



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:56 PM GMT

PDB ID : 4QDV  
Title : Dcps in complex with covalent ligand  
Authors : Liu, S.  
Deposited on : 2014-05-14  
Resolution : 2.80 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

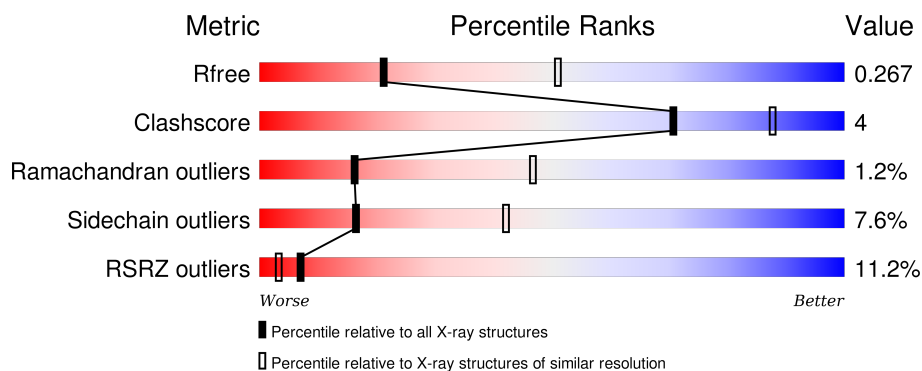
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	337	<div> <div>9%</div> <div>69%</div> <div>15%</div> <div>•</div> <div>15%</div> </div>
1	B	337	<div> <div>6%</div> <div>70%</div> <div>13%</div> <div>•</div> <div>15%</div> </div>
1	C	337	<div> <div>11%</div> <div>68%</div> <div>17%</div> <div>•</div> <div>14%</div> </div>
1	D	337	<div> <div>12%</div> <div>71%</div> <div>15%</div> <div>•</div> <div>13%</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
3	PO4	A	403	-	-	-	X
3	PO4	A	404	-	-	-	X
3	PO4	B	401	-	-	X	-
3	PO4	B	402	-	-	-	X
3	PO4	B	403	-	-	-	X
3	PO4	D	402	-	-	-	X
4	GOL	D	404	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9697 atoms, of which 34 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.

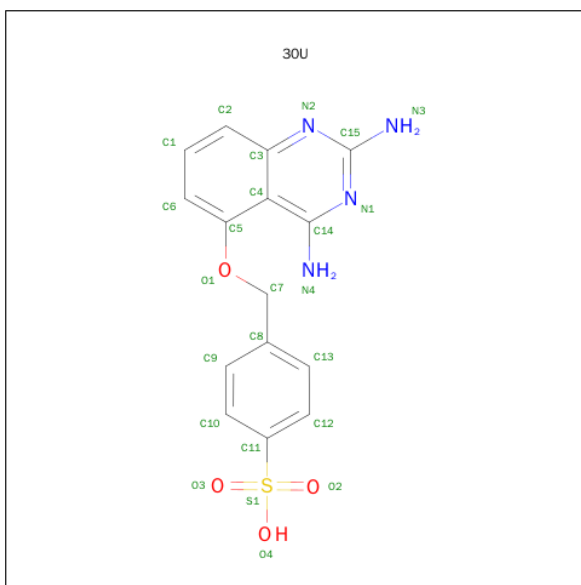
- Molecule 1 is a protein called m7GpppX diphosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	287	Total	C	N	O	S	0	0	0
			2377	1523	425	426	3			
1	B	288	Total	C	N	O	S	0	0	0
			2384	1526	427	428	3			
1	C	289	Total	C	N	O	S	0	0	0
			2389	1529	427	430	3			
1	D	292	Total	C	N	O	S	0	0	0
			2411	1542	430	436	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	EXPRESSION TAG	UNP Q96C86
B	1	GLY	-	EXPRESSION TAG	UNP Q96C86
C	1	GLY	-	EXPRESSION TAG	UNP Q96C86
D	1	GLY	-	EXPRESSION TAG	UNP Q96C86

- Molecule 2 is 4-([(2,4-DIAMINOQUINAZOLIN-5-YL)OXY]METHYL}BENZENESULFONIC ACID (three-letter code: 30U) (formula: C<sub>15</sub>H<sub>14</sub>N<sub>4</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	S	13	0
			36	15	13	4	3	1		
2	D	1	Total	C	H	N	O	S	13	0
			36	15	13	4	3	1		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O P	0	0
			5	4 1		
3	A	1	Total	O P	0	0
			5	4 1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).

