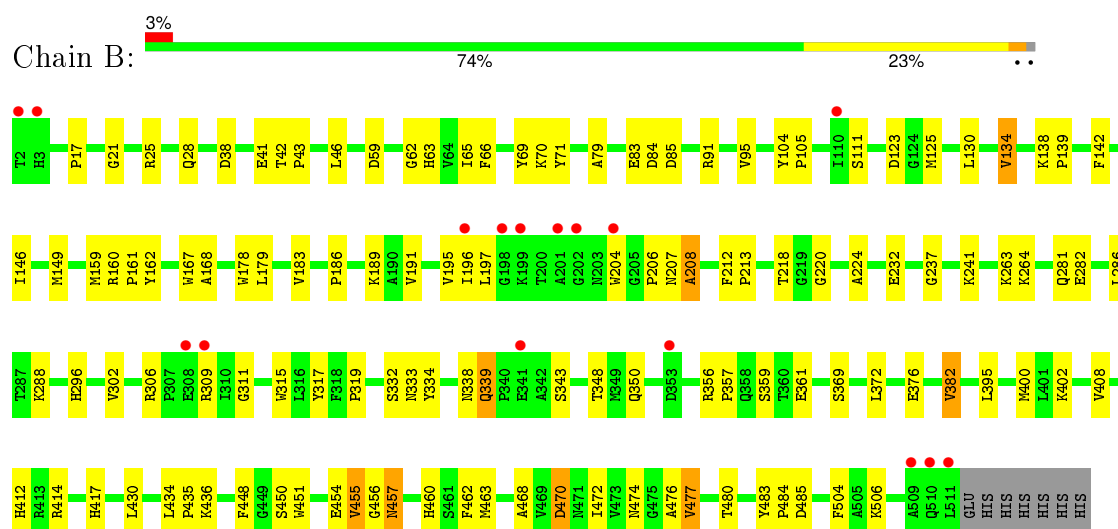
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ( $RSRZ > 2$ ). 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: UDP-galactopyranose mutase

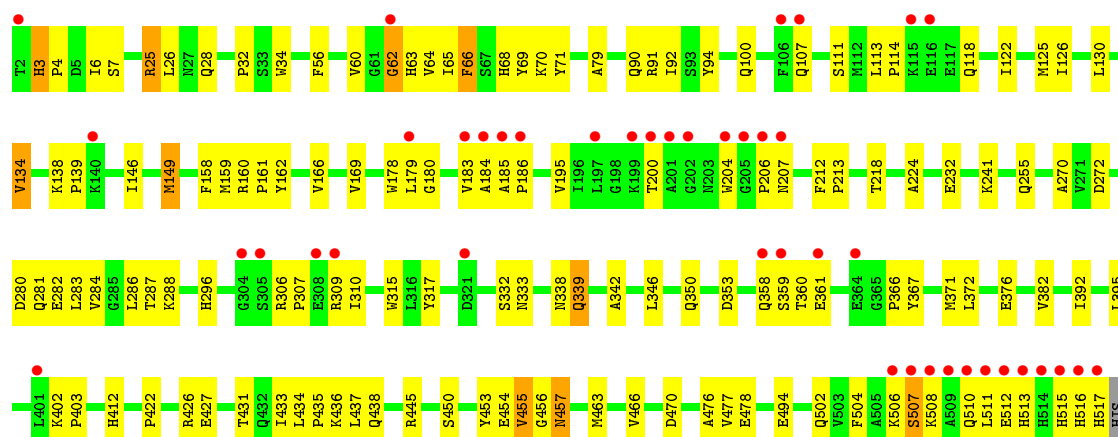


#### • Molecule 1: UDP-galactopyranose mutase

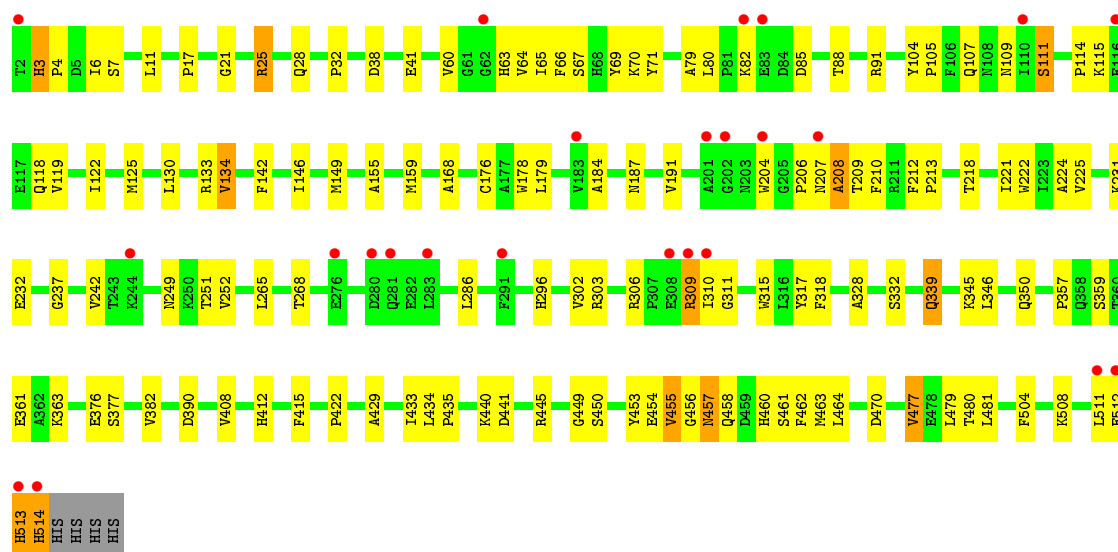


#### • Molecule 1: UDP-galactopyranose mutase





• Molecule 1: UDP-galactopyranose mutase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.66Å 123.66Å 156.37Å 90.00° 103.26° 90.00°	Depositor
Resolution (Å)	47.99 – 2.75 47.99 – 2.75	Depositor EDS
% Data completeness (in resolution range)	93.4 (47.99-2.75) 93.5 (47.99-2.75)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.30 (at 2.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, $R_{free}$	0.183 , 0.241 0.185 , 0.240	Depositor DCC
$R_{free}$ test set	3182 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.5	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 54.3	EDS
Estimated twinning fraction	0.031 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 63632 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	16649	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FDA, UDP, FAD

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	0.26	0/4176	0.43	0/5675
1	B	0.26	0/4101	0.43	0/5573
1	C	0.27	0/4165	0.44	0/5660
1	D	0.25	0/4132	0.43	0/5615
All	All	0.26	0/16574	0.43	0/22523

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4071	0	3973	87	0
1	B	4002	0	3925	92	0
1	C	4061	0	3966	104	0
1	D	4031	0	3945	96	0
2	A	53	0	30	2	0
2	B	53	0	30	5	0
2	D	53	0	30	3	0
3	A	25	0	11	1	0
3	B	25	0	11	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	25	0	11	2	0
3	D	25	0	11	2	0
4	C	53	0	30	3	0
5	A	54	0	0	1	0
5	B	53	0	0	6	0
5	C	37	0	0	1	0
5	D	28	0	0	4	0
All	All	16649	0	15973	366	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 11.

