



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 8, 2021 – 04:03 PM EST

PDB ID : 7LPX  
Title : Crystal Structure of HIV-1 RT in Complex with NBD-14270  
Authors : Losada, N.; Ruiz, F.X.; Arnold, E.  
Deposited on : 2021-02-12  
Resolution : 2.45 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.2

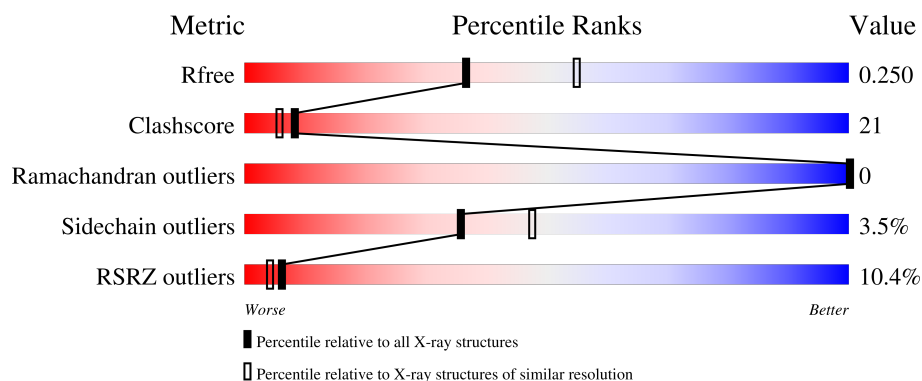
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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))
$R_{free}$	130704	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	557	<div> <div>10%</div> <div>68%</div> <div>30%</div> <div>.</div> </div>
2	B	429	<div> <div>11%</div> <div>66%</div> <div>27%</div> <div>..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	602	-	-	X	-
3	SO4	B	501	-	-	X	-
3	SO4	B	502	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8103 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 Reverse transcriptase p66.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	556	Total	C	N	O	S	0	0	0
			4516	2923	750	835	8			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP P03366
A	0	VAL	-	expression tag	UNP P03366
A	172	ALA	LYS	engineered mutation	UNP P03366
A	173	ALA	LYS	engineered mutation	UNP P03366
A	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 2 is a protein called Reverse transcriptase p51.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	412	Total	C	N	O	S	0	0	0
			3409	2220	564	618	7			

There are 2 discrepancies between the modelled and reference sequences:

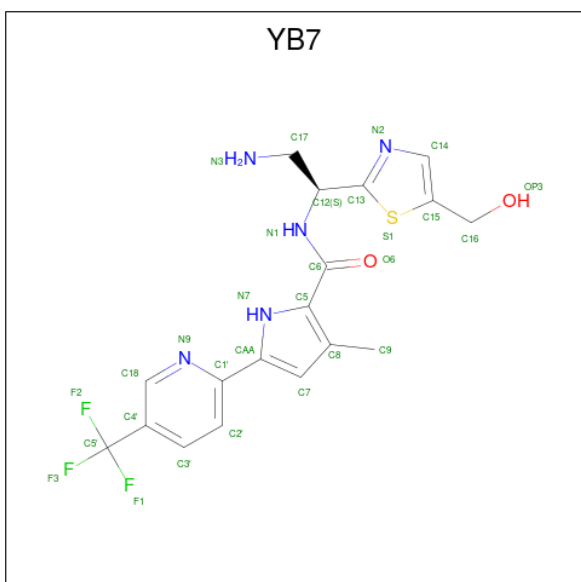
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP P03366
B	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 4 is {N}-[(1 {S})-2-azanyl-1-[5-(hydroxymethyl)-1,3-thiazol-2-yl]ethyl]-3-methyl-5-[5-(trifluoromethyl)pyridin-2-yl]-1 {H}-pyrrole-2-carboxamide (three-letter code: YB7) (formula: C<sub>18</sub>H<sub>18</sub>F<sub>3</sub>N<sub>5</sub>O<sub>2</sub>S) (labeled as "Ligand of Interest" by depositor).

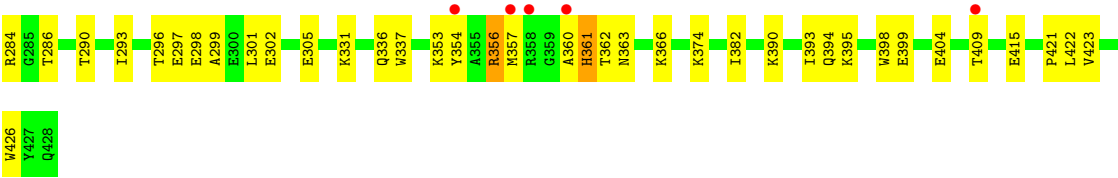


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	S	0	0
			29	18	3	5	2	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	71	Total	O	0	0
			71	71		
5	B	58	Total	O	0	0
			58	58		







## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	161.60Å 73.06Å 107.40Å 90.00° 100.11° 90.00°	Depositor
Resolution (Å)	30.31 – 2.45 30.31 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.3 (30.31-2.45) 99.3 (30.31-2.45)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.78 (at 2.45Å)	Xtriage
Refinement program	PHENIX dev_3051	Depositor
R, $R_{free}$	0.215 , 0.250 0.215 , 0.250	Depositor DCC
$R_{free}$ test set	1998 reflections (4.41%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	69.8	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 67.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8103	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.92% 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: YB7, 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	0/4634	0.57	0/6299
2	B	0.32	0/3506	0.53	0/4762
All	All	0.34	0/8140	0.55	0/11061

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

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	4516	0	4572	217	0
2	B	3409	0	3441	135	0
3	A	10	0	0	2	0
3	B	10	0	0	5	0
4	A	29	0	0	5	0
5	A	71	0	0	44	0
5	B	58	0	0	39	0
All	All	8103	0	8013	336	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 21.

All (336) 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:543:GLY:CA	2:B:284:ARG:HA	1.55	1.37
1:A:210:LEU:HA	5:A:756:HOH:O	1.44	1.17
1:A:101:LYS:HE3	5:A:720:HOH:O	1.43	1.16
1:A:536:VAL:HG21	1:A:542:ILE:HD11	1.25	1.13
1:A:108:VAL:HG21	4:A:603:YB7:C7	1.82	1.09
1:A:210:LEU:HD23	5:A:756:HOH:O	1.54	1.07
1:A:543:GLY:HA3	2:B:283:LEU:O	1.55	1.06
1:A:64:LYS:HZ1	1:A:69:THR:HA	1.16	1.03
1:A:64:LYS:NZ	1:A:69:THR:HA	1.71	1.03
1:A:543:GLY:HA2	2:B:284:ARG:HA	1.04	1.03
1:A:111:VAL:HG22	1:A:185:ASP:O	1.60	1.02
2:B:404:GLU:HG3	3:B:502:SO4:O1	1.61	0.99
1:A:543:GLY:CA	2:B:284:ARG:CA	2.43	0.97
1:A:203:GLU:HA	5:A:736:HOH:O	1.65	0.95
1:A:541:GLY:C	1:A:546:GLU:HB2	1.89	0.93
1:A:115:TYR:HD1	5:A:711:HOH:O	1.53	0.91
1:A:543:GLY:HA2	2:B:284:ARG:CA	1.98	0.91
2:B:206:ARG:HD3	5:B:612:HOH:O	1.70	0.89
2:B:6:GLU:HA	5:B:652:HOH:O	1.72	0.88
1:A:543:GLY:HA3	2:B:284:ARG:HA	1.55	0.86
2:B:278:GLN:OE1	2:B:298:GLU:HG3	1.77	0.85
1:A:63:ILE:HD13	5:A:745:HOH:O	1.78	0.83
1:A:206:ARG:HD3	5:A:736:HOH:O	1.79	0.83
1:A:536:VAL:CG2	1:A:542:ILE:HD11	2.09	0.82
2:B:360:ALA:HB1	2:B:363:ASN:O	1.79	0.82
1:A:111:VAL:CG2	1:A:185:ASP:O	2.27	0.82
1:A:88:TRP:CH2	5:B:624:HOH:O	2.33	0.80
1:A:61:PHE:HD1	1:A:62:ALA:H	1.28	0.80
1:A:7:THR:HG22	5:A:757:HOH:O	1.81	0.79
2:B:149:LEU:HD23	2:B:156:SER:HA	1.63	0.79
2:B:163:SER:HB3	5:B:622:HOH:O	1.81	0.79
1:A:536:VAL:HG21	1:A:542:ILE:CD1	2.12	0.78