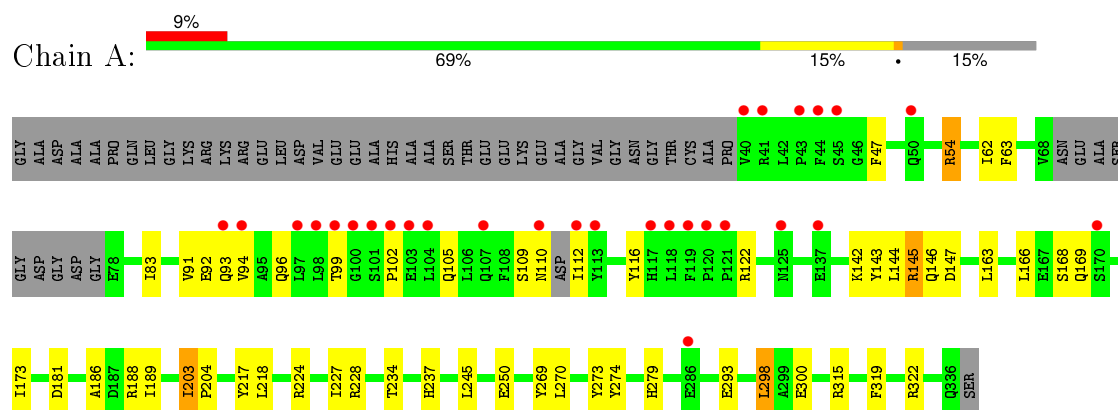


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	C	H	O	0	0
			14	3	8	3		

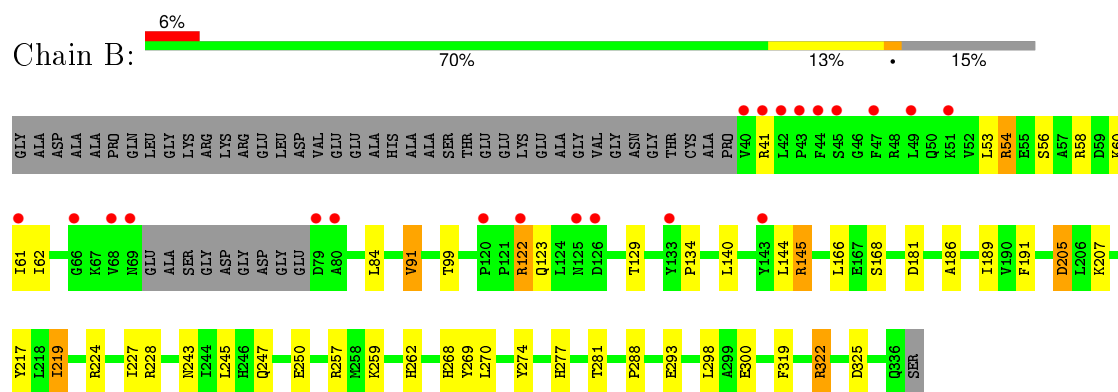
### 3 Residue-property plots [i](#)

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.

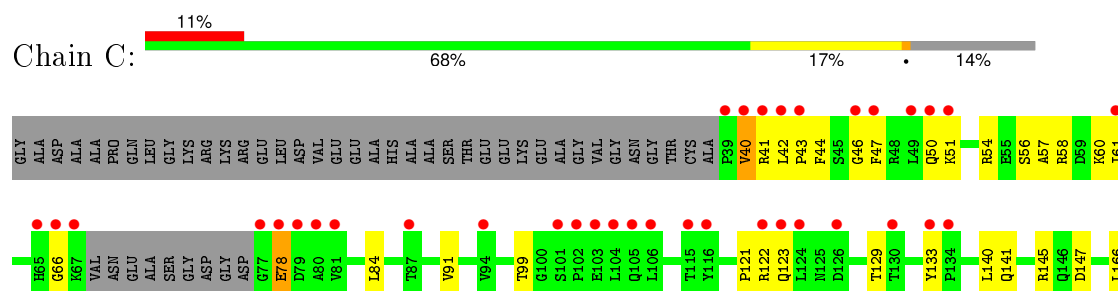
#### • Molecule 1: m7GpppX diphosphatase