All (366) 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:C:66:PHE:CE2	1:C:206:PRO:HB3	2.00	0.95
1:A:456:GLY:O	1:A:457:ASN:HB2	1.71	0.90
1:C:456:GLY:O	1:C:457:ASN:HB2	1.72	0.88
1:D:63:HIS:HB2	1:D:218:THR:HG21	1.54	0.87
1:C:91:ARG:HD3	1:C:207:ASN:HB2	1.55	0.85
1:A:91:ARG:HH11	1:A:207:ASN:HB2	1.43	0.83
1:D:107:GLN:HE21	1:D:184:ALA:HB3	1.45	0.81
1:A:296:HIS:HD2	1:A:412:HIS:HE1	1.29	0.78
1:C:309:ARG:HH21	1:C:402:LYS:HE2	1.49	0.78
1:C:64:VAL:HG21	1:C:315:TRP:CZ3	2.18	0.78
1:B:296:HIS:HD2	1:B:412:HIS:HE1	1.30	0.78
1:C:3:HIS:H	1:C:3:HIS:CD2	1.98	0.77
1:C:66:PHE:CZ	1:C:206:PRO:HB3	2.19	0.76
1:C:513:HIS:HA	1:C:516:HIS:HD1	1.52	0.75
1:B:504:PHE:CD2	1:C:32:PRO:HB3	2.21	0.75
1:C:309:ARG:NH2	1:C:402:LYS:HE2	2.02	0.74
1:C:296:HIS:HD2	1:C:412:HIS:HE1	1.34	0.73
1:D:508:LYS:HA	1:D:511:LEU:HD13	1.70	0.73
1:A:134:VAL:HG22	1:C:134:VAL:HG22	1.69	0.72
1:C:511:LEU:O	1:C:515:HIS:HD2	1.72	0.72
1:A:296:HIS:HD2	1:A:412:HIS:CE1	2.08	0.71
1:B:332:SER:HA	1:B:339:GLN:NE2	2.04	0.71
1:D:508:LYS:HG3	1:D:511:LEU:HD22	1.72	0.70
1:B:63:HIS:HB2	1:B:218:THR:HG21	1.73	0.69
1:A:296:HIS:CD2	1:A:412:HIS:HE1	2.09	0.69
1:A:504:PHE:CD2	1:D:32:PRO:HB3	2.28	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:66:PHE:HE2	1:C:68:HIS:NE2	1.91	0.69
1:C:296:HIS:HD2	1:C:412:HIS:CE1	2.11	0.68
1:C:296:HIS:CD2	1:C:412:HIS:HE1	2.11	0.68
1:C:111:SER:HB3	1:C:195:VAL:HA	1.77	0.67
1:D:296:HIS:HD2	1:D:412:HIS:HE1	1.41	0.67
1:D:511:LEU:HG	1:D:512:GLU:H	1.59	0.67
1:C:125:MET:HE1	1:C:186:PRO:HB2	1.75	0.67
1:D:67:SER:N	5:D:722:HOH:O	2.27	0.66
1:C:91:ARG:HG3	1:C:315:TRP:CH2	2.30	0.65
1:D:146:ILE:HD13	1:D:159:MET:HB3	1.77	0.65
1:C:3:HIS:N	1:C:3:HIS:CD2	2.63	0.65
1:B:306:ARG:HD3	1:B:333:ASN:HD21	1.61	0.65
1:A:372:LEU:HD21	1:A:395:LEU:HD21	1.77	0.65
1:B:296:HIS:HD2	1:B:412:HIS:CE1	2.15	0.65
1:A:306:ARG:HD3	1:A:333:ASN:HD21	1.60	0.65
1:D:212:PHE:CG	1:D:213:PRO:HD2	2.33	0.64
1:A:115:LYS:HB3	1:B:197:LEU:HD23	1.79	0.64
1:C:502:GLN:O	1:C:506:LYS:HG3	1.97	0.64
1:C:107:GLN:HE21	1:C:184:ALA:HB3	1.62	0.64
1:D:296:HIS:HD2	1:D:412:HIS:CE1	2.16	0.64
1:A:434:LEU:HB2	1:A:435:PRO:HD3	1.80	0.63
1:C:91:ARG:NH2	1:C:204:TRP:O	2.31	0.63
1:C:513:HIS:HA	1:C:516:HIS:ND1	2.14	0.62
1:A:502:GLN:O	1:A:506:LYS:HD3	1.99	0.62
1:C:296:HIS:HE1	1:C:376:GLU:OE2	1.83	0.62
1:B:296:HIS:CD2	1:B:412:HIS:HE1	2.16	0.62
1:C:63:HIS:HB2	1:C:218:THR:HG21	1.82	0.61
1:D:429:ALA:O	1:D:433:ILE:HG13	2.01	0.61
1:C:66:PHE:HE2	1:C:68:HIS:CE1	2.19	0.60
1:C:287:THR:HG22	1:C:433:ILE:HD13	1.83	0.60
1:A:178:TRP:HB2	1:A:454:GLU:HG3	1.83	0.60
1:D:69:TYR:CG	1:D:463:MET:HG3	2.36	0.60
1:C:338:ASN:HB2	1:C:339:GLN:HE21	1.66	0.60
1:B:178:TRP:HB2	1:B:454:GLU:HG3	1.84	0.59
1:B:306:ARG:HD2	1:B:311:GLY:O	2.02	0.59
1:A:91:ARG:NH1	1:A:207:ASN:HB2	2.16	0.59
1:B:69:TYR:CG	1:B:463:MET:HG3	2.38	0.59
1:C:306:ARG:HD3	1:C:333:ASN:HD21	1.67	0.58
1:A:457:ASN:HA	2:A:601:FDA:H1'2	1.86	0.58
1:D:511:LEU:O	1:D:512:GLU:HB2	2.02	0.58
1:B:91:ARG:HD3	1:B:207:ASN:CB	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:456:GLY:O	1:C:457:ASN:CB	2.50	0.58
1:B:91:ARG:HD3	1:B:207:ASN:HB2	1.84	0.58
1:D:455:VAL:HG13	1:D:455:VAL:O	2.01	0.58
1:B:91:ARG:HH11	1:B:207:ASN:HB2	1.69	0.58
1:D:38:ASP:OD1	2:D:601:FDA:O3B	2.22	0.58
1:A:25:ARG:HH21	1:A:28:GLN:HE22	1.50	0.58
1:A:456:GLY:O	1:A:457:ASN:CB	2.48	0.57
1:C:332:SER:HA	1:C:339:GLN:NE2	2.18	0.57
1:A:91:ARG:NH2	1:A:204:TRP:O	2.34	0.57
1:A:66:PHE:CE1	1:A:206:PRO:HB2	2.40	0.57
1:C:178:TRP:HB2	1:C:454:GLU:HG3	1.87	0.57
1:A:38:ASP:OD1	2:A:601:FDA:O3B	2.22	0.57
1:D:296:HIS:CD2	1:D:412:HIS:HE1	2.22	0.57
1:C:353:ASP:HB3	1:C:403:PRO:HB3	1.87	0.57
1:C:232:GLU:N	1:C:232:GLU:OE1	2.36	0.56
1:D:231:LYS:NZ	5:D:711:HOH:O	2.39	0.56
1:A:298:ILE:HG13	1:A:391:CYS:SG	2.46	0.56
1:C:512:GLU:O	1:C:516:HIS:ND1	2.39	0.56
1:C:504:PHE:O	1:C:508:LYS:HG3	2.05	0.56
1:C:502:GLN:HB3	1:C:506:LYS:HE2	1.88	0.56
1:B:69:TYR:CD1	1:B:463:MET:HG3	2.41	0.55
1:A:494:GLU:HG2	1:D:477:VAL:HA	1.88	0.55
1:C:453:TYR:OH	3:C:602:UDP:O2B	2.22	0.55
1:A:455:VAL:HG13	1:A:455:VAL:O	2.06	0.55
1:C:338:ASN:HB2	1:C:339:GLN:NE2	2.21	0.55
