



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2018 – 02:10 pm GMT

PDB ID : 1Y1Q  
Title : Crystal Structure of the Uridine Phosphorylase from Salmonella Typhimurium in Complex with Uridine-5p-monophosphate and Sulfate Ion at 2.35Å Resolution  
Authors : Gabdoulkhakov, A.G.; Dontsova, M.V.; Kachalova, G.S.; Betzel, C.; Ealick, S.E.; Mikhailov, A.M.  
Deposited on : 2004-11-19  
Resolution : 2.35 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

<https://www.wwpdb.org/validation/2017/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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk31020  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk31020

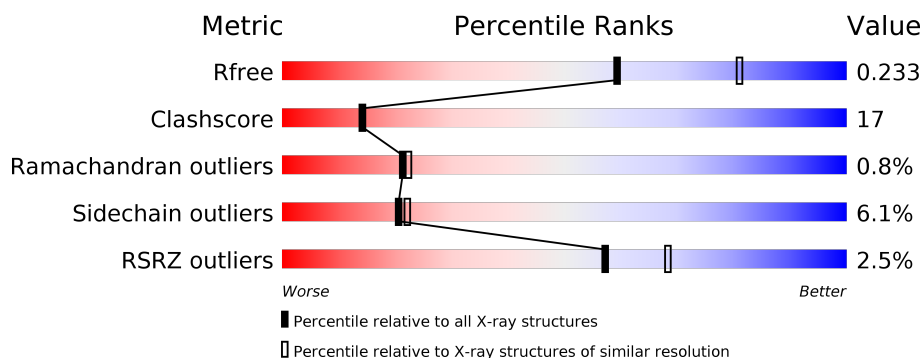
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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))
$R_{free}$	111664	1015 (2.36-2.36)
Clashscore	122126	1081 (2.36-2.36)
Ramachandran outliers	120053	1066 (2.36-2.36)
Sidechain outliers	120020	1067 (2.36-2.36)
RSRZ outliers	108989	1002 (2.36-2.36)

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	253	<div> <div>4%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div>• •</div> </div> </div>
1	B	253	<div> <div>3%</div> <div> <div></div> <div>62%</div> <div>30%</div> <div>• 6%</div> </div> </div>
1	C	253	<div> <div>2%</div> <div> <div></div> <div>62%</div> <div>29%</div> <div>• 5%</div> </div> </div>
1	D	253	<div> <div>4%</div> <div> <div></div> <div>63%</div> <div>29%</div> <div>• •</div> </div> </div>
1	E	253	<div> <div>%</div> <div> <div></div> <div>64%</div> <div>27%</div> <div>• 6%</div> </div> </div>
1	F	253	<div> <div>%</div> <div> <div></div> <div>66%</div> <div>28%</div> <div>• •</div> </div> </div>

## 2 Entry composition [i](#)

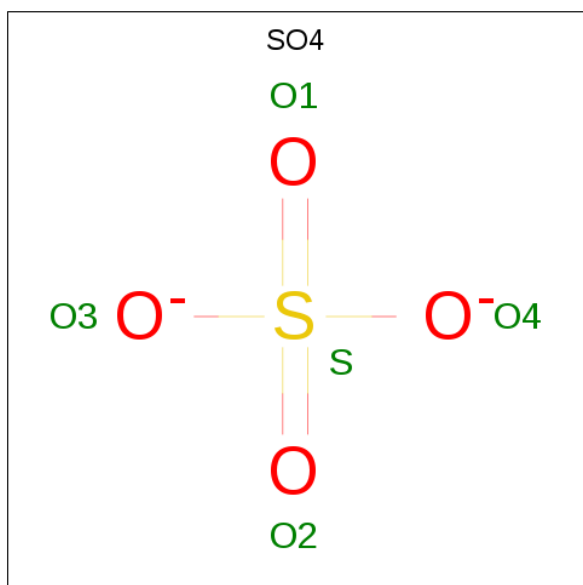
There are 4 unique types of molecules in this entry. The entry contains 11160 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Uridine phosphorylase.

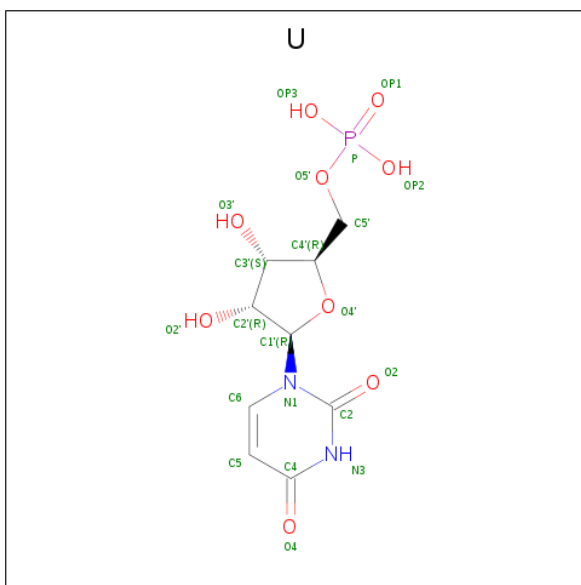
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1877	1174	330	361	12			
1	B	239	Total	C	N	O	S	0	0	0
			1789	1121	315	342	11			
1	C	240	Total	C	N	O	S	0	0	0
			1798	1126	317	344	11			
1	D	245	Total	C	N	O	S	0	0	0
			1836	1149	323	352	12			
1	E	238	Total	C	N	O	S	0	0	0
			1782	1117	314	340	11			
1	F	244	Total	C	N	O	S	0	0	0
			1830	1146	322	351	11			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0

- Molecule 3 is URIDINE-5'-MONOPHOSPHATE (three-letter code: U) (formula: C<sub>9</sub>H<sub>13</sub>N<sub>2</sub>O<sub>9</sub>P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C N O P 21 9 2 9 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	32	Total O 32 32	0	0
4	B	34	Total O 34 34	0	0
4	C	30	Total O 30 30	0	0
4	D	35	Total O 35 35	0	0
4	E	35	Total O 35 35	0	0

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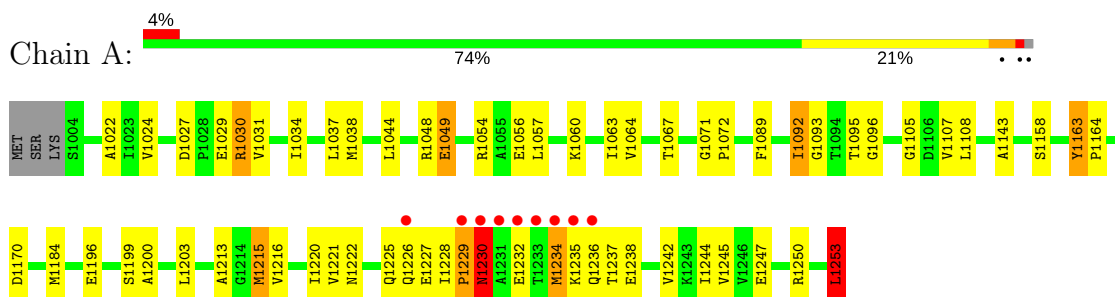
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	41	Total	O	0	0
			41	41		