#### • Molecule 1: m7GpppX diphosphatase

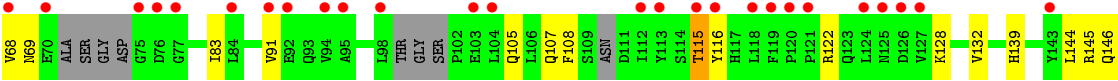
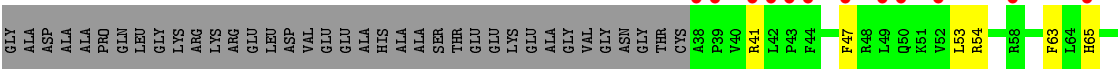


#### • Molecule 1: m7GpppX diphosphatase





● Molecule 1: m7GpppX diphosphatase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.09Å 105.51Å 140.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.26 – 2.80 64.72 – 2.80	Depositor EDS
% Data completeness (in resolution range)	91.5 (84.26-2.80) 91.5 (64.72-2.80)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.14 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, $R_{free}$	0.205 , 0.250 0.222 , 0.267	Depositor DCC
$R_{free}$ test set	1777 reflections (5.45%)	DCC
Wilson B-factor (Å <sup>2</sup> )	45.1	Xtriage
Anisotropy	0.753	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 60.5	EDS
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	2 of 34391 reflections (0.006%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9697	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.47 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.7561e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PO4, 30U

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	0.51	0/2432	0.75	3/3298 (0.1%)
1	B	0.51	0/2440	0.73	2/3311 (0.1%)
1	C	0.50	0/2446	0.74	2/3318 (0.1%)
1	D	0.52	0/2466	0.74	2/3342 (0.1%)
All	All	0.51	0/9784	0.74	9/13269 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	269	TYR	C-N-CA	7.61	140.72	121.70
1	C	269	TYR	C-N-CA	7.53	140.52	121.70
1	D	269	TYR	C-N-CA	7.26	139.85	121.70
1	A	269	TYR	C-N-CA	7.22	139.76	121.70
1	C	269	TYR	N-CA-CB	5.61	120.70	110.60
1	D	269	TYR	N-CA-CB	5.59	120.67	110.60
1	B	269	TYR	N-CA-CB	5.33	120.19	110.60
1	A	269	TYR	N-CA-CB	5.31	120.16	110.60
1	A	168	SER	C-N-CA	5.03	134.28	121.70

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	2377	0	2383	22	0
1	B	2384	0	2388	26	0
1	C	2389	0	2390	22	0
1	D	2411	0	2404	26	0
2	A	23	13	13	1	0
2	D	23	13	13	0	0
3	A	15	0	0	0	0
3	B	15	0	0	3	0
3	C	10	0	0	0	0
3	D	10	0	0	0	0
4	D	6	8	8	0	0
All	All	9663	34	9599	84	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 4.