1:D:21:GLY:HA2	1:D:462:PHE:CE1	2.42	0.55
1:D:60:VAL:HG13	1:D:415:PHE:CE2	2.42	0.55
1:B:146:ILE:HD13	1:B:159:MET:HB3	1.89	0.54
1:C:427:GLU:O	1:C:431:THR:HG23	2.08	0.54
1:C:359:SER:OG	1:C:361:GLU:HG2	2.08	0.54
1:B:296:HIS:HE1	1:B:376:GLU:OE2	1.90	0.54
1:D:350:GLN:HA	1:D:357:PRO:HD3	1.90	0.54
1:D:296:HIS:HE1	1:D:376:GLU:OE2	1.91	0.54
1:C:342:ALA:HB2	1:C:366:PRO:HB3	1.89	0.54
1:C:66:PHE:O	1:C:66:PHE:CD2	2.61	0.54
1:D:332:SER:HA	1:D:339:GLN:NE2	2.23	0.54
1:A:296:HIS:HE1	1:A:376:GLU:OE2	1.91	0.53
1:D:178:TRP:HB2	1:D:454:GLU:HG3	1.89	0.53
1:A:91:ARG:HD3	1:A:207:ASN:HB3	1.90	0.53
1:C:455:VAL:O	1:C:455:VAL:CG1	2.56	0.53
1:D:11:LEU:O	1:D:265:LEU:HD12	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:350:GLN:HA	1:B:357:PRO:HD3	1.90	0.53
3:D:602:UDP:H3'	5:D:724:HOH:O	2.09	0.53
1:A:96:ARG:HB2	1:A:101:TRP:CZ3	2.44	0.53
1:C:178:TRP:HA	1:C:454:GLU:HG2	1.91	0.53
1:B:134:VAL:HG22	1:D:134:VAL:HG22	1.90	0.53
1:A:69:TYR:CG	1:A:463:MET:HG3	2.44	0.53
1:A:455:VAL:O	1:A:460:HIS:HB3	2.09	0.53
1:A:183:VAL:HG22	3:A:602:UDP:H1'	1.91	0.53
1:B:281:GLN:OE1	1:B:281:GLN:HA	2.09	0.53
1:A:332:SER:HA	1:A:339:GLN:NE2	2.24	0.53
1:A:178:TRP:HA	1:A:454:GLU:HG2	1.90	0.53
1:D:82:LYS:HB2	1:D:85:ASP:OD1	2.08	0.53
1:C:114:PRO:O	1:C:118:GLN:HG3	2.09	0.53
1:A:514:HIS:O	1:A:518:HIS:HB2	2.10	0.53
1:B:95:VAL:HG22	1:B:317:TYR:HB2	1.91	0.52
1:B:309:ARG:NH1	1:B:400:MET:O	2.42	0.52
1:C:392:ILE:HA	1:C:395:LEU:HD12	1.92	0.52
1:B:241:LYS:NZ	5:B:708:HOH:O	2.42	0.52
1:C:307:PRO:HB2	1:C:310:ILE:HG12	1.92	0.52
1:A:178:TRP:CB	1:A:454:GLU:HG3	2.39	0.52
1:B:359:SER:OG	1:B:361:GLU:HG2	2.10	0.52
1:B:455:VAL:HG21	1:B:480:THR:HG22	1.91	0.52
1:B:372:LEU:HD21	1:B:395:LEU:HD21	1.92	0.52
1:C:66:PHE:CE2	1:C:68:HIS:CE1	2.99	0.51
1:D:345:LYS:HA	1:D:363:LYS:O	2.10	0.51
1:A:345:LYS:HA	1:A:363:LYS:O	2.09	0.51
1:A:134:VAL:HG22	1:C:134:VAL:CG2	2.39	0.51
1:C:434:LEU:HB2	1:C:435:PRO:HD3	1.92	0.51
1:D:434:LEU:HB2	1:D:435:PRO:HD3	1.91	0.51
1:A:66:PHE:CD1	1:A:206:PRO:HB2	2.46	0.51
2:B:601:FDA:O2'	2:B:601:FDA:H9	2.10	0.51
1:D:25:ARG:HH21	1:D:28:GLN:HE22	1.59	0.51
1:B:332:SER:HA	1:B:339:GLN:HE21	1.72	0.51
1:B:456:GLY:O	1:B:457:ASN:HB2	2.10	0.51
1:D:309:ARG:HG3	1:D:310:ILE:HD12	1.93	0.51
1:C:358:GLN:N	5:C:721:HOH:O	2.42	0.51
1:A:507:SER:O	1:A:511:LEU:HD13	2.10	0.51
1:C:62:GLY:N	1:C:371:MET:SD	2.84	0.51
1:B:455:VAL:HG13	1:B:455:VAL:O	2.10	0.51
1:B:232:GLU:N	1:B:232:GLU:OE1	2.36	0.50
1:C:26:LEU:HD13	1:C:34:TRP:CB	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:114:PRO:O	1:D:118:GLN:HG3	2.11	0.50
1:C:130:LEU:HD23	1:D:130:LEU:HD23	1.93	0.50
1:C:69:TYR:CG	1:C:463:MET:HG3	2.46	0.50
1:D:508:LYS:HG3	1:D:511:LEU:CD2	2.40	0.50
1:B:408:VAL:HG12	1:B:408:VAL:O	2.10	0.50
1:C:122:ILE:O	1:C:126:ILE:HG13	2.12	0.50
1:A:50:ASP:OD2	1:A:413:ARG:NH1	2.42	0.50
1:A:212:PHE:CG	1:A:213:PRO:HD2	2.47	0.50
1:D:79:ALA:HB1	1:D:224:ALA:HB1	1.93	0.50
1:A:232:GLU:N	1:A:232:GLU:OE1	2.34	0.50
1:C:60:VAL:HB	1:C:63:HIS:NE2	2.27	0.49
1:B:28:GLN:HE22	1:B:71:TYR:HE2	1.60	0.49
1:A:67:SER:HB2	1:A:72:PHE:HD2	1.77	0.49
1:D:25:ARG:HH21	1:D:28:GLN:NE2	2.10	0.49
1:A:249:ASN:O	1:A:251:THR:HG23	2.12	0.49
1:C:91:ARG:HG3	1:C:315:TRP:CZ2	2.48	0.49
1:D:66:PHE:CE1	1:D:206:PRO:HB2	2.47	0.49
1:B:38:ASP:OD1	2:B:601:FDA:O3B	2.31	0.49
1:B:338:ASN:HB2	1:B:339:GLN:NE2	2.27	0.49
1:D:332:SER:HA	1:D:339:GLN:HE21	1.78	0.49
1:A:32:PRO:HB3	1:D:504:PHE:CD2	2.48	0.49
1:C:506:LYS:O	1:C:510:GLN:HB2	2.13	0.48
1:A:178:TRP:HA	1:A:454:GLU:CG	2.42	0.48
1:D:187:ASN:O	1:D:191:VAL:HG23	2.13	0.48
1:C:66:PHE:CD2	1:C:206:PRO:HB3	2.46	0.48
1:B:343:SER:N	5:B:727:HOH:O	2.46	0.48
1:D:232:GLU:H	1:D:232:GLU:CD	2.14	0.48
1:C:63:HIS:HD1	4:C:601:FAD:C4X	2.26	0.48
1:D:38:ASP:OD1	2:D:601:FDA:H1B	2.14	0.48
1:A:359:SER:OG	1:A:361:GLU:HG2	2.14	0.48
1:A:91:ARG:HD3	1:A:207:ASN:CB	2.43	0.48
4:C:601:FAD:H1'1	4:C:601:FAD:H9	1.60	0.48
1:B:376:GLU:HG3	1:B:382:VAL:HG13	1.96	0.48
1:B:178:TRP:HA	1:B:454:GLU:HG2	1.95	0.48
1:D:231:LYS:HA	1:D:231:LYS:HD3	1.74	0.48
1:D:242:VAL:HG13	1:D:252:VAL:HG13	1.96	0.48
1:D:453:TYR:OH	3:D:602:UDP:O2B	2.27	0.48