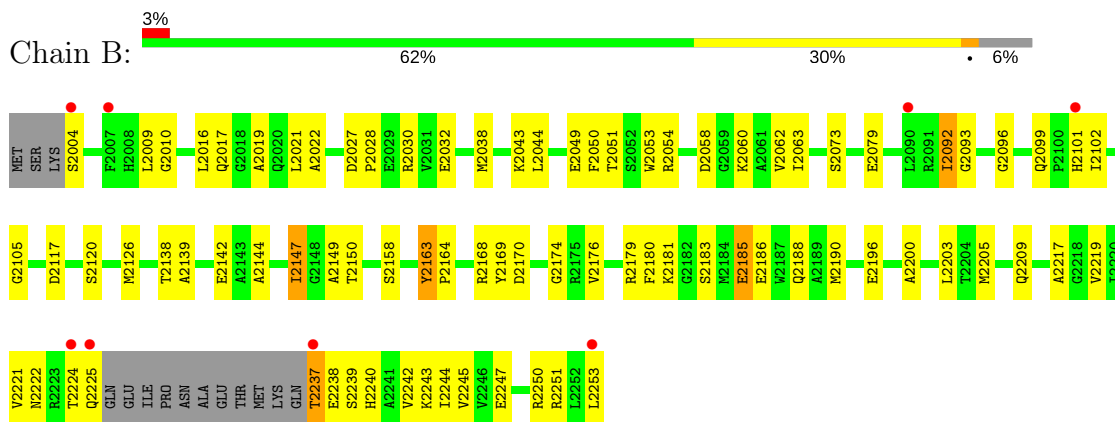
### 3 Residue-property plots

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.

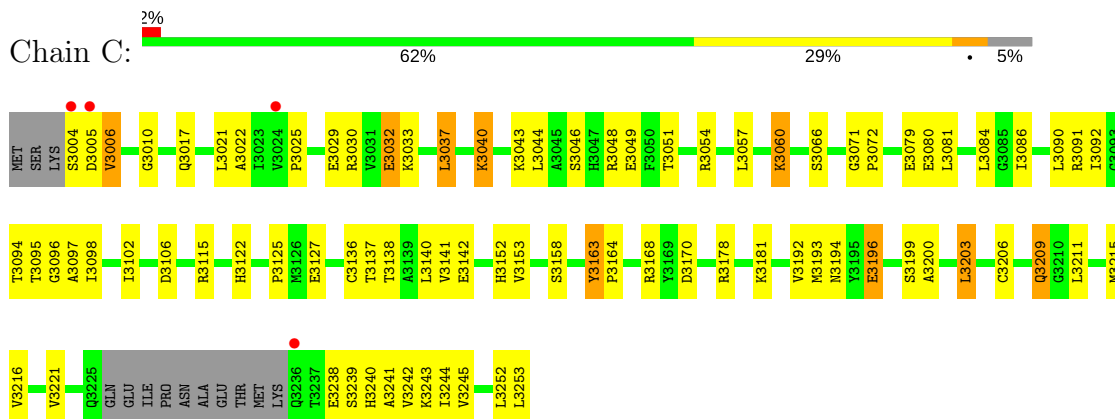
#### • Molecule 1: Uridine phosphorylase



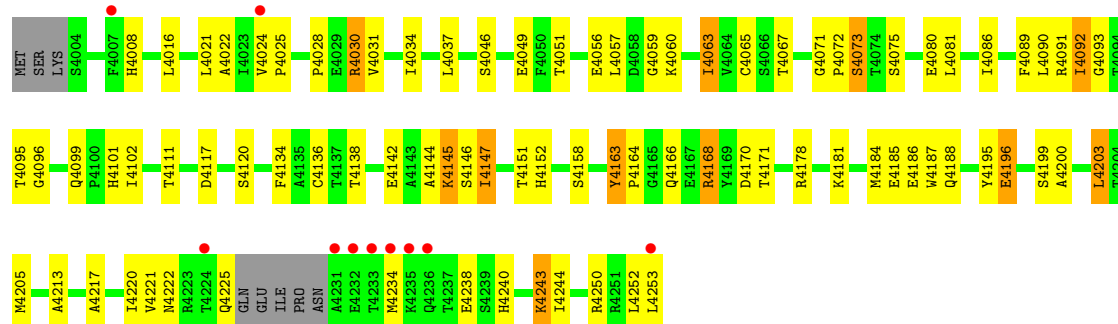
#### • Molecule 1: Uridine phosphorylase



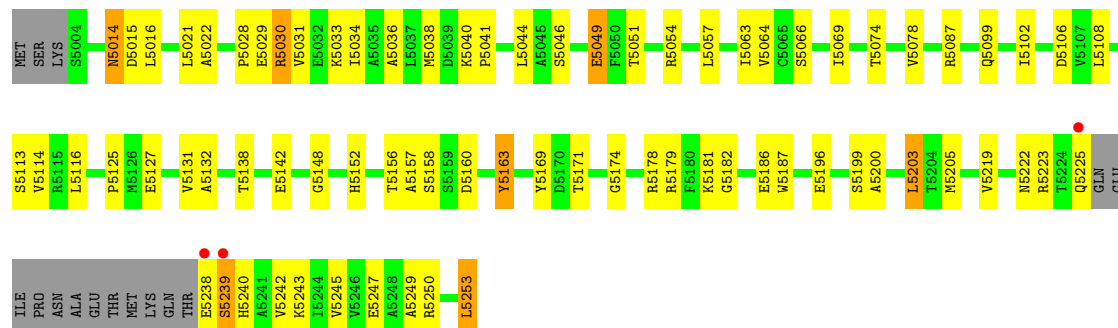
#### • Molecule 1: Uridine phosphorylase



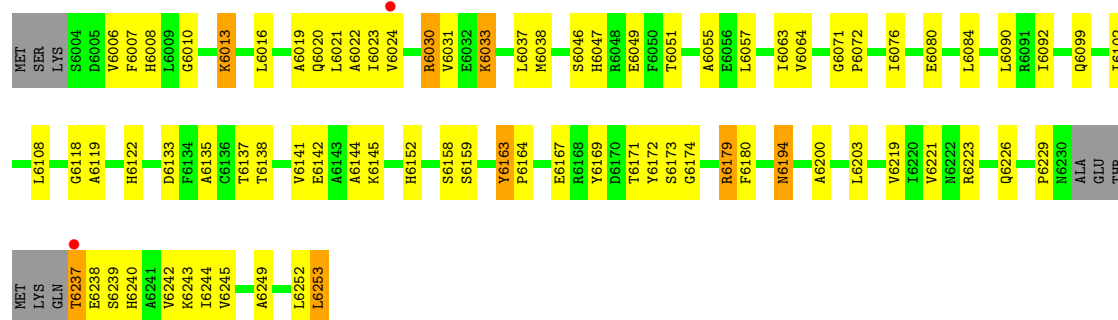
## ● Molecule 1: Uridine phosphorylase

Chain D: 