All (84) 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:D:234:THR:H	1:D:237:HIS:HD2	1.23	0.86
1:A:234:THR:H	1:A:237:HIS:HD2	1.30	0.80
1:A:173:ILE:HD11	1:A:273:TYR:HB2	1.64	0.79
1:A:63:PHE:CD2	1:A:83:ILE:HD12	2.19	0.77
1:D:203:ILE:HD11	1:D:221:ILE:HD12	1.71	0.71
1:B:54:ARG:HH11	1:B:145:ARG:HE	1.40	0.70
1:B:205:ASP:OD1	1:B:207:LYS:HG2	1.96	0.66
1:C:217:TYR:CD1	1:C:281:THR:HG22	2.31	0.66
1:A:228:ARG:HB3	1:A:274:TYR:HB3	1.77	0.65
1:B:228:ARG:HB3	1:B:274:TYR:HB3	1.80	0.64
1:D:228:ARG:HB3	1:D:274:TYR:HB3	1.78	0.63
1:C:228:ARG:HB3	1:C:274:TYR:HB3	1.81	0.63
1:C:56:SER:HB3	1:C:61:ILE:HG22	1.82	0.62
1:B:219:ILE:HD12	1:B:277:HIS:HB2	1.80	0.62
1:D:63:PHE:CD2	1:D:83:ILE:HD12	2.36	0.60
1:C:322:ARG:HG3	1:C:325:ASP:HB2	1.83	0.60
1:A:146:GLN:HB2	1:A:322:ARG:HD2	1.84	0.60
1:C:57:ALA:HB1	1:D:215:ASP:HB3	1.83	0.59
1:A:47:PHE:O	1:B:99:THR:HG22	2.03	0.59
1:D:203:ILE:HD13	1:D:203:ILE:N	2.17	0.59
1:B:191:PHE:CZ	1:D:254:GLN:HB2	2.37	0.59
1:D:234:THR:H	1:D:237:HIS:CD2	2.13	0.58
1:C:54:ARG:HG3	1:C:145:ARG:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:203:ILE:H	1:D:203:ILE:HD13	1.70	0.57
1:A:203:ILE:HG13	1:A:204:PRO:HD2	1.87	0.56
1:D:128:LYS:HE3	1:D:207:LYS:HA	1.88	0.55
1:B:243:ASN:O	1:B:247:GLN:HB2	2.08	0.54
1:B:53:LEU:HD21	1:B:140:LEU:HD23	1.90	0.52
1:B:217:TYR:CD1	1:B:281:THR:HG22	2.45	0.52
1:D:132:VAL:HG11	1:D:139:HIS:CD2	2.45	0.52
1:A:173:ILE:CD1	1:A:273:TYR:HB2	2.38	0.51
1:D:201:VAL:HG12	1:D:203:ILE:HD12	1.92	0.51
1:B:56:SER:HB3	1:B:61:ILE:HG22	1.93	0.51
1:C:40:VAL:H	1:D:105:GLN:HG2	1.76	0.51
1:D:53:LEU:HD11	1:D:65:HIS:HB2	1.92	0.50
1:C:217:TYR:HD1	1:C:281:THR:HG22	1.76	0.50
1:A:54:ARG:HD2	1:A:145:ARG:HG2	1.94	0.50
1:C:58:ARG:HD3	1:D:286:GLU:O	2.12	0.49
1:C:186:ALA:HA	1:C:189:ILE:HD12	1.94	0.49
1:A:62:ILE:HD11	1:B:91:VAL:HG12	1.95	0.49
1:A:142:LYS:HA	1:A:322:ARG:HH22	1.78	0.49
1:B:53:LEU:HA	1:B:144:LEU:HD12	1.95	0.48
1:A:94:VAL:HG11	1:B:62:ILE:HD11	1.95	0.47
1:D:217:TYR:CD1	1:D:281:THR:HG22	2.48	0.47
1:B:277:HIS:CE1	3:B:401:PO4:O4	2.68	0.47