1:A:338:ASN:HB2	1:A:339:GLN:NE2	2.29	0.48
1:D:64:VAL:HG21	1:D:315:TRP:CZ3	2.49	0.48
1:B:414:ARG:NH1	5:B:731:HOH:O	2.21	0.48
1:B:160:ARG:N	1:B:161:PRO:HD2	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:474:ASN:ND2	5:B:753:HOH:O	2.46	0.48
1:A:195:VAL:HG11	1:B:196:ILE:HG12	1.96	0.48
1:C:184:ALA:HB2	1:C:204:TRP:CE2	2.49	0.47
1:C:280:ASP:O	1:C:284:VAL:HG23	2.14	0.47
1:B:21:GLY:HA2	1:B:462:PHE:CE1	2.49	0.47
1:C:25:ARG:HB2	1:C:466:VAL:HG13	1.95	0.47
1:A:309:ARG:NH1	1:A:400:MET:O	2.47	0.47
1:C:149:MET:HG3	1:C:185:ALA:HB1	1.96	0.47
1:D:69:TYR:CD1	1:D:463:MET:HG3	2.49	0.47
1:B:456:GLY:O	1:B:457:ASN:CB	2.62	0.47
1:D:91:ARG:HG3	1:D:315:TRP:CH2	2.50	0.47
1:C:79:ALA:HB1	1:C:224:ALA:CB	2.44	0.47
1:B:41:GLU:HG2	1:B:237:GLY:HA2	1.95	0.47
1:D:445:ARG:NE	1:D:481:LEU:HD22	2.29	0.47
1:C:65:ILE:HG22	1:C:66:PHE:N	2.30	0.47
1:C:113:LEU:HB3	1:C:114:PRO:HD2	1.97	0.47
1:D:41:GLU:HG2	1:D:237:GLY:HA3	1.97	0.47
1:B:417:HIS:HB3	1:B:448:PHE:CZ	2.50	0.47
1:C:160:ARG:N	1:C:161:PRO:HD2	2.30	0.47
1:B:83:GLU:C	1:B:85:ASP:H	2.18	0.47
1:D:212:PHE:CD2	1:D:213:PRO:HD2	2.50	0.47
1:C:372:LEU:HD21	1:C:395:LEU:HD21	1.96	0.47
1:C:69:TYR:CD1	1:C:463:MET:HG3	2.50	0.47
1:A:63:HIS:HB2	1:A:218:THR:HG21	1.96	0.47
1:B:162:TYR:HB2	1:B:319:PRO:HB3	1.97	0.47
1:B:207:ASN:O	1:B:208:ALA:C	2.54	0.46
1:D:64:VAL:HG12	1:D:66:PHE:HD2	1.79	0.46
1:B:483:TYR:N	1:B:484:PRO:HD3	2.30	0.46
1:A:114:PRO:O	1:A:118:GLN:HG3	2.15	0.46
1:A:207:ASN:O	1:A:208:ALA:C	2.53	0.46
1:D:207:ASN:O	1:D:208:ALA:C	2.54	0.46
1:B:434:LEU:HB2	1:B:435:PRO:HD3	1.97	0.46
1:C:284:VAL:O	1:C:288:LYS:HG2	2.16	0.46
1:A:64:VAL:HG21	1:A:315:TRP:CZ3	2.51	0.46
1:D:155:ALA:HA	1:D:159:MET:HB2	1.96	0.46
1:C:422:PRO:HA	1:C:426:ARG:HD3	1.98	0.46
1:B:191:VAL:O	1:B:195:VAL:HG23	2.16	0.46
1:A:245:VAL:HG22	1:A:252:VAL:HG22	1.98	0.46
1:A:333:ASN:ND2	5:A:733:HOH:O	2.48	0.46
1:C:392:ILE:O	1:C:395:LEU:HB2	2.15	0.46
1:C:158:PHE:HE2	1:C:159:MET:HE1	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:SER:HA	1:A:339:GLN:HE21	1.80	0.46
1:D:455:VAL:HG22	1:D:460:HIS:HB3	1.98	0.46
1:B:455:VAL:HG22	1:B:460:HIS:HB3	1.97	0.46
1:B:70:LYS:HA	1:B:70:LYS:HD2	1.75	0.46
1:D:79:ALA:HB1	1:D:224:ALA:CB	2.46	0.45
1:C:162:TYR:O	1:C:166:VAL:HG12	2.16	0.45
1:B:91:ARG:HG3	1:B:315:TRP:CH2	2.52	0.45
1:C:92:ILE:HG22	1:C:94:TYR:CE2	2.51	0.45
1:D:91:ARG:HH11	1:D:207:ASN:HB2	1.82	0.45
1:C:56:PHE:CE1	1:C:339:GLN:HB3	2.52	0.45
1:B:220:GLY:HA3	5:B:748:HOH:O	2.15	0.45
1:A:421:THR:HA	1:A:422:PRO:HD3	1.78	0.45
1:C:306:ARG:CD	1:C:333:ASN:HD21	2.30	0.45
1:C:162:TYR:HH	1:C:317:TYR:HD1	1.63	0.45
1:A:25:ARG:HD3	1:A:470:ASP:OD1	2.16	0.45
1:C:28:GLN:NE2	1:C:71:TYR:OH	2.49	0.45
1:C:183:VAL:HG22	3:C:602:UDP:H1'	1.99	0.45
1:B:348:THR:CG2	1:B:357:PRO:HB3	2.46	0.45
1:A:338:ASN:HB2	1:A:339:GLN:HE21	1.82	0.45
1:C:282:GLU:OE2	1:C:436:LYS:HE2	2.16	0.45
1:B:263:LYS:NZ	1:C:507:SER:HB3	2.32	0.45
1:D:508:LYS:CG	1:D:511:LEU:HD22	2.44	0.45
1:D:318:PHE:HE1	1:D:328:ALA:HB3	1.82	0.45
1:B:65:ILE:N	1:B:65:ILE:HD12	2.32	0.45
1:B:69:TYR:CD2	1:B:463:MET:HG3	2.52	0.45
1:D:17:PRO:HG2	2:D:601:FDA:H4'	1.98	0.44
1:A:408:VAL:HG12	1:A:408:VAL:O	2.17	0.44
1:D:408:VAL:HG12	1:D:408:VAL:O	2.17	0.44
1:A:168:ALA:HB1	1:A:377:SER:OG	2.17	0.44
1:C:281:GLN:OE1	1:C:281:GLN:HA	2.17	0.44
1:A:351:LEU:HD12	1:A:355:SER:OG	2.15	0.44
1:A:69:TYR:CD2	1:A:463:MET:HG3	2.52	0.44
1:D:41:GLU:HG2	1:D:237:GLY:CA	2.48	0.44
1:B:46:LEU:HD13	2:B:601:FDA:HM81	2.00	0.44
1:C:346:LEU:HD12	1:C:367:TYR:CZ	2.53	0.44
1:B:468:ALA:O	1:B:472:ILE:HG13	2.18	0.44
1:D:268:THR:HA	1:D:445:ARG:O	2.18	0.44
1:A:280:ASP:O	1:A:284:VAL:HG23	2.18	0.44
1:D:184:ALA:HB2	1:D:204:TRP:CE2	2.53	0.44
1:D:508:LYS:HA	1:D:511:LEU:HD22	2.00	0.44
1:B:59:ASP:HB2	1:B:62:GLY:HA2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:264:LYS:HG3	1:B:472:ILE:HG23	2.00	0.44
1:A:290:LEU:HD13	1:A:451:TRP:CD2	2.52	0.44
1:B:212:PHE:CG	1:B:213:PRO:HD2	2.53	0.44
1:D:249:ASN:OD1	1:D:251:THR:HG23	2.18	0.43
1:A:7:SER:HB2	1:D:514:HIS:HA	2.00	0.43
1:C:470:ASP:HB3	1:C:476:ALA:HB3	2.00	0.43
1:D:142:PHE:HA	1:D:176:CYS:HB3	2.00	0.43