## ● Molecule 1: Uridine phosphorylase

Chain E: 

## ● Molecule 1: Uridine phosphorylase

Chain F: 

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.37Å 123.73Å 134.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.66 – 2.35 28.77 – 2.29	Depositor EDS
% Data completeness (in resolution range)	97.6 (28.66-2.35) 97.5 (28.77-2.29)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.02 (at 2.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.194 , 0.234 0.194 , 0.233	Depositor DCC
$R_{free}$ test set	3020 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.6	Xtriage
Anisotropy	0.597	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 68.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	11160	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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, 0.333 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: SO4

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	0.35	0/1907	0.67	1/2584 (0.0%)
1	B	0.36	0/1817	0.63	0/2461
1	C	0.33	0/1826	0.63	0/2473
1	D	0.35	0/1864	0.65	0/2523
1	E	0.38	0/1810	0.64	0/2451
1	F	0.36	0/1859	0.62	0/2519
All	All	0.35	0/11083	0.64	1/15011 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1253	LEU	N-CA-C	6.03	127.27	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	1877	0	1887	59	0
1	B	1789	0	1800	61	0
1	C	1798	0	1808	73	0
1	D	1836	0	1848	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1782	0	1793	60	0
1	F	1830	0	1838	60	0
2	A	10	0	0	1	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	C	21	0	11	6	0
4	A	32	0	0	0	0
4	B	34	0	0	2	0
4	C	30	0	0	0	0
4	D	35	0	0	1	0
4	E	35	0	0	0	0
4	F	41	0	0	3	0
All	All	11160	0	10985	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 17.