1:A:96:GLN:O	1:A:99:THR:HG22	2.14	0.47
1:A:186:ALA:HA	1:A:189:ILE:HD12	1.96	0.47
1:B:219:ILE:CD1	1:B:277:HIS:HB2	2.44	0.47
1:B:186:ALA:HA	1:B:189:ILE:HD12	1.96	0.47
1:D:54:ARG:HG3	1:D:145:ARG:HB2	1.97	0.46
1:A:143:TYR:CZ	2:A:401:30U:S1	3.03	0.46
1:D:224:ARG:HD3	1:D:227:ILE:HD11	1.98	0.46
1:C:121:PRO:HB2	1:C:123:GLN:HE22	1.82	0.45
1:C:243:ASN:O	1:C:247:GLN:HB2	2.17	0.45
1:B:322:ARG:HG3	1:B:325:ASP:HB2	1.99	0.44
1:C:293:GLU:O	1:C:319:PHE:HA	2.18	0.44
1:D:107:GLN:HB3	1:D:115:THR:HB	1.99	0.44
1:A:116:TYR:HB2	1:B:129:THR:HB	2.00	0.44
1:C:129:THR:HB	1:D:116:TYR:HB2	2.00	0.44
1:C:240:LEU:O	1:C:244:ILE:HG13	2.18	0.43
1:B:54:ARG:HD2	1:B:145:ARG:HE	1.83	0.43
1:B:268:HIS:HB2	3:B:401:PO4:O2	2.19	0.43
1:B:259:LYS:HB2	1:B:262:HIS:HD1	1.84	0.43
1:D:243:ASN:O	1:D:247:GLN:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:GLU:O	1:B:319:PHE:HA	2.19	0.42
1:D:186:ALA:HA	1:D:189:ILE:HD12	2.00	0.42
1:C:287:ALA:HB3	1:C:290:SER:HB3	2.01	0.42
1:B:191:PHE:CE1	1:D:254:GLN:HB2	2.55	0.42
1:C:99:THR:HG22	1:D:47:PHE:O	2.19	0.42
1:C:245:LEU:HD22	1:C:249:GLN:OE1	2.19	0.41
1:D:68:VAL:HG23	1:D:69:ASN:HD22	1.85	0.41
1:A:245:LEU:HB2	1:A:298:LEU:HD13	2.02	0.41
1:C:47:PHE:CE1	1:C:66:GLY:HA3	2.56	0.41
1:A:293:GLU:O	1:A:319:PHE:HA	2.20	0.41
1:A:234:THR:H	1:A:237:HIS:CD2	2.21	0.41
1:C:44:PHE:CD2	1:C:78:GLU:HG2	2.56	0.41
1:C:78:GLU:HG3	1:C:133:TYR:CE1	2.55	0.41
1:C:54:ARG:NE	1:C:145:ARG:HD3	2.36	0.41
1:D:240:LEU:O	1:D:244:ILE:HG13	2.21	0.41
1:A:224:ARG:HD3	1:A:227:ILE:HD11	2.02	0.41
1:A:217:TYR:HH	1:A:279:HIS:CE1	2.39	0.41
1:A:105:GLN:HE22	1:B:122:ARG:HH22	1.69	0.40
1:B:224:ARG:HD3	1:B:227:ILE:HD11	2.03	0.40
1:B:277:HIS:HE1	3:B:401:PO4:O4	2.02	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	281/337 (83%)	266 (95%)	12 (4%)	3 (1%)	17	50
1	B	284/337 (84%)	267 (94%)	13 (5%)	4 (1%)	14	42
1	C	285/337 (85%)	266 (93%)	14 (5%)	5 (2%)	11	34
1	D	284/337 (84%)	266 (94%)	16 (6%)	2 (1%)	26	62
All	All	1134/1348 (84%)	1065 (94%)	55 (5%)	14 (1%)	16	47