1:D:168:ALA:HB1	1:D:377:SER:OG	2.18	0.43
1:B:183:VAL:HG13	3:B:602:UDP:O2	2.19	0.43
1:C:118:GLN:O	1:C:122:ILE:HG12	2.18	0.43
1:D:222:TRP:HE1	1:D:458:GLN:NE2	2.16	0.43
1:C:455:VAL:O	1:C:455:VAL:HG13	2.19	0.43
1:A:212:PHE:CD2	1:A:213:PRO:HD2	2.54	0.43
1:A:398:THR:O	1:A:399:GLU:HB2	2.19	0.43
1:C:4:PRO:HB2	1:C:6:ILE:O	2.19	0.43
1:D:3:HIS:HA	1:D:4:PRO:HD3	1.79	0.43
1:B:125:MET:HE1	1:B:186:PRO:HB2	2.01	0.43
1:D:115:LYS:O	1:D:119:VAL:HG23	2.19	0.43
1:B:315:TRP:HE3	1:B:334:TYR:HH	1.65	0.43
1:D:455:VAL:HG21	1:D:480:THR:CG2	2.49	0.43
1:A:146:ILE:HD13	1:A:159:MET:HB3	2.01	0.43
1:D:65:ILE:O	1:D:210:PHE:HB2	2.19	0.43
1:A:306:ARG:HD2	1:A:311:GLY:O	2.19	0.42
1:B:457:ASN:HA	2:B:601:FDA:H1'2	2.01	0.42
1:A:130:LEU:HD23	1:B:130:LEU:HD23	2.00	0.42
1:D:66:PHE:CD1	1:D:206:PRO:HB2	2.55	0.42
1:A:142:PHE:CZ	1:A:146:ILE:HD11	2.54	0.42
1:D:440:LYS:O	1:D:441:ASP:HB2	2.19	0.42
1:D:315:TRP:HE1	1:D:317:TYR:HH	1.65	0.42
1:D:359:SER:OG	1:D:361:GLU:HG2	2.19	0.42
1:C:66:PHE:CE2	1:C:68:HIS:NE2	2.81	0.42
1:A:69:TYR:CD1	1:A:463:MET:HG3	2.54	0.42
1:A:138:LYS:HG2	1:A:139:PRO:HD2	2.01	0.42
1:B:142:PHE:O	1:B:146:ILE:HG13	2.19	0.42
1:D:125:MET:HE1	1:D:191:VAL:HG21	2.01	0.42
1:D:445:ARG:O	1:D:449:GLY:HA3	2.19	0.42
1:C:270:ALA:HB1	1:C:272:ASP:OD1	2.19	0.42
1:C:70:LYS:HA	1:C:70:LYS:HD3	1.50	0.42
1:B:104:TYR:CD1	1:B:105:PRO:HA	2.55	0.42
1:B:470:ASP:HB3	1:B:476:ALA:HB3	2.01	0.42
1:D:118:GLN:O	1:D:122:ILE:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:306:ARG:HD2	1:D:311:GLY:O	2.20	0.42
1:C:25:ARG:HD3	1:C:470:ASP:OD1	2.20	0.42
1:B:42:THR:HA	1:B:43:PRO:HD2	1.94	0.42
1:B:79:ALA:HB1	1:B:224:ALA:CB	2.50	0.42
1:B:167:TRP:O	1:B:168:ALA:HB3	2.20	0.41
1:B:91:ARG:NH1	1:B:104:TYR:HE2	2.17	0.41
1:D:71:TYR:HB2	5:D:709:HOH:O	2.19	0.41
1:D:80:LEU:HB3	1:D:85:ASP:HB3	2.03	0.41
1:B:477:VAL:HA	1:C:494:GLU:HG2	2.00	0.41
1:A:477:VAL:HG11	1:D:479:LEU:HD11	2.02	0.41
1:D:104:TYR:CD1	1:D:105:PRO:HA	2.55	0.41
1:A:166:VAL:HG23	1:A:326:TYR:CZ	2.55	0.41
1:A:218:THR:O	1:A:221:ILE:HB	2.21	0.41
1:A:272:ASP:OD1	1:A:273:PHE:N	2.54	0.41
1:C:241:LYS:HB3	1:C:255:GLN:HB2	2.02	0.41
1:C:146:ILE:HD13	1:C:159:MET:HB3	2.01	0.41
1:B:430:LEU:HD11	1:B:451:TRP:HB3	2.02	0.41
1:D:133:ARG:HG3	1:D:133:ARG:O	2.19	0.41
1:C:26:LEU:HD13	1:C:34:TRP:HB2	2.03	0.41
1:C:283:LEU:CD1	1:C:437:LEU:HD21	2.51	0.41
1:D:107:GLN:NE2	1:D:184:ALA:HB3	2.24	0.41
1:A:127:ASP:OD1	1:B:189:LYS:HE3	2.21	0.41
1:D:303:ARG:NH2	1:D:346:LEU:O	2.39	0.41
1:C:138:LYS:HG2	1:C:139:PRO:HD2	2.02	0.41
1:B:332:SER:HB3	1:B:369:SER:H	1.85	0.41
4:C:601:FAD:O4'	4:C:601:FAD:O2'	2.35	0.41
1:B:315:TRP:HE1	1:B:317:TYR:HH	1.69	0.41
1:B:455:VAL:O	1:B:460:HIS:HB3	2.21	0.41
1:C:445:ARG:HH21	1:C:478:GLU:CD	2.24	0.41
1:A:70:LYS:HD2	1:A:70:LYS:HA	1.79	0.41
1:A:60:VAL:HG12	1:A:60:VAL:O	2.21	0.41
1:D:6:ILE:HG22	1:D:7:SER:N	2.36	0.41
1:A:160:ARG:N	1:A:161:PRO:HD2	2.36	0.41
1:B:17:PRO:HG2	2:B:601:FDA:H4'	2.03	0.41
1:D:461:SER:O	1:D:464:LEU:HB2	2.21	0.41
1:B:282:GLU:OE2	1:B:436:LYS:HE2	2.20	0.40
1:A:383:ASN:HB3	1:A:386:THR:OG1	2.21	0.40
1:B:66:PHE:CD1	1:B:206:PRO:HB2	2.56	0.40
1:D:109:ASN:C	1:D:111:SER:N	2.74	0.40
1:B:91:ARG:NH2	1:B:204:TRP:O	2.47	0.40
1:B:91:ARG:HD3	1:B:207:ASN:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:ASP:OD2	1:A:263:LYS:NZ	2.51	0.40
1:B:485:ASP:OD1	5:B:720:HOH:O	2.21	0.40
1:D:221:ILE:O	1:D:225:VAL:HG23	2.22	0.40
1:D:456:GLY:O	1:D:457:ASN:CB	2.69	0.40
1:B:138:LYS:HG2	1:B:139:PRO:HD2	2.04	0.40
1:A:306:ARG:CD	1:A:333:ASN:HD21	2.31	0.40
1:B:309:ARG:HH21	1:B:402:LYS:HE3	1.87	0.40
1:A:122:ILE:HG13	1:B:196:ILE:HD11	2.03	0.40
1:B:21:GLY:HA2	1:B:462:PHE:CZ	2.56	0.40
1:A:158:PHE:HE2	1:A:159:MET:HE1	1.86	0.40
1:D:70:LYS:HD2	1:D:70:LYS:HA	1.85	0.40
1:C:212:PHE:CG	1:C:213:PRO:HD2	2.56	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	515/517 (100%)	494 (96%)	19 (4%)	2 (0%)	39	72
1	B	508/517 (98%)	487 (96%)	18 (4%)	3 (1%)	30	62
1	C	514/517 (99%)	486 (95%)	25 (5%)	3 (1%)	30	62
1	D	511/517 (99%)	479 (94%)	29 (6%)	3 (1%)	30	62
All	All	2048/2068 (99%)	1946 (95%)	91 (4%)	11 (0%)	34	67