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:A:1049:GLU:HG3	1:E:5049:GLU:HG2	1.09	1.09
1:D:4144:ALA:HA	1:D:4244:ILE:HD12	1.43	1.00
1:A:1049:GLU:HG3	1:E:5049:GLU:CG	1.93	0.98
1:C:3163:TYR:HB2	1:C:3164:PRO:HD3	1.47	0.95
1:A:1049:GLU:CG	1:E:5049:GLU:HG2	1.97	0.92
1:C:3022:ALA:HB2	1:C:3086:ILE:HD13	1.52	0.91
1:B:2049:GLU:HG3	1:D:4049:GLU:HG3	1.53	0.89
1:B:2049:GLU:CG	1:D:4049:GLU:HG3	2.03	0.88
1:F:6099:GLN:HB2	1:F:6102:ILE:HD13	1.56	0.87
1:A:1220:ILE:O	1:A:1229:PRO:HG3	1.76	0.85
1:E:5250:ARG:HA	1:E:5253:LEU:HD22	1.57	0.85
1:B:2105:GLY:HA2	1:B:2237:THR:HB	1.61	0.82
1:D:4030:ARG:O	1:D:4034:ILE:HG12	1.79	0.82
1:F:6194:ASN:HD22	1:F:6194:ASN:N	1.77	0.82
1:A:1238:GLU:O	1:A:1242:VAL:HG23	1.79	0.81
1:A:1049:GLU:OE1	1:E:5069:ILE:HD12	1.81	0.80
1:C:3049:GLU:HG2	1:F:6049:GLU:HB3	1.63	0.80
1:A:1027:ASP:HB3	1:A:1030:ARG:HG2	1.62	0.79
1:C:3158:SER:HB3	1:C:3200:ALA:HB2	1.65	0.78
1:A:1048:ARG:HD3	1:E:5069:ILE:HD11	1.64	0.78
1:D:4181:LYS:HB3	1:D:4181:LYS:NZ	1.96	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:6144:ALA:HA	1:F:6244:ILE:HD12	1.64	0.78
1:C:3239:SER:HB3	1:C:3243:LYS:HE3	1.66	0.77
1:A:1230:ASN:ND2	1:A:1230:ASN:H	1.82	0.77
1:B:2158:SER:HB3	1:B:2200:ALA:HB2	1.67	0.77
1:F:6240:HIS:O	1:F:6244:ILE:HG12	1.86	0.76
1:D:4037:LEU:HD21	1:D:4243:LYS:HE2	1.67	0.76
1:A:1230:ASN:HD22	1:A:1230:ASN:N	1.83	0.75
1:A:1242:VAL:O	1:A:1245:VAL:HG12	1.88	0.74
1:C:3040:LYS:HB2	1:C:3040:LYS:HZ3	1.53	0.73
1:D:4145:LYS:HD2	1:D:4146:SER:N	2.03	0.73
1:F:6158:SER:HB3	1:F:6200:ALA:HB2	1.69	0.73
1:D:4240:HIS:O	1:D:4244:ILE:HG12	1.88	0.73
1:D:4092:ILE:HD13	1:D:4093:GLY:N	2.05	0.72
1:E:5247:GLU:O	1:E:5250:ARG:HG2	1.90	0.72
1:A:1037:LEU:HD22	1:A:1242:VAL:HG12	1.71	0.71
1:E:5099:GLN:HB2	1:E:5102:ILE:HD12	1.73	0.71
1:C:3092:ILE:HD11	1:C:3241:ALA:HB1	1.72	0.70
1:B:2147:ILE:HD11	1:B:2149:ALA:CB	2.21	0.70
1:A:1230:ASN:O	1:A:1234:MET:HB2	1.92	0.69
1:C:3137:THR:O	1:C:3141:VAL:HG23	1.93	0.69
1:E:5125:PRO:HB2	1:E:5127:GLU:OE2	1.93	0.69
1:B:2222:ASN:HB3	1:B:2225:GLN:HB2	1.74	0.68
1:B:2058:ASP:OD1	1:B:2250:ARG:HD2	1.92	0.68
1:E:5138:THR:O	1:E:5142:GLU:HG3	1.93	0.68
1:C:3163:TYR:HA	1:C:3168:ARG:HD2	1.76	0.67
1:A:1158:SER:HB3	1:A:1200:ALA:HB2	1.76	0.67
1:D:4057:LEU:HB3	1:D:4253:LEU:HD11	1.76	0.67
1:F:6239:SER:O	1:F:6243:LYS:HG3	1.95	0.67
1:D:4134:PHE:O	1:D:4138:THR:HG23	1.96	0.66
1:C:3044:LEU:HD21	1:C:3054:ARG:NH1	2.11	0.66
1:D:4147:ILE:HD11	1:D:4243:LYS:HG2	1.76	0.66
1:E:5021:LEU:HD23	1:E:5022:ALA:N	2.10	0.66
1:C:3040:LYS:HB2	1:C:3040:LYS:NZ	2.12	0.65
1:F:6099:GLN:HB2	1:F:6102:ILE:CD1	2.25	0.65
1:B:2093:GLY:O	1:B:2217:ALA:HA	1.96	0.65
1:C:3079:GLU:OE1	1:F:6171:THR:HB	1.96	0.64
1:A:1230:ASN:ND2	1:A:1230:ASN:N	2.41	0.64
1:D:4086:ILE:H	1:D:4086:ILE:HD12	1.62	0.64
1:F:6249:ALA:O	1:F:6253:LEU:HD13	1.97	0.64
1:B:2147:ILE:HD11	1:B:2149:ALA:HB2	1.80	0.63
1:D:4163:TYR:HA	1:D:4168:ARG:HG3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1031:VAL:HG13	1:A:1064:VAL:HG12	1.81	0.63
1:A:1230:ASN:H	1:A:1230:ASN:HD22	1.44	0.63
1:D:4086:ILE:HD12	1:D:4086:ILE:N	2.13	0.62
1:C:3240:HIS:O	1:C:3244:ILE:HG13	1.99	0.62
1:E:5158:SER:HB3	1:E:5200:ALA:HB2	1.81	0.61
1:E:5044:LEU:HD11	1:E:5054:ARG:HB2	1.82	0.61
1:B:2092:ILE:HD13	1:B:2093:GLY:N	2.15	0.61
1:E:5030:ARG:HD3	1:E:5238:GLU:OE2	2.00	0.61
1:C:3017:GLN:HG3	1:C:3054:ARG:NE	2.15	0.61
1:D:4181:LYS:HZ3	1:D:4181:LYS:HB3	1.63	0.61
1:B:2179:ARG:HD2	4:B:9133:HOH:O	1.99	0.61
1:B:2247:GLU:O	1:B:2250:ARG:HB3	2.01	0.60
1:F:6194:ASN:HD22	1:F:6194:ASN:H	1.48	0.60
1:F:6194:ASN:N	1:F:6194:ASN:ND2	2.48	0.60
1:E:5030:ARG:HD3	1:E:5238:GLU:CD	2.23	0.59
1:C:3152:HIS:C	1:C:3193:MET:HE1	2.23	0.59
1:C:3199:SER:HB3	1:C:3215:MET:HE2	1.83	0.59
1:D:4163:TYR:HB2	1:D:4164:PRO:CD	2.33	0.58
1:F:6108:LEU:HD22	1:F:6152:HIS:HB2	1.86	0.58
1:C:3199:SER:HB3	1:C:3215:MET:CE	2.33	0.58
1:A:1027:ASP:HB3	1:A:1030:ARG:CG	2.33	0.58
1:D:4178:ARG:HA	1:D:4181:LYS:HG3	1.86	0.57
1:E:5030:ARG:NE	1:E:5238:GLU:HG2	2.19	0.57
1:A:1229:PRO:HB2	1:A:1235:LYS:HE2	1.85	0.57
1:C:3046:SER:OG	1:C:3051:THR:HG22	2.04	0.57
1:B:2188:GLN:NE2	1:B:2224:THR:HG21	2.20	0.57
1:A:1092:ILE:HD13	1:A:1093:GLY:N	2.20	0.56
1:C:3081:LEU:HB3	1:C:3086:ILE:HD12	1.86	0.56
1:F:6007:PHE:HD2	1:F:6008:HIS:CE1	2.24	0.56
1:C:3152:HIS:HB3	1:C:3193:MET:CE	2.35	0.56
1:B:2239:SER:O	1:B:2243:LYS:HG3	2.06	0.56
1:A:1143:ALA:HB1	1:A:1247:GLU:HB3	1.88	0.56
1:D:4093:GLY:O	1:D:4217:ALA:HA	2.06	0.56
1:C:3163:TYR:CB	1:C:3164:PRO:HD3	2.31	0.55
1:E:5222:ASN:HB3	1:E:5225:GLN:HB2	1.87	0.55
1:C:3238:GLU:O	1:C:3242:VAL:HG23	2.06	0.55
1:C:3095:THR:HA	3:C:8003:U:C5	2.41	0.55
1:D:4046:SER:OG	1:D:4051:THR:HG22	2.06	0.55
1:C:3004:SER:OG	1:C:3010:GLY:HA2	2.06	0.55
1:D:4184:MET:O	1:D:4188:GLN:HG3	2.07	0.55
1:F:6030:ARG:HA	1:F:6033:LYS:HD3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4168:ARG:HD3	4:D:9149:HOH:O	2.05	0.55
1:F:6240:HIS:HA	1:F:6243:LYS:HE2	1.88	0.55
1:B:2060:LYS:HD3	1:B:2253:LEU:HB3	1.89	0.54
1:B:2139:ALA:HA	1:B:2251:ARG:HD2	1.89	0.54
1:C:3122:HIS:HE1	1:F:6159:SER:HB2	1.73	0.54
1:E:5046:SER:OG	1:E:5051:THR:HG22	2.07	0.54
1:F:6226:GLN:NE2	1:F:6229:PRO:HA	2.22	0.54
1:E:5033:LYS:O	1:E:5036:ALA:HB3	2.07	0.54
1:A:1230:ASN:HB2	1:A:1234:MET:HB2	1.89	0.54
1:B:2147:ILE:CD1	1:B:2149:ALA:H	2.21	0.54
1:C:3095:THR:HA	3:C:8003:U:H5	1.72	0.54
1:D:4186:GLU:OE2	1:E:5178:ARG:HB2	2.09	0.53
1:B:2138:THR:O	1:B:2142:GLU:HG2	2.08	0.53
1:B:2096:GLY:HA2	1:B:2221:VAL:O	2.08	0.53
1:E:5178:ARG:HA	1:E:5181:LYS:HE3	1.91	0.53
1:C:3092:ILE:HD11	1:C:3241:ALA:CB	2.38	0.53
1:D:4067:THR:O	1:D:4073:SER:HB3	2.08	0.53
1:D:4151:THR:HG22	1:D:4152:HIS:N	2.24	0.53
1:F:6145:LYS:C	1:F:6145:LYS:HD3	2.30	0.53
1:F:6137:THR:O	1:F:6141:VAL:HG23	2.09	0.53
1:C:3006:VAL:HG12	1:C:3006:VAL:O	2.09	0.52