2:B:193:LEU:HD21	2:B:197:GLN:CB	2.14	0.77
2:B:193:LEU:HD21	2:B:197:GLN:HB2	1.66	0.77
1:A:90:VAL:CG2	5:B:613:HOH:O	2.32	0.77
2:B:296:THR:CB	5:B:604:HOH:O	2.31	0.77
1:A:257:ILE:HG23	1:A:260:LEU:HB3	1.67	0.77
1:A:415:GLU:HB2	5:A:712:HOH:O	1.85	0.77
1:A:543:GLY:HA3	2:B:284:ARG:CA	2.12	0.76
2:B:293:ILE:HB	5:B:635:HOH:O	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:LEU:CD1	1:A:307:ARG:NE	2.49	0.76
1:A:543:GLY:CA	2:B:283:LEU:O	2.34	0.76
1:A:11:LYS:HD3	1:A:12:LEU:N	2.02	0.75
1:A:240:THR:OG1	1:A:315:HIS:HA	1.87	0.75
2:B:236:PRO:HA	2:B:239:TRP:CH2	2.22	0.74
1:A:49:LYS:HD3	1:A:142:ILE:HD11	1.70	0.74
1:A:246:LEU:HD11	1:A:264:LEU:HD21	1.70	0.74
1:A:427:TYR:HB2	3:A:602:SO4:O4	1.88	0.74
1:A:84:THR:HG21	1:A:153:TRP:HE1	1.53	0.73
2:B:193:LEU:CD2	2:B:197:GLN:HB2	2.18	0.73
1:A:11:LYS:HD3	1:A:12:LEU:H	1.53	0.73
2:B:22:LYS:HD2	5:B:624:HOH:O	1.87	0.73
1:A:303:LEU:HD11	1:A:307:ARG:HE	1.54	0.72
1:A:300:GLU:CD	1:A:300:GLU:O	2.27	0.72
1:A:108:VAL:HG12	1:A:223:LYS:O	1.90	0.72
1:A:542:ILE:O	1:A:546:GLU:HB2	1.90	0.72
1:A:63:ILE:HA	5:A:745:HOH:O	1.89	0.71
2:B:337:TRP:HB2	2:B:354:TYR:HB3	1.72	0.71
2:B:22:LYS:CD	5:B:624:HOH:O	2.39	0.71
2:B:244:ILE:HA	5:B:605:HOH:O	1.90	0.71
1:A:260:LEU:O	1:A:264:LEU:HG	1.91	0.71
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.24	0.70
2:B:336:GLN:HB3	2:B:353:LYS:HE3	1.73	0.70
1:A:396:GLU:HG2	5:A:761:HOH:O	1.89	0.70
2:B:337:TRP:O	2:B:354:TYR:N	2.20	0.70
1:A:66:LYS:CE	1:A:66:LYS:HA	2.20	0.70
2:B:46:LYS:HE2	2:B:116:PHE:HB3	1.74	0.70
2:B:180:ILE:HG13	2:B:189:VAL:HG22	1.73	0.70
2:B:360:ALA:HB2	2:B:366:LYS:HB3	1.73	0.69
1:A:435:VAL:HG12	2:B:290:THR:HG21	1.74	0.69
1:A:88:TRP:HH2	5:B:624:HOH:O	1.71	0.69
1:A:182:GLN:HB3	1:A:187:LEU:HD23	1.75	0.69
2:B:276:VAL:N	3:B:501:SO4:O1	2.23	0.68
2:B:206:ARG:CD	5:B:612:HOH:O	2.35	0.68
1:A:90:VAL:HG21	5:B:613:HOH:O	1.94	0.68
1:A:206:ARG:NH1	1:A:218:ASP:OD1	2.26	0.68
1:A:246:LEU:CD1	1:A:264:LEU:HD21	2.24	0.68
1:A:122:GLU:HA	1:A:125:ARG:HG3	1.76	0.67
1:A:63:ILE:CD1	5:A:745:HOH:O	2.38	0.67
1:A:541:GLY:HA2	1:A:546:GLU:CG	2.25	0.67
2:B:296:THR:HB	5:B:604:HOH:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:354:TYR:CE1	2:B:374:LYS:HE3	2.30	0.67
2:B:361:HIS:O	2:B:361:HIS:ND1	2.27	0.67
1:A:114:ALA:HB1	1:A:214:LEU:HD22	1.77	0.66
2:B:163:SER:CB	5:B:622:HOH:O	2.39	0.66
1:A:21:VAL:HG11	1:A:59:PRO:HD3	1.77	0.66
2:B:58:THR:HG23	2:B:76:ASP:O	1.95	0.65
2:B:169:GLU:O	2:B:173:LYS:HB2	1.97	0.65
2:B:277:ARG:HB2	3:B:501:SO4:O2	1.97	0.64
1:A:66:LYS:HE3	1:A:67:ASP:H	1.62	0.64
2:B:293:ILE:CG2	5:B:635:HOH:O	2.46	0.64
1:A:206:ARG:HH22	1:A:218:ASP:HB2	1.63	0.63
2:B:94:ILE:HD11	5:B:628:HOH:O	1.98	0.63