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	457	ASN
1	B	457	ASN
1	C	457	ASN

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Mol	Chain	Res	Type
1	D	457	ASN
1	B	208	ALA
1	D	208	ALA
1	D	513	HIS
1	A	208	ALA
1	B	84	ASP
1	C	62	GLY
1	C	180	GLY

### 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	439/439 (100%)	425 (97%)	14 (3%)	46	78
1	B	432/439 (98%)	415 (96%)	17 (4%)	39	72
1	C	438/439 (100%)	416 (95%)	22 (5%)	30	61
1	D	435/439 (99%)	414 (95%)	21 (5%)	31	63
All	All	1744/1756 (99%)	1670 (96%)	74 (4%)	36	68

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	ARG
1	A	111	SER
1	A	134	VAL
1	A	149	MET
1	A	209	THR
1	A	286	LEU
1	A	302	VAL
1	A	339	GLN
1	A	382	VAL
1	A	450	SER
1	A	455	VAL
1	A	470	ASP
1	A	477	VAL

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Mol	Chain	Res	Type
1	A	510	GLN
1	B	25	ARG
1	B	111	SER
1	B	123	ASP
1	B	134	VAL
1	B	149	MET
1	B	179	LEU
1	B	286	LEU
1	B	288	LYS
1	B	302	VAL
1	B	339	GLN
1	B	356	ARG
1	B	382	VAL
1	B	450	SER
1	B	455	VAL
1	B	470	ASP
1	B	477	VAL
1	B	506	LYS
1	C	3	HIS
1	C	7	SER
1	C	25	ARG
1	C	66	PHE
1	C	90	GLN
1	C	100	GLN
1	C	134	VAL
1	C	149	MET
1	C	169	VAL
1	C	179	LEU
1	C	200	THR
1	C	286	LEU
1	C	339	GLN
1	C	350	GLN
1	C	360	THR
1	C	382	VAL
1	C	438	GLN
1	C	450	SER
1	C	455	VAL
1	C	477	VAL
1	C	507	SER
1	C	517	HIS
1	D	3	HIS
1	D	25	ARG

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Mol	Chain	Res	Type
1	D	88	THR
1	D	111	SER
1	D	134	VAL
1	D	149	MET
1	D	179	LEU
1	D	209	THR
1	D	286	LEU
1	D	302	VAL
1	D	309	ARG
1	D	339	GLN
1	D	382	VAL
1	D	390	ASP
1	D	422	PRO
1	D	450	SER
1	D	455	VAL
1	D	470	ASP
1	D	477	VAL
1	D	513	HIS
1	D	514	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	GLN
1	A	90	GLN
1	A	98	GLN
1	A	118	GLN
1	A	296	HIS
1	A	333	ASN
1	A	338	ASN
1	A	339	GLN
1	A	393	GLN
1	A	397	ASN
1	A	412	HIS
1	A	458	GLN
1	B	28	GLN
1	B	98	GLN
1	B	118	GLN
1	B	248	ASN
1	B	296	HIS
1	B	333	ASN
1	B	338	ASN

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Mol	Chain	Res	Type
1	B	339	GLN
1	B	383	ASN
1	B	384	GLN
1	B	393	GLN
1	B	397	ASN
1	B	412	HIS
1	B	471	ASN
1	C	3	HIS
1	C	28	GLN
1	C	90	GLN
1	C	98	GLN
1	C	118	GLN
1	C	203	ASN
1	C	296	HIS
1	C	333	ASN
1	C	338	ASN
1	C	339	GLN
1	C	358	GLN
1	C	412	HIS
1	C	417	HIS
1	C	458	GLN
1	C	471	ASN
1	C	515	HIS
1	D	27	ASN
1	D	28	GLN
1	D	98	GLN
1	D	118	GLN
1	D	296	HIS
1	D	333	ASN
1	D	338	ASN
1	D	339	GLN
1	D	384	GLN
1	D	412	HIS
1	D	417	HIS
1	D	458	GLN
1	D	471	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 ⓘ

8 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	$\# Z  > 2$
2	FDA	A	601	-	48,58,58	2.34	21 (43%)	54,89,89	2.51	17 (31%)
3	UDP	A	602	-	18,26,26	1.18	1 (5%)	26,40,40	1.48	4 (15%)
2	FDA	B	601	-	48,58,58	2.33	23 (47%)	54,89,89	2.40	15 (27%)
3	UDP	B	602	-	18,26,26	1.18	1 (5%)	26,40,40	1.45	2 (7%)
4	FAD	C	601	-	48,58,58	2.20	12 (25%)	54,89,89	2.15	14 (25%)
3	UDP	C	602	-	18,26,26	1.18	1 (5%)	26,40,40	1.49	2 (7%)
2	FDA	D	601	-	48,58,58	2.30	22 (45%)	54,89,89	2.44	16 (29%)
3	UDP	D	602	-	18,26,26	1.20	1 (5%)	26,40,40	1.58	2 (7%)

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
2	FDA	A	601	-	-	0/30/50/50	0/6/6/6
3	UDP	A	602	-	-	0/12/32/32	0/2/2/2
2	FDA	B	601	-	-	0/30/50/50	0/6/6/6
3	UDP	B	602	-	-	0/12/32/32	0/2/2/2
4	FAD	C	601	-	-	0/30/50/50	0/6/6/6

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	UDP	C	602	-	-	0/12/32/32	0/2/2/2
2	FDA	D	601	-	-	0/30/50/50	0/6/6/6
3	UDP	D	602	-	-	0/12/32/32	0/2/2/2