1:C:3092:ILE:CD1	1:C:3241:ALA:HB1	2.39	0.52
1:A:1232:GLU:O	1:A:1235:LYS:HB2	2.09	0.52
1:F:6023:ILE:O	1:F:6064:VAL:HA	2.08	0.52
1:B:2019:ALA:HB3	1:B:2063:ILE:HD13	1.91	0.52
1:F:6016:LEU:HD11	1:F:6084:LEU:HB3	1.89	0.52
1:A:1049:GLU:HG3	1:E:5049:GLU:CB	2.40	0.52
1:D:4144:ALA:HA	1:D:4244:ILE:CD1	2.28	0.52
1:E:5239:SER:O	1:E:5243:LYS:HG3	2.09	0.52
1:F:6144:ALA:HA	1:F:6244:ILE:CD1	2.38	0.52
1:E:5028:PRO:HA	1:E:5066:SER:HB3	1.92	0.52
1:A:1107:VAL:HG21	1:A:1244:ILE:HD12	1.90	0.52
1:B:2250:ARG:HH11	1:B:2250:ARG:HG2	1.74	0.52
1:B:2022:ALA:HA	1:B:2063:ILE:O	2.10	0.52
1:F:6016:LEU:HA	1:F:6063:ILE:HD11	1.92	0.52
1:C:3091:ARG:HB3	1:C:3215:MET:HG2	1.92	0.51
1:C:3239:SER:HB3	1:C:3243:LYS:CE	2.40	0.51
1:A:1044:LEU:HD11	1:A:1054:ARG:HB2	1.93	0.51
3:C:8003:U:H2'	4:F:9094:HOH:O	2.10	0.51
1:D:4081:LEU:HB3	1:D:4086:ILE:HD13	1.92	0.51
1:D:4220:ILE:HB	1:D:4234:MET:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3136:CYS:HA	1:C:3252:LEU:HD11	1.91	0.51
1:F:6200:ALA:HB3	4:F:9159:HOH:O	2.11	0.51
1:C:3209:GLN:HG2	1:F:6173:SER:HB3	1.93	0.51
1:B:2009:LEU:HD22	1:B:2050:PHE:HB3	1.92	0.51
1:F:6019:ALA:CB	1:F:6063:ILE:HD13	2.41	0.51
1:E:5031:VAL:HG13	1:E:5064:VAL:HG12	1.92	0.50
1:E:5238:GLU:HG3	1:E:5242:VAL:HG21	1.93	0.50
1:D:4117:ASP:OD1	1:D:4120:SER:HB2	2.10	0.50
1:D:4158:SER:HB3	1:D:4200:ALA:HB2	1.93	0.50
1:A:1092:ILE:C	1:A:1092:ILE:HD13	2.32	0.50
1:A:1222:ASN:HB3	1:A:1225:GLN:HG3	1.94	0.50
1:F:6021:LEU:C	1:F:6021:LEU:HD23	2.32	0.50
1:F:6221:VAL:HG23	1:F:6226:GLN:HE21	1.76	0.50
1:D:4025:PRO:HD2	1:D:4065:CYS:O	2.12	0.50
1:E:5030:ARG:CZ	1:E:5238:GLU:HG2	2.42	0.50
1:E:5169:TYR:O	1:E:5174:GLY:HA2	2.12	0.50
1:B:2169:TYR:O	1:B:2174:GLY:HA2	2.11	0.50
1:E:5016:LEU:HA	1:E:5063:ILE:HD11	1.94	0.50
1:D:4181:LYS:HB3	1:D:4181:LYS:HZ2	1.75	0.49
1:F:6119:ALA:O	1:F:6122:HIS:HB2	2.12	0.49
1:A:1038:MET:HG2	1:A:1057:LEU:HD13	1.95	0.49
1:C:3152:HIS:HB3	1:C:3193:MET:HE2	1.95	0.49
1:A:1199:SER:HB3	1:A:1215:MET:HE2	1.94	0.49
1:C:3163:TYR:HB2	1:C:3164:PRO:CD	2.30	0.49
1:A:1158:SER:HA	1:A:1196:GLU:O	2.12	0.49
1:B:2144:ALA:O	1:B:2147:ILE:HD13	2.13	0.49
1:F:6090:LEU:HD11	1:F:6252:LEU:HD12	1.95	0.49
1:A:1029:GLU:C	1:A:1030:ARG:HE	2.17	0.49
1:A:1089:PHE:O	1:A:1213:ALA:HA	2.13	0.49
1:C:3060:LYS:HB2	1:C:3060:LYS:NZ	2.28	0.49
1:F:6024:VAL:HG23	1:F:6024:VAL:O	2.13	0.48
1:D:4142:GLU:O	1:D:4145:LYS:HE3	2.13	0.48
1:E:5078:VAL:HB	1:E:5205:MET:HE1	1.94	0.48
1:C:3178:ARG:HA	1:C:3181:LYS:HE3	1.96	0.48
1:D:4057:LEU:CD2	1:D:4250:ARG:HG2	2.43	0.48
1:B:2163:TYR:HA	1:B:2168:ARG:HD3	1.95	0.48
1:E:5015:ASP:O	1:E:5054:ARG:HD3	2.13	0.48
1:A:1060:LYS:HD3	1:A:1060:LYS:HA	1.64	0.48
1:C:3029:GLU:O	1:C:3033:LYS:HE2	2.12	0.48
1:F:6010:GLY:HA3	1:F:6047:HIS:CD2	2.49	0.48
1:A:1107:VAL:HG21	1:A:1244:ILE:CD1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:5099:GLN:HB2	1:E:5102:ILE:CD1	2.43	0.48
1:A:1037:LEU:CD2	1:A:1242:VAL:HG12	2.41	0.48
1:D:4147:ILE:O	1:D:4147:ILE:CG2	2.61	0.48
1:E:5040:LYS:N	1:E:5041:PRO:CD	2.77	0.48
1:A:1247:GLU:O	1:A:1250:ARG:HB2	2.13	0.48
1:C:3080:GLU:O	1:C:3084:LEU:HG	2.13	0.48
1:A:1030:ARG:HE	1:A:1030:ARG:N	2.12	0.47
1:B:2179:ARG:HG2	1:B:2180:PHE:CD1	2.48	0.47
1:D:4060:LYS:HB2	1:D:4253:LEU:HD13	1.96	0.47
1:B:2183:SER:O	1:B:2186:GLU:HB2	2.14	0.47
1:D:4136:CYS:HA	1:D:4252:LEU:HD11	1.96	0.47
1:B:2028:PRO:HB3	1:B:2051:THR:HG23	1.97	0.47
1:B:2222:ASN:CB	1:B:2225:GLN:HB2	2.43	0.47
1:B:2163:TYR:HB2	1:B:2164:PRO:CD	2.45	0.47
1:E:5074:THR:O	1:E:5078:VAL:HG23	2.15	0.47
1:B:2147:ILE:HD13	1:B:2149:ALA:H	1.80	0.47
1:C:3096:GLY:HA2	1:C:3221:VAL:O	2.15	0.47
1:D:4021:LEU:C	1:D:4021:LEU:HD23	2.35	0.47
1:D:4016:LEU:CD1	1:D:4086:ILE:HD11	2.44	0.47
1:D:4199:SER:O	1:D:4203:LEU:HB2	2.14	0.47
1:E:5114:VAL:HB	1:E:5157:ALA:HA	1.97	0.47
1:F:6033:LYS:H	1:F:6033:LYS:HD2	1.79	0.47
1:B:2044:LEU:HD11	1:B:2054:ARG:HB2	1.96	0.47
1:E:5014:ASN:HA	1:E:5014:ASN:HD22	1.58	0.46
1:D:4095:THR:OG1	1:D:4096:GLY:N	2.47	0.46
1:E:5106:ASP:O	1:E:5219:VAL:HG23	2.15	0.46
1:B:2163:TYR:O	1:B:2168:ARG:HG3	2.14	0.46
1:D:4022:ALA:HA	1:D:4063:ILE:O	2.15	0.46
1:C:3125:PRO:HB2	1:C:3127:GLU:OE1	2.16	0.46
1:F:6242:VAL:O	1:F:6245:VAL:HG12	2.16	0.46
1:F:6006:VAL:HG11	1:F:6080:GLU:HB3	1.98	0.46
1:F:6038:MET:HE1	1:F:6055:ALA:HB3	1.98	0.46
1:A:1221:VAL:HG23	1:A:1229:PRO:HD2	1.96	0.46
2:A:7003:SO4:O4	1:D:4111:THR:HB	2.16	0.46
1:B:2176:VAL:O	1:B:2181:LYS:HG3	2.14	0.46
1:E:5199:SER:O	1:E:5203:LEU:HB2	2.15	0.46
1:B:2032:GLU:HG3	1:B:2053:TRP:CH2	2.49	0.46
1:E:5242:VAL:O	1:E:5245:VAL:HG12	2.16	0.46
1:D:4030:ARG:HD2	1:D:4238:GLU:OE2	2.16	0.46
1:F:6179:ARG:HG2	1:F:6180:PHE:CE1	2.50	0.46
1:B:2043:LYS:HD2	1:B:2053:TRP:NE1	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4089:PHE:O	1:D:4213:ALA:HA	2.16	0.46
1:F:6013:LYS:HE3	1:F:6084:LEU:HA	1.98	0.46
1:F:6223:ARG:HH11	1:F:6223:ARG:HG3	1.80	0.46
1:E:5238:GLU:O	1:E:5242:VAL:HG23	2.16	0.46
1:B:2038:MET:SD	1:B:2062:VAL:HG21	2.56	0.45
1:B:2147:ILE:HD11	1:B:2149:ALA:HB3	1.96	0.45
1:C:3006:VAL:CG1	1:C:3006:VAL:O	2.64	0.45
1:D:4037:LEU:HD21	1:D:4243:LYS:CE	2.40	0.45
1:C:3096:GLY:O	1:C:3194:ASN:HB2	2.17	0.45
1:C:3153:VAL:N	1:C:3193:MET:HE1	2.30	0.45
1:D:4024:VAL:HG23	1:D:4024:VAL:O	2.16	0.45
1:B:2021:LEU:HD23	1:B:2022:ALA:N	2.32	0.45
1:D:4091:ARG:HG3	1:D:4091:ARG:HH11	1.82	0.45
1:C:3097:ALA:HA	1:C:3194:ASN:HB3	1.98	0.45
1:D:4142:GLU:CA	1:D:4145:LYS:HE3	2.46	0.45
1:F:6021:LEU:HD23	1:F:6022:ALA:N	2.32	0.45
1:C:3017:GLN:HG3	1:C:3054:ARG:CD	2.46	0.45
1:C:3097:ALA:HB1	1:C:3102:ILE:HD12	1.99	0.45
1:E:5029:GLU:O	1:E:5033:LYS:HE2	2.16	0.45
1:F:6033:LYS:N	1:F:6033:LYS:HD2	2.32	0.45
1:A:1199:SER:HB3	1:A:1215:MET:CE	2.47	0.45
1:C:3140:LEU:HD22	1:C:3216:VAL:HB	1.99	0.45
1:D:4185:GLU:HA	1:D:4188:GLN:OE1	2.17	0.45