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	169	GLN
1	C	46	GLY
1	B	288	PRO
1	B	91	VAL
1	B	122	ARG
1	C	43	PRO
1	C	91	VAL
1	C	40	VAL
1	D	122	ARG
1	A	122	ARG
1	B	41	ARG
1	C	122	ARG
1	D	91	VAL
1	A	91	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	261/294 (89%)	240 (92%)	21 (8%)	15	40
1	B	262/294 (89%)	243 (93%)	19 (7%)	17	44
1	C	262/294 (89%)	239 (91%)	23 (9%)	12	35
1	D	264/294 (90%)	247 (94%)	17 (6%)	22	52
All	All	1049/1176 (89%)	969 (92%)	80 (8%)	16	42

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	ARG
1	A	92	GLU
1	A	93	GLN
1	A	102	PRO
1	A	109	SER
1	A	110	ASN

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Mol	Chain	Res	Type
1	A	112	ILE
1	A	144	LEU
1	A	145	ARG
1	A	147	ASP
1	A	163	LEU
1	A	166	LEU
1	A	181	ASP
1	A	188	ARG
1	A	203	ILE
1	A	218	LEU
1	A	250	GLU
1	A	270	LEU
1	A	298	LEU
1	A	300	GLU
1	A	315	ARG
1	B	54	ARG
1	B	58	ARG
1	B	60	LYS
1	B	84	LEU
1	B	123	GLN
1	B	134	PRO
1	B	145	ARG
1	B	166	LEU
1	B	168	SER
1	B	181	ASP
1	B	205	ASP
1	B	219	ILE
1	B	245	LEU
1	B	250	GLU
1	B	257	ARG
1	B	270	LEU
1	B	298	LEU
1	B	300	GLU
1	B	322	ARG
1	C	41	ARG
1	C	42	LEU
1	C	50	GLN
1	C	51	LYS
1	C	60	LYS
1	C	78	GLU
1	C	84	LEU
1	C	140	LEU

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Mol	Chain	Res	Type
1	C	141	GLN
1	C	147	ASP
1	C	166	LEU
1	C	171	LEU
1	C	181	ASP
1	C	206	LEU
1	C	207	LYS
1	C	219	ILE
1	C	245	LEU
1	C	250	GLU
1	C	254	GLN
1	C	270	LEU
1	C	286	GLU
1	C	298	LEU
1	C	300	GLU
1	D	41	ARG
1	D	108	PHE
1	D	115	THR
1	D	144	LEU
1	D	146	GLN
1	D	163	LEU
1	D	166	LEU
1	D	181	ASP
1	D	188	ARG
1	D	203	ILE
1	D	219	ILE
1	D	250	GLU
1	D	254	GLN
1	D	270	LEU
1	D	298	LEU
1	D	300	GLU
1	D	315	ARG

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	105	GLN
1	A	146	GLN
1	A	237	HIS
1	A	249	GLN
1	B	277	HIS
1	C	123	GLN

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Mol	Chain	Res	Type
1	C	169	GLN
1	D	69	ASN
1	D	169	GLN
1	D	237	HIS
1	D	254	GLN

### 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 ⓘ

13 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	30U	A	401	1	23,25,26	2.32	5 (21%)	30,35,38	1.69	5 (16%)
3	PO4	A	402	-	4,4,4	1.68	0	6,6,6	0.28	0
3	PO4	A	403	-	4,4,4	1.71	1 (25%)	6,6,6	0.28	0
3	PO4	A	404	-	4,4,4	1.71	0	6,6,6	0.28	0
3	PO4	B	401	-	4,4,4	1.70	0	6,6,6	0.27	0
3	PO4	B	402	-	4,4,4	1.75	1 (25%)	6,6,6	0.29	0
3	PO4	B	403	-	4,4,4	1.85	2 (50%)	6,6,6	0.27	0
3	PO4	C	401	-	4,4,4	1.69	0	6,6,6	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	PO4	C	402	-	4,4,4	1.73	2 (50%)	6,6,6	0.26	0
2	30U	D	401	1	23,25,26	2.17	5 (21%)	30,35,38	1.72	5 (16%)
3	PO4	D	402	-	4,4,4	1.73	1 (25%)	6,6,6	0.30	0
3	PO4	D	403	-	4,4,4	1.63	0	6,6,6	0.28	0
4	GOL	D	404	-	5,5,5	0.14	0	5,5,5	0.54	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	30U	A	401	1	-	0/9/9/11	0/3/3/3
3	PO4	A	402	-	-	0/0/0/0	0/0/0/0
3	PO4	A	403	-	-	0/0/0/0	0/0/0/0
3	PO4	A	404	-	-	0/0/0/0	0/0/0/0
3	PO4	B	401	-	-	0/0/0/0	0/0/0/0
3	PO4	B	402	-	-	0/0/0/0	0/0/0/0
3	PO4	B	403	-	-	0/0/0/0	0/0/0/0
3	PO4	C	401	-	-	0/0/0/0	0/0/0/0
3	PO4	C	402	-	-	0/0/0/0	0/0/0/0
2	30U	D	401	1	-	0/9/9/11	0/3/3/3
3	PO4	D	402	-	-	0/0/0/0	0/0/0/0
3	PO4	D	403	-	-	0/0/0/0	0/0/0/0
4	GOL	D	404	-	-	0/4/4/4	0/0/0/0