2:B:94:ILE:CD1	5:B:628:HOH:O	2.46	0.63
1:A:12:LEU:HD23	1:A:84:THR:HA	1.81	0.63
1:A:315:HIS:CD2	5:A:724:HOH:O	2.51	0.63
2:B:88:TRP:HB3	2:B:92:LEU:HD23	1.80	0.63
1:A:303:LEU:CD1	1:A:307:ARG:HE	2.10	0.63
1:A:107:THR:HG22	1:A:109:LEU:CD1	2.29	0.62
1:A:229:TRP:CD1	4:A:603:YB7:N7	2.67	0.62
2:B:293:ILE:CB	5:B:635:HOH:O	2.44	0.62
1:A:113:ASP:C	5:A:711:HOH:O	2.37	0.61
1:A:264:LEU:HD13	1:A:306:ASN:OD1	2.00	0.61
1:A:245:VAL:CG1	5:A:759:HOH:O	2.48	0.61
1:A:325:LEU:HB2	1:A:385:LYS:HE2	1.81	0.61
1:A:84:THR:HG22	1:A:124:PHE:HZ	1.66	0.61
2:B:213:GLY:CA	5:B:640:HOH:O	2.48	0.61
1:A:21:VAL:CG1	1:A:59:PRO:HD3	2.32	0.60
1:A:357:MET:CE	5:A:737:HOH:O	2.49	0.60
1:A:315:HIS:HD2	5:A:724:HOH:O	1.85	0.60
1:A:116:PHE:HE2	5:A:739:HOH:O	1.83	0.60
2:B:104:LYS:HA	2:B:237:ASP:HB2	1.82	0.60
2:B:293:ILE:HG22	5:B:635:HOH:O	2.01	0.60
2:B:193:LEU:HD21	2:B:197:GLN:HB3	1.83	0.59
1:A:12:LEU:HG	1:A:124:PHE:HE1	1.68	0.59
1:A:473:THR:HG23	1:A:476:LYS:H	1.67	0.59
1:A:541:GLY:HA2	1:A:546:GLU:HG2	1.84	0.59
1:A:544:GLY:HA2	2:B:286:THR:HG22	1.84	0.59
1:A:315:HIS:HB2	5:A:724:HOH:O	2.03	0.58
2:B:197:GLN:HA	2:B:200:THR:HG23	1.85	0.58
2:B:354:TYR:HE1	2:B:374:LYS:HE3	1.67	0.58
2:B:8:VAL:HG21	2:B:159:ILE:HG12	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:193:LEU:CD2	2:B:197:GLN:CB	2.79	0.58
2:B:409:THR:HG21	5:B:619:HOH:O	2.04	0.58
2:B:360:ALA:C	2:B:362:THR:H	2.07	0.58
1:A:303:LEU:O	1:A:307:ARG:HG3	2.04	0.58
1:A:64:LYS:NZ	1:A:68:SER:O	2.37	0.57
2:B:191:SER:OG	2:B:198:HIS:ND1	2.32	0.57
1:A:109:LEU:HD23	1:A:216:THR:CG2	2.35	0.57
1:A:542:ILE:O	1:A:546:GLU:CB	2.52	0.57
2:B:72:ARG:NH2	2:B:151:GLN:OE1	2.37	0.57
2:B:175:ASN:HB3	2:B:178:ILE:HG12	1.85	0.57
1:A:88:TRP:CD1	1:A:90:VAL:HG23	2.39	0.57
2:B:50:ILE:HG13	2:B:145:GLN:HB3	1.86	0.57
1:A:64:LYS:HZ3	1:A:69:THR:HA	1.68	0.57
1:A:246:LEU:HD12	1:A:260:LEU:HD11	1.86	0.57
1:A:245:VAL:HG12	5:A:759:HOH:O	2.03	0.56
1:A:406:TRP:HA	5:A:715:HOH:O	2.04	0.56
1:A:541:GLY:CA	1:A:546:GLU:CG	2.83	0.56
2:B:233:GLU:OE1	2:B:233:GLU:N	2.37	0.56
1:A:168:LEU:HD11	1:A:187:LEU:HD22	1.88	0.56
1:A:91:GLN:H	1:A:91:GLN:CD	2.09	0.56
2:B:103:LYS:NZ	2:B:192:ASP:OD2	2.31	0.56
1:A:53:GLU:OE2	1:A:53:GLU:N	2.31	0.56
1:A:112:GLY:C	5:A:711:HOH:O	2.43	0.56
1:A:303:LEU:HD13	1:A:307:ARG:NE	2.20	0.55
1:A:434:ILE:HA	5:A:763:HOH:O	2.06	0.55
1:A:116:PHE:CE2	5:A:739:HOH:O	2.53	0.55
1:A:50:ILE:HG13	1:A:143:ARG:HB3	1.89	0.55
2:B:277:ARG:HB2	3:B:501:SO4:S	2.47	0.55
2:B:185:ASP:HB2	5:B:619:HOH:O	2.06	0.55
2:B:6:GLU:HB2	5:B:652:HOH:O	2.06	0.54
2:B:296:THR:HG21	5:B:604:HOH:O	2.07	0.54
1:A:206:ARG:NH2	1:A:218:ASP:HB2	2.23	0.54
2:B:88:TRP:HA	2:B:91:GLN:