All (82) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	601	FAD	C1'-N10	-6.80	1.41	1.48
2	A	601	FDA	P-O1P	-5.60	1.30	1.51
2	B	601	FDA	P-O1P	-5.52	1.31	1.51
2	D	601	FDA	P-O1P	-5.50	1.31	1.51
4	C	601	FAD	C2B-C3B	-4.99	1.39	1.53
2	B	601	FDA	PA-O1A	-4.25	1.35	1.51
2	A	601	FDA	C10-N10	-4.25	1.34	1.39
2	B	601	FDA	PA-O2A	-4.19	1.37	1.54
2	B	601	FDA	C10-N10	-4.13	1.34	1.39
2	D	601	FDA	PA-O1A	-4.10	1.36	1.51
2	A	601	FDA	PA-O1A	-4.08	1.36	1.51
2	A	601	FDA	PA-O2A	-4.05	1.37	1.54
2	D	601	FDA	PA-O2A	-4.01	1.37	1.54
2	B	601	FDA	P-O2P	-3.64	1.39	1.54
2	D	601	FDA	C10-N10	-3.55	1.35	1.39
2	A	601	FDA	P-O2P	-3.51	1.40	1.54
2	A	601	FDA	O4'-C4'	-3.43	1.35	1.43
2	B	601	FDA	O4'-C4'	-3.42	1.35	1.43
2	D	601	FDA	P-O2P	-3.41	1.40	1.54
2	D	601	FDA	O4'-C4'	-3.38	1.35	1.43
4	C	601	FAD	C9A-C5X	-3.36	1.35	1.42
2	D	601	FDA	C6-C5X	-3.34	1.36	1.41
2	B	601	FDA	C1'-N10	-3.34	1.44	1.48
2	B	601	FDA	C6-C5X	-3.20	1.36	1.41
2	A	601	FDA	C1'-N10	-3.16	1.45	1.48
2	A	601	FDA	O3B-C3B	-3.14	1.35	1.43
2	D	601	FDA	O3B-C3B	-3.08	1.35	1.43
4	C	601	FAD	O3'-C3'	-3.06	1.35	1.43
2	D	601	FDA	C1'-N10	-2.94	1.45	1.48
2	B	601	FDA	O3B-C3B	-2.93	1.35	1.43
2	B	601	FDA	O5B-C5B	-2.86	1.33	1.44
2	A	601	FDA	C6-C5X	-2.84	1.37	1.41
2	D	601	FDA	O5B-C5B	-2.81	1.33	1.44
2	A	601	FDA	O5B-C5B	-2.81	1.33	1.44
2	A	601	FDA	C5A-N7A	-2.78	1.30	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	FDA	C5A-N7A	-2.74	1.30	1.39
2	B	601	FDA	P-O5'	-2.73	1.46	1.59
2	B	601	FDA	C5A-N7A	-2.73	1.30	1.39
2	A	601	FDA	P-O5'	-2.71	1.46	1.59
2	B	601	FDA	C4A-N3A	-2.69	1.31	1.35
2	A	601	FDA	C4A-N3A	-2.63	1.31	1.35
2	D	601	FDA	P-O5'	-2.61	1.47	1.59
4	C	601	FAD	C4'-C3'	-2.59	1.48	1.53
2	B	601	FDA	C8A-N7A	-2.57	1.29	1.34
2	D	601	FDA	C4A-N3A	-2.55	1.31	1.35
4	C	601	FAD	C9A-N10	-2.54	1.35	1.38
2	A	601	FDA	C8A-N7A	-2.44	1.29	1.34
2	A	601	FDA	C2A-N1A	-2.40	1.29	1.33
2	D	601	FDA	C8A-N7A	-2.39	1.30	1.34
2	A	601	FDA	O4-C4	-2.34	1.19	1.24
2	A	601	FDA	C5A-C4A	-2.29	1.35	1.40
2	B	601	FDA	O4-C4	-2.26	1.19	1.24
2	B	601	FDA	C5A-C4A	-2.26	1.35	1.40
2	D	601	FDA	O4-C4	-2.25	1.19	1.24
2	D	601	FDA	C5A-C4A	-2.23	1.35	1.40
2	A	601	FDA	O5'-C5'	-2.20	1.35	1.44
2	B	601	FDA	C2A-N1A	-2.19	1.29	1.33
2	D	601	FDA	C2A-N1A	-2.18	1.29	1.33
2	D	601	FDA	O5'-C5'	-2.17	1.35	1.44
2	B	601	FDA	O5'-C5'	-2.16	1.36	1.44
2	D	601	FDA	PA-O5B	-2.15	1.49	1.59
2	A	601	FDA	PA-O5B	-2.14	1.49	1.59
2	D	601	FDA	O3'-C3'	-2.14	1.37	1.43
2	B	601	FDA	O3'-C3'	-2.09	1.38	1.43
2	B	601	FDA	PA-O5B	-2.06	1.49	1.59
2	B	601	FDA	O2B-C2B	-2.03	1.38	1.43
2	D	601	FDA	C2'-C3'	2.14	1.57	1.53
2	A	601	FDA	C2'-C3'	2.17	1.57	1.53
2	B	601	FDA	C2'-C3'	2.19	1.57	1.53
4	C	601	FAD	O4'-C4'	2.43	1.48	1.43
4	C	601	FAD	P-O1P	2.44	1.60	1.51
3	A	602	UDP	C4-N3	2.89	1.38	1.33
3	C	602	UDP	C4-N3	2.95	1.38	1.33
3	B	602	UDP	C4-N3	2.97	1.38	1.33
3	D	602	UDP	C4-N3	3.05	1.38	1.33
4	C	601	FAD	C4-C4X	3.43	1.48	1.41
4	C	601	FAD	C7M-C7	4.09	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	FDA	O4B-C1B	4.15	1.46	1.41
4	C	601	FAD	C4-N3	4.58	1.41	1.33
2	A	601	FDA	O4B-C1B	4.65	1.47	1.41
2	D	601	FDA	O4B-C1B	4.93	1.47	1.41
4	C	601	FAD	C10-N1	5.12	1.44	1.35