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	30U	C11-S1	-9.04	1.64	1.80
2	D	401	30U	C11-S1	-7.99	1.66	1.80
3	C	402	PO4	P-O4	2.00	1.60	1.53
3	C	402	PO4	P-O3	2.01	1.60	1.53
3	B	403	PO4	P-O4	2.03	1.60	1.53
3	B	403	PO4	P-O3	2.03	1.60	1.53
3	A	403	PO4	P-O3	2.03	1.60	1.53
3	B	402	PO4	P-O2	2.04	1.60	1.53
3	D	402	PO4	P-O4	2.04	1.60	1.53
2	A	401	30U	C1-C6	2.06	1.43	1.38
2	D	401	30U	C10-C11	2.39	1.42	1.38
2	A	401	30U	C15-N1	2.47	1.39	1.35
2	D	401	30U	C1-C6	2.65	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	30U	C10-C11	2.78	1.42	1.38
2	D	401	30U	C12-C11	2.87	1.43	1.38
2	A	401	30U	C12-C11	2.96	1.43	1.38
2	D	401	30U	C15-N1	3.27	1.41	1.35

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	30U	C10-C11-C12	-3.60	117.35	121.58
2	A	401	30U	C10-C11-C12	-3.20	117.82	121.58
2	A	401	30U	O3-S1-C11	2.31	109.50	104.38
2	A	401	30U	O2-S1-C11	2.53	109.98	104.38
2	A	401	30U	C13-C12-C11	2.69	121.72	119.42
2	D	401	30U	O3-S1-C11	2.82	110.63	104.38
2	D	401	30U	C13-C12-C11	3.00	121.99	119.42
2	D	401	30U	O2-S1-C11	3.05	111.12	104.38
2	D	401	30U	C7-O1-C5	4.68	124.30	117.54
2	A	401	30U	C7-O1-C5	5.46	125.43	117.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	30U	1	0
3	B	401	PO4	3	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	287/337 (85%)	0.46	29 (10%) <b>9</b> <b>4</b>	23, 50, 135, 151	0
1	B	288/337 (85%)	0.34	21 (7%) <b>18</b> <b>10</b>	26, 53, 123, 156	0
1	C	289/337 (85%)	0.51	38 (13%) <b>5</b> <b>2</b>	28, 56, 126, 144	0
1	D	292/337 (86%)	0.58	41 (14%) <b>4</b> <b>2</b>	20, 54, 132, 155	0
All	All	1156/1348 (85%)	0.47	129 (11%) <b>7</b> <b>3</b>	20, 54, 128, 156	0

All (129) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	41	ARG	9.0
1	D	75	GLY	7.3
1	A	40	VAL	7.1
1	D	39	PRO	7.1
1	D	120	PRO	7.0
1	D	125	ASN	6.7
1	D	38	ALA	6.7
1	A	104	LEU	5.5
1	B	80	ALA	5.5
1	C	80	ALA	5.5
1	D	77	GLY	5.1
1	C	66	GLY	5.1
1	A	112	ILE	5.1
1	B	40	VAL	5.0
1	A	99	THR	4.9
1	A	98	LEU	4.8
1	D	76	ASP	4.7
1	D	43	PRO	4.7
1	D	124	LEU	4.7
1	C	65	HIS	4.6
1	B	79	ASP	4.5