1:D:4196:GLU:CD	1:D:4199:SER:H	2.20	0.45
1:A:1095:THR:HG21	1:A:1108:LEU:HD12	1.99	0.44
1:C:3091:ARG:NH1	1:C:3091:ARG:HG3	2.32	0.44
1:C:3094:THR:O	3:C:8003:U:H5'	2.17	0.44
1:A:1096:GLY:HA2	1:A:1221:VAL:O	2.17	0.44
1:B:2004:SER:N	4:B:9201:HOH:O	2.49	0.44
1:B:2019:ALA:CB	1:B:2063:ILE:HD13	2.47	0.44
1:F:6167:GLU:HG2	1:F:6169:TYR:CE1	2.52	0.44
1:C:3071:GLY:N	1:C:3072:PRO:CD	2.81	0.44
1:D:4099:GLN:HG2	1:D:4101:HIS:CE1	2.53	0.44
1:F:6076:ILE:O	1:F:6080:GLU:HG3	2.17	0.44
1:A:1024:VAL:HB	1:A:1067:THR:CG2	2.48	0.44
1:B:2099:GLN:HB3	1:B:2101:HIS:CE1	2.52	0.44
1:B:2179:ARG:HG2	1:B:2180:PHE:CE1	2.53	0.44
1:A:1072:PRO:HA	1:E:5160:ASP:O	2.17	0.44
1:C:3199:SER:HB2	1:C:3203:LEU:HD22	2.00	0.44
1:E:5031:VAL:HG13	1:E:5064:VAL:CG1	2.48	0.44
1:E:5249:ALA:O	1:E:5253:LEU:HD13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1220:ILE:O	1:A:1229:PRO:CG	2.58	0.44
1:C:3090:LEU:HD11	1:C:3252:LEU:HD12	1.99	0.44
1:D:4075:SER:HA	1:D:4205:MET:SD	2.58	0.44
1:D:4090:LEU:HD11	1:D:4252:LEU:HD12	1.99	0.44
1:B:2242:VAL:O	1:B:2245:VAL:HG12	2.18	0.44
1:C:3206:CYS:HB3	1:C:3211:LEU:O	2.18	0.44
1:B:2102:ILE:CG2	1:B:2219:VAL:HG21	2.48	0.43
1:C:3025:PRO:O	1:C:3066:SER:HA	2.18	0.43
1:C:3138:THR:O	1:C:3142:GLU:HG3	2.18	0.43
1:B:2185:GLU:HA	1:B:2188:GLN:OE1	2.18	0.43
1:C:3095:THR:CA	3:C:8003:U:H5	2.31	0.43
1:D:4091:ARG:HG3	1:D:4091:ARG:NH1	2.33	0.43
1:D:4166:GLN:HG2	1:D:4195:TYR:CD1	2.53	0.43
1:A:1163:TYR:HB2	1:A:1164:PRO:CD	2.48	0.43
1:F:6102:ILE:CG2	1:F:6219:VAL:HG21	2.48	0.43
1:F:6163:TYR:HB2	1:F:6164:PRO:CD	2.48	0.43
1:A:1030:ARG:O	1:A:1034:ILE:HD13	2.18	0.43
1:A:1071:GLY:N	1:A:1072:PRO:CD	2.82	0.43
1:E:5108:LEU:CD2	1:E:5152:HIS:HB2	2.48	0.43
1:A:1105:GLY:HA2	1:A:1237:THR:OG1	2.19	0.43
1:E:5108:LEU:HD23	1:E:5152:HIS:HB2	2.01	0.43
1:B:2021:LEU:C	1:B:2021:LEU:HD23	2.39	0.43
1:D:4102:ILE:HG12	1:D:4152:HIS:CD2	2.53	0.43
1:E:5038:MET:HG2	1:E:5057:LEU:HD13	1.99	0.43
1:F:6046:SER:OG	1:F:6051:THR:HG22	2.18	0.43
1:A:1226:GLN:OE1	1:A:1227:GLU:HG2	2.19	0.43
1:D:4028:PRO:O	1:D:4031:VAL:HG23	2.19	0.43
1:B:2102:ILE:HG22	1:B:2219:VAL:HG21	2.00	0.43
1:B:2250:ARG:NH1	1:B:2250:ARG:HG2	2.33	0.43
1:C:3152:HIS:HB3	1:C:3193:MET:HE1	1.99	0.43
1:B:2186:GLU:O	1:B:2190:MET:HG3	2.19	0.43
1:D:4063:ILE:HD11	1:D:4065:CYS:HB2	2.01	0.43
1:F:6031:VAL:HG13	1:F:6064:VAL:HG12	2.00	0.43
1:C:3196:GLU:HA	3:C:8003:U:C1'	2.49	0.42
1:E:5187:TRP:HA	1:E:5187:TRP:CE3	2.54	0.42
1:F:6049:GLU:HG2	1:F:6049:GLU:H	1.58	0.42
1:E:5113:SER:HA	1:E:5156:THR:O	2.19	0.42
1:F:6057:LEU:HB3	1:F:6253:LEU:HD21	1.99	0.42
1:E:5087:ARG:HH11	1:E:5087:ARG:HG3	1.84	0.42
1:F:6019:ALA:HB3	1:F:6063:ILE:HD13	2.02	0.42
1:D:4071:GLY:N	1:D:4072:PRO:CD	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4008:HIS:HD2	1:D:4080:GLU:OE2	2.03	0.42
1:E:5116:LEU:HB2	1:E:5158:SER:O	2.19	0.42
1:F:6169:TYR:O	1:F:6174:GLY:HA2	2.19	0.42
1:A:1049:GLU:HG3	1:E:5049:GLU:HB3	2.02	0.42
1:C:3091:ARG:HH11	1:C:3091:ARG:HG3	1.84	0.42
1:D:4102:ILE:O	1:D:4222:ASN:ND2	2.52	0.42
1:E:5158:SER:HB3	1:E:5200:ALA:CB	2.48	0.42
1:F:6038:MET:HG2	1:F:6057:LEU:HD13	2.01	0.42
1:C:3040:LYS:CB	1:C:3040:LYS:NZ	2.81	0.42
1:C:3049:GLU:HG2	1:F:6049:GLU:CB	2.43	0.42
1:B:2126:MET:SD	1:C:3127:GLU:HG3	2.59	0.42
1:B:2205:MET:O	1:B:2209:GLN:HG3	2.19	0.42
1:D:4147:ILE:O	1:D:4147:ILE:HG23	2.19	0.42
1:D:4016:LEU:HD13	1:D:4086:ILE:HD11	2.02	0.41
1:D:4037:LEU:CD2	1:D:4243:LYS:HE2	2.42	0.41
1:A:1108:LEU:O	1:A:1216:VAL:HA	2.20	0.41
1:B:2028:PRO:HB3	1:B:2051:THR:CG2	2.50	0.41
1:A:1229:PRO:HB2	1:A:1235:LYS:CE	2.50	0.41
1:A:1250:ARG:HA	1:A:1253:LEU:HD22	2.02	0.41
1:C:3033:LYS:O	1:C:3037:LEU:HD12	2.20	0.41
1:E:5127:GLU:OE2	1:E:5127:GLU:N	2.46	0.41
1:D:4187:TRP:HA	1:D:4187:TRP:CE3	2.55	0.41
1:E:5182:GLY:O	1:E:5186:GLU:HG3	2.20	0.41
1:B:2016:LEU:O	1:B:2017:GLN:HB2	2.21	0.41
1:E:5238:GLU:HG3	1:E:5242:VAL:CG2	2.50	0.41
1:A:1022:ALA:HA	1:A:1063:ILE:O	2.19	0.41
1:B:2079:GLU:OE1	1:D:4171:THR:HB	2.21	0.41
1:C:3211:LEU:HD21	1:F:6172:TYR:CE1	2.55	0.41
1:E:5163:TYR:CD2	1:E:5171:THR:HG22	2.56	0.41
1:E:5034:ILE:HG12	1:E:5242:VAL:HG13	2.02	0.41
1:E:5033:LYS:CD	1:E:5033:LYS:H	2.34	0.41
1:A:1234:MET:C	1:A:1236:GLN:H	2.24	0.41
1:B:2117:ASP:OD1	1:B:2120:SER:HB3	2.21	0.41
1:C:3098:ILE:HD11	1:C:3192:VAL:HB	2.03	0.41
1:C:3239:SER:O	1:C:3243:LYS:HG3	2.21	0.41
1:E:5131:VAL:HG22	1:E:5132:ALA:O	2.20	0.41
1:F:6237:THR:O	1:F:6240:HIS:HB2	2.20	0.41
1:A:1031:VAL:HG13	1:A:1064:VAL:CG1	2.51	0.41
1:B:2004:SER:OG	1:B:2010:GLY:HA2	2.21	0.41
1:B:2240:HIS:O	1:B:2244:ILE:HG13	2.21	0.41
1:C:3048:ARG:HD3	4:F:9105:HOH:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3158:SER:CB	1:C:3200:ALA:HB2	2.45	0.41
1:D:4092:ILE:HD13	1:D:4092:ILE:C	2.42	0.41
1:C:3095:THR:OG1	1:C:3096:GLY:N	2.54	0.40
1:D:4056:GLU:OE2	1:D:4059:GLY:HA2	2.21	0.40
1:A:1228:ILE:HA	1:A:1229:PRO:HD2	1.86	0.40
1:B:2027:ASP:HA	1:B:2028:PRO:HD3	1.94	0.40
1:C:3032:GLU:HG3	1:C:3033:LYS:N	2.36	0.40
1:F:6133:ASP:OD1	1:F:6135:ALA:N	2.54	0.40
1:F:6138:THR:O	1:F:6142:GLU:HG3	2.22	0.40
1:A:1163:TYR:HB2	1:A:1164:PRO:HD3	2.04	0.40
1:C:3021:LEU:HD23	1:C:3021:LEU:C	2.42	0.40
1:D:4057:LEU:HD21	1:D:4250:ARG:HG2	2.03	0.40
1:B:2163:TYR:CB	1:B:2164:PRO:CD	2.99	0.40
1:C:3057:LEU:O	1:C:3253:LEU:HD21	2.22	0.40
1:D:4187:TRP:HA	1:D:4187:TRP:HE3	1.87	0.40
1:F:6071:GLY:N	1:F:6072:PRO:CD	2.84	0.40
1:F:6006:VAL:HB	1:F:6080:GLU:OE1	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/253 (98%)	235 (95%)	10 (4%)	3 (1%)	14	13
1	B	235/253 (93%)	225 (96%)	9 (4%)	1 (0%)	36	41
1	C	236/253 (93%)	218 (92%)	17 (7%)	1 (0%)	36	41
1	D	241/253 (95%)	228 (95%)	11 (5%)	2 (1%)	21	22
1	E	234/253 (92%)	218 (93%)	13 (6%)	3 (1%)	13	11
1	F	240/253 (95%)	227 (95%)	11 (5%)	2 (1%)	21	22
All	All	1434/1518 (94%)	1351 (94%)	71 (5%)	12 (1%)	21	22