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	601	FAD	N3A-C2A-N1A	-8.93	122.06	128.89
2	D	601	FDA	N3A-C2A-N1A	-7.88	122.86	128.89
2	A	601	FDA	N3A-C2A-N1A	-7.80	122.92	128.89
2	B	601	FDA	N3A-C2A-N1A	-7.48	123.17	128.89
4	C	601	FAD	O5B-PA-O1A	-4.87	90.72	109.62
2	B	601	FDA	C4-C4X-C10	-4.84	116.84	119.94
2	A	601	FDA	C4-C4X-C10	-4.27	117.21	119.94
2	B	601	FDA	C4X-C4-N3	-3.85	118.33	123.59
4	C	601	FAD	O5'-P-O1P	-3.42	96.33	109.62
2	D	601	FDA	C4X-C4-N3	-3.28	119.11	123.59
3	D	602	UDP	PA-O3A-PB	-3.26	121.73	132.67
2	A	601	FDA	C4X-C4-N3	-3.22	119.19	123.59
2	D	601	FDA	C4-C4X-C10	-3.03	118.00	119.94
3	C	602	UDP	PA-O3A-PB	-2.94	122.82	132.67
4	C	601	FAD	C4B-O4B-C1B	-2.82	106.62	109.72
2	A	601	FDA	P-O3P-PA	-2.68	125.21	132.73
4	C	601	FAD	C4X-C4-N3	-2.62	120.00	123.59
4	C	601	FAD	C4X-C10-N10	-2.53	119.03	120.52
3	A	602	UDP	PA-O3A-PB	-2.45	124.45	132.67
3	B	602	UDP	PA-O3A-PB	-2.35	124.78	132.67
2	D	601	FDA	O4B-C4B-C3B	-2.22	100.68	105.15
2	B	601	FDA	C4A-C5A-N7A	-2.20	107.46	109.48
4	C	601	FAD	C4A-C5A-N7A	-2.12	107.53	109.48
2	D	601	FDA	C4B-O4B-C1B	-2.10	107.41	109.72
3	A	602	UDP	C6-N1-C2	-2.10	117.88	121.28
2	A	601	FDA	C4A-C5A-N7A	-2.06	107.59	109.48
2	A	601	FDA	C4B-O4B-C1B	-2.02	107.49	109.72
2	A	601	FDA	O5'-P-O1P	-2.02	101.79	109.62
2	D	601	FDA	C2B-C3B-C4B	-2.00	98.49	102.61
2	B	601	FDA	C1'-N10-C9A	2.00	121.11	118.86
3	A	602	UDP	O2A-PA-O3A	2.09	114.55	105.09
2	D	601	FDA	C4X-N5-C5X	2.11	119.19	116.76
2	B	601	FDA	O5B-C5B-C4B	2.17	117.13	109.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	601	FDA	O3'-C3'-C2'	2.22	114.34	108.75
4	C	601	FAD	C2B-C3B-C4B	2.23	107.20	102.61
2	B	601	FDA	O3P-P-O5'	2.26	108.93	102.94
2	A	601	FDA	C4X-N5-C5X	2.30	119.40	116.76
4	C	601	FAD	C4X-N5-C5X	2.34	119.45	116.76
2	D	601	FDA	C5X-C9A-N10	2.34	119.40	117.62
2	A	601	FDA	O2'-C2'-C1'	2.36	115.74	109.94
2	D	601	FDA	C4-C4X-N5	2.39	121.62	118.72
2	B	601	FDA	O3'-C3'-C2'	2.46	114.94	108.75
2	A	601	FDA	O3'-C3'-C2'	2.66	115.46	108.75
2	B	601	FDA	O2'-C2'-C1'	2.72	116.62	109.94
4	C	601	FAD	O2A-PA-O3P	2.80	117.78	105.09
2	B	601	FDA	O4B-C1B-N9A	2.89	114.16	108.10
4	C	601	FAD	O5B-C5B-C4B	2.94	119.95	109.12
4	C	601	FAD	O2P-P-O3P	2.99	118.66	105.09
4	C	601	FAD	C5X-C9A-N10	3.03	119.92	117.62
2	A	601	FDA	C1'-N10-C9A	3.25	122.51	118.86
2	D	601	FDA	O2'-C2'-C1'	3.42	118.34	109.94
2	A	601	FDA	C4-C4X-N5	3.74	123.26	118.72
2	D	601	FDA	O2'-C2'-C3'	3.91	118.84	109.02
2	A	601	FDA	O2'-C2'-C3'	3.98	119.02	109.02
2	B	601	FDA	O2'-C2'-C3'	3.99	119.05	109.02
2	B	601	FDA	C4-C4X-N5	4.09	123.68	118.72
2	A	601	FDA	O4B-C1B-N9A	4.23	116.96	108.10
2	D	601	FDA	O4B-C1B-N9A	4.24	116.96	108.10
2	B	601	FDA	O3B-C3B-C4B	4.55	124.71	111.05
2	A	601	FDA	O3B-C3B-C4B	4.82	125.50	111.05
2	D	601	FDA	O3B-C3B-C4B	5.03	126.15	111.05
2	A	601	FDA	C5B-C4B-C3B	5.09	135.41	115.21
2	D	601	FDA	C5B-C4B-C3B	5.21	135.89	115.21
2	B	601	FDA	C5B-C4B-C3B	5.27	136.13	115.21
3	A	602	UDP	C4-N3-C2	5.46	119.55	114.14
4	C	601	FAD	C4-N3-C2	5.59	120.08	115.25
3	B	602	UDP	C4-N3-C2	5.75	119.83	114.14
3	C	602	UDP	C4-N3-C2	5.81	119.90	114.14
3	D	602	UDP	C4-N3-C2	6.15	120.23	114.14
2	B	601	FDA	C4-N3-C2	7.75	121.94	115.25
2	D	601	FDA	C4-N3-C2	8.09	122.24	115.25
2	A	601	FDA	C4-N3-C2	8.24	122.37	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	FDA	2	0
3	A	602	UDP	1	0
2	B	601	FDA	5	0
3	B	602	UDP	1	0
4	C	601	FAD	3	0
3	C	602	UDP	2	0
2	D	601	FDA	3	0
3	D	602	UDP	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
1	A	517/517 (100%)	0.24	19 (3%)	45	38	18, 44, 85, 112	0
1	B	510/517 (98%)	0.15	16 (3%)	52	46	17, 43, 83, 112	0
1	C	516/517 (99%)	0.27	43 (8%)	14	9	18, 45, 94, 152	0
1	D	513/517 (99%)	0.21	24 (4%)	35	28	19, 49, 88, 126	0
All	All	2056/2068 (99%)	0.22	102 (4%)	32	25	17, 46, 88, 152	0

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	507	SER	7.6
1	B	511	LEU	7.3
1	C	514	HIS	5.9
1	C	2	THR	5.1
1	C	184	ALA	4.9
1	D	511	LEU	4.8
1	D	514	HIS	4.5
1	B	509	ALA	4.5
1	A	358	GLN	4.4
1	A	511	LEU	4.3
1	C	515	HIS	4.2
1	C	201	ALA	4.1
1	C	202	GLY	4.0
1	D	310	ILE	4.0
1	C	183	VAL	3.8
1	A	2	THR	3.7
1	D	201	ALA	3.7
1	C	511	LEU	3.7
1	C	304	GLY	3.6
1	D	280	ASP	3.5
1	B	308	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	2	THR	3.4
1	C	516	HIS	3.3
1	B	309	ARG	3.3
1	B	510	GLN	3.3
1	C	506	LYS	3.3
1	A	62	GLY	3.3
1	C	186	PRO	3.2
1	C	512	GLU	3.2
1	C	358	GLN	3.1
1	C	309	ARG	3.1
1	D	83	GLU	3.1
1	C	517	HIS	2.9
1	C	62	GLY	2.8
1	D	183	VAL	2.8
1	D	308	GLU	2.8
1	C	510	GLN	2.8
1	C	185	ALA	2.8
1	C	206	PRO	2.8
1	C	179	LEU	2.8
1	A	516	HIS	2.7
1	A	283	LEU	2.7
1	A	281	GLN	2.7
1	C	359	SER	2.7
1	C	361	GLU	2.7
1	D	62	GLY	2.6
1	D	202	GLY	2.6
1	B	2	THR	2.6
1	C	207	ASN	2.6
1	D	276	GLU	2.6
1	B	110	ILE	2.6
1	C	106	PHE	2.6
1	D	110	ILE	2.5
1	C	199	LYS	2.5
1	A	201	ALA	2.5
1	D	281	GLN	2.5
1	D	207	ASN	2.5
1	C	115	LYS	2.5
1	D	513	HIS	2.5
1	B	198	GLY	2.5
1	A	515	HIS	2.4
1	A	512	GLU	2.4
1	D	512	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	3	HIS	2.4
1	C	197	LEU	2.4
1	B	353	ASP	2.4
1	C	116	GLU	2.4
1	C	513	HIS	2.4
1	B	202	GLY	2.4
1	A	341	GLU	2.4
1	D	204	TRP	2.3
1	A	200	THR	2.3
1	C	107	GLN	2.3
1	A	82	LYS	2.3
1	D	116	GLU	2.3
1	B	199	LYS	2.3
1	C	321	ASP	2.3
1	C	509	ALA	2.3
1	B	204	TRP	2.2
1	B	201	ALA	2.2
1	C	308	GLU	2.2
1	B	196	ILE	2.2
1	A	321	ASP	2.2
1	C	305	SER	2.2
1	A	119	VAL	2.2
1	C	204	TRP	2.2
1	A	508	LYS	2.1
1	C	205	GLY	2.1
1	A	199	LYS	2.1
1	D	291	PHE	2.1
1	B	341	GLU	2.1
1	D	244	LYS	2.1
1	C	364	GLU	2.1
1	C	401	LEU	2.1
1	C	508	LYS	2.1
1	D	82	LYS	2.1
1	C	200	THR	2.1
1	A	506	LYS	2.1
1	C	140	LYS	2.1
1	A	61	GLY	2.1
1	D	283	LEU	2.0
1	D	309	ARG	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( $\text{\AA}^2$ )	Q<0.9
3	UDP	C	602	25/25	0.81	0.25	0.33	68,99,141,156	0
2	FDA	D	601	53/53	0.97	0.16	0.04	32,53,78,99	0
4	FAD	C	601	53/53	0.98	0.17	0.04	16,39,65,74	0
2	FDA	A	601	53/53	0.97	0.18	0.03	17,38,65,71	0
2	FDA	B	601	53/53	0.98	0.18	-0.20	13,33,56,67	0
3	UDP	D	602	25/25	0.91	0.18	-0.30	55,95,117,134	0
3	UDP	A	602	25/25	0.94	0.17	-0.50	23,66,98,123	0
3	UDP	B	602	25/25	0.92	0.18	-0.54	45,79,109,134	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.