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Mol	Chain	Res	Type	RSRZ
1	B	44	PHE	4.4
1	D	121	PRO	4.4
1	D	115	THR	4.2
1	A	102	PRO	4.2
1	A	120	PRO	4.2
1	C	130	THR	4.1
1	B	126	ASP	4.0
1	A	44	PHE	4.0
1	C	40	VAL	3.9
1	B	45	SER	3.9
1	D	113	TYR	3.9
1	A	43	PRO	3.8
1	D	44	PHE	3.8
1	A	101	SER	3.7
1	B	68	VAL	3.7
1	D	171	LEU	3.6
1	A	119	PHE	3.6
1	C	78	GLU	3.6
1	B	43	PRO	3.6
1	B	133	TYR	3.6
1	A	103	GLU	3.5
1	A	117	HIS	3.5
1	D	112	ILE	3.5
1	C	133	TYR	3.5
1	A	125	ASN	3.5
1	B	47	PHE	3.5
1	C	61	ILE	3.4
1	D	337	SER	3.4
1	C	42	LEU	3.4
1	D	52	VAL	3.4
1	A	118	LEU	3.4
1	C	102	PRO	3.3
1	C	104	LEU	3.2
1	B	66	GLY	3.2
1	D	126	ASP	3.2
1	B	49	LEU	3.2
1	D	118	LEU	3.2
1	C	77	GLY	3.2
1	C	101	SER	3.1
1	C	39	PRO	3.1
1	D	95	ALA	3.1
1	D	94	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	51	LYS	3.1
1	C	49	LEU	3.1
1	C	41	ARG	3.0
1	C	124	LEU	3.0
1	C	123	GLN	3.0
1	C	43	PRO	3.0
1	A	286	GLU	3.0
1	B	61	ILE	2.9
1	B	41	ARG	2.9
1	C	46	GLY	2.9
1	B	42	LEU	2.9
1	C	105	GLN	2.9
1	C	51	LYS	2.9
1	C	126	ASP	2.9
1	C	81	VAL	2.8
1	A	170	SER	2.8
1	D	143	TYR	2.8
1	A	107	GLN	2.7
1	C	67	LYS	2.7
1	D	42	LEU	2.6
1	C	79	ASP	2.6
1	D	65	HIS	2.6
1	D	104	LEU	2.6
1	C	168	SER	2.6
1	D	119	PHE	2.6
1	D	70	GLU	2.6
1	C	115	THR	2.6
1	C	103	GLU	2.5
1	C	134	PRO	2.5
1	A	93	GLN	2.5
1	B	125	ASN	2.5
1	D	127	VAL	2.5
1	A	110	ASN	2.5
1	C	47	PHE	2.5
1	C	94	VAL	2.5
1	C	122	ARG	2.5
1	A	50	GLN	2.5
1	D	98	LEU	2.5
1	D	41	ARG	2.5
1	A	100	GLY	2.4
1	A	137	GLU	2.4
1	C	50	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	122	ARG	2.4
1	D	84	LEU	2.4
1	B	143	TYR	2.4
1	A	94	VAL	2.4
1	A	121	PRO	2.4
1	D	58	ARG	2.4
1	C	106	LEU	2.3
1	D	50	GLN	2.3
1	D	49	LEU	2.3
1	D	47	PHE	2.2
1	A	97	LEU	2.2
1	D	336	GLN	2.2
1	C	116	TYR	2.2
1	D	116	TYR	2.2
1	D	92	GLU	2.1
1	A	45	SER	2.1
1	D	103	GLU	2.1
1	B	69	ASN	2.1
1	A	113	TYR	2.1
1	C	288	PRO	2.1
1	D	68	VAL	2.1
1	D	91	VAL	2.1
1	C	87	THR	2.0
1	B	120	PRO	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	PO4	D	402	5/5	0.81	0.29	8.21	91,93,96,97	0
3	PO4	A	404	5/5	0.69	0.43	6.43	151,152,152,153	0
3	PO4	B	403	5/5	0.89	0.26	4.77	79,79,81,83	0
3	PO4	B	402	5/5	0.87	0.22	3.86	82,84,87,87	0
4	GOL	D	404	6/6	0.44	0.39	3.03	94,99,104,104	0
3	PO4	A	403	5/5	0.94	0.23	3.01	70,75,76,78	0
3	PO4	C	401	5/5	0.95	0.23	1.43	48,50,52,53	0
2	30U	D	401	23/24	0.91	0.32	0.99	35,61,99,102	13
3	PO4	C	402	5/5	0.91	0.18	0.75	85,85,88,90	0
2	30U	A	401	23/24	0.95	0.21	-0.07	32,47,93,96	13
3	PO4	A	402	5/5	0.98	0.18	-0.72	57,58,62,63	0
3	PO4	D	403	5/5	0.98	0.16	-0.89	59,63,66,67	0
3	PO4	B	401	5/5	0.98	0.13	-1.97	47,47,48,49	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.