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	4163	TYR
1	A	1229	PRO
1	A	1230	ASN
1	A	1163	TYR
1	B	2163	TYR
1	C	3163	TYR
1	E	5163	TYR
1	E	5223	ARG
1	F	6163	TYR
1	D	4221	VAL
1	E	5148	GLY
1	F	6118	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	199/202 (98%)	188 (94%)	11 (6%)	24	26
1	B	189/202 (94%)	178 (94%)	11 (6%)	22	24
1	C	190/202 (94%)	175 (92%)	15 (8%)	13	13
1	D	194/202 (96%)	182 (94%)	12 (6%)	20	21
1	E	188/202 (93%)	179 (95%)	9 (5%)	28	33
1	F	194/202 (96%)	182 (94%)	12 (6%)	20	21
All	All	1154/1212 (95%)	1084 (94%)	70 (6%)	20	22

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1030	ARG
1	A	1049	GLU
1	A	1056	GLU
1	A	1092	ILE
1	A	1170	ASP

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Mol	Chain	Res	Type
1	A	1184	MET
1	A	1203	LEU
1	A	1215	MET
1	A	1230	ASN
1	A	1234	MET
1	A	1253	LEU
1	B	2030	ARG
1	B	2073	SER
1	B	2092	ILE
1	B	2147	ILE
1	B	2150	THR
1	B	2170	ASP
1	B	2185	GLU
1	B	2196	GLU
1	B	2203	LEU
1	B	2237	THR
1	B	2238	GLU
1	C	3005	ASP
1	C	3006	VAL
1	C	3030	ARG
1	C	3032	GLU
1	C	3037	LEU
1	C	3040	LYS
1	C	3043	LYS
1	C	3060	LYS
1	C	3106	ASP
1	C	3115	ARG
1	C	3170	ASP
1	C	3196	GLU
1	C	3203	LEU
1	C	3209	GLN
1	C	3245	VAL
1	D	4030	ARG
1	D	4063	ILE
1	D	4073	SER
1	D	4092	ILE
1	D	4145	LYS
1	D	4147	ILE
1	D	4168	ARG
1	D	4170	ASP
1	D	4196	GLU
1	D	4203	LEU

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Mol	Chain	Res	Type
1	D	4225	GLN
1	D	4243	LYS
1	E	5014	ASN
1	E	5030	ARG
1	E	5049	GLU
1	E	5179	ARG
1	E	5196	GLU
1	E	5203	LEU
1	E	5239	SER
1	E	5240	HIS
1	E	5253	LEU
1	F	6013	LYS
1	F	6020	GLN
1	F	6030	ARG
1	F	6033	LYS
1	F	6037	LEU
1	F	6092	ILE
1	F	6179	ARG
1	F	6194	ASN
1	F	6203	LEU
1	F	6237	THR
1	F	6238	GLU
1	F	6253	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1188	GLN
1	A	1225	GLN
1	A	1230	ASN
1	B	2017	GLN
1	B	2020	GLN
1	B	2152	HIS
1	C	3020	GLN
1	D	4008	HIS
1	D	4020	GLN
1	D	4099	GLN
1	D	4225	GLN
1	E	5014	ASN
1	E	5209	GLN
1	F	6020	GLN
1	F	6047	HIS

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Mol	Chain	Res	Type
1	F	6188	GLN
1	F	6194	ASN
1	F	6226	GLN
1	F	6240	HIS

### 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](#)

5 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	SO4	A	7003	-	4,4,4	0.34	0	6,6,6	0.07	0
2	SO4	A	7004	-	4,4,4	0.36	0	6,6,6	0.11	0
3	U	C	8003	-	17,22,22	1.11	1 (5%)	21,33,33	3.39	2 (9%)
2	SO4	E	7001	-	4,4,4	0.33	0	6,6,6	0.13	0
2	SO4	F	7005	-	4,4,4	0.34	0	6,6,6	0.13	0

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	SO4	A	7003	-	-	0/0/0/0	0/0/0/0
2	SO4	A	7004	-	-	0/0/0/0	0/0/0/0
3	U	C	8003	-	-	0/6/26/26	0/2/2/2
2	SO4	E	7001	-	-	0/0/0/0	0/0/0/0
2	SO4	F	7005	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	8003	U	C4-N3	3.34	1.39	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	8003	U	C5-C4-N3	-3.73	114.51	123.17
3	C	8003	U	C4-N3-C2	14.89	126.95	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	7003	SO4	1	0
3	C	8003	U	6	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	250/253 (98%)	-0.13	9 (3%)	42	56	8, 23, 61, 91	0
1	B	239/253 (94%)	-0.00	8 (3%)	46	60	10, 29, 54, 87	0
1	C	240/253 (94%)	-0.07	4 (1%)	70	79	13, 29, 59, 104	0
1	D	245/253 (96%)	-0.10	10 (4%)	37	50	10, 25, 54, 128	0
1	E	238/253 (94%)	-0.19	3 (1%)	77	85	7, 24, 52, 96	0
1	F	244/253 (96%)	-0.23	2 (0%)	86	92	12, 26, 52, 96	0
All	All	1456/1518 (95%)	-0.12	36 (2%)	57	68	7, 26, 56, 128	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1234	MET	6.9
1	A	1233	THR	6.1
1	D	4232	GLU	5.2
1	D	4233	THR	5.1
1	A	1232	GLU	5.0
1	E	5225	GLN	4.9
1	A	1230	ASN	4.7
1	D	4234	MET	4.4
1	B	2224	THR	4.4
1	A	1231	ALA	4.3
1	B	2007	PHE	4.3
1	D	4235	LYS	4.2
1	A	1236	GLN	3.8
1	A	1229	PRO	3.7
1	C	3236	GLN	3.7
1	B	2225	GLN	3.1
1	D	4236	GLN	3.0
1	E	5238	GLU	2.9
1	C	3024	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	4224	THR	2.7
1	B	2101	HIS	2.6
1	C	3005	ASP	2.6
1	C	3004	SER	2.5
1	B	2253	LEU	2.4
1	D	4007	PHE	2.4
1	F	6237	THR	2.4
1	B	2090	LEU	2.3
1	D	4253	LEU	2.2
1	D	4231	ALA	2.2
1	D	4024	VAL	2.2
1	F	6024	VAL	2.1
1	A	1235	LYS	2.1
1	E	5239	SER	2.1
1	A	1226	GLN	2.1
1	B	2004	SER	2.1
1	B	2237	THR	2.1

## 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	A	7003	5/5	0.81	0.28	109,124,126,126	0
3	U	C	8003	21/21	0.88	0.30	35,58,71,71	0
2	SO4	A	7004	5/5	0.94	0.16	14,60,71,89	0
2	SO4	E	7001	5/5	0.98	0.13	26,50,67,74	0
2	SO4	F	7005	5/5	0.98	0.17	36,54,58,81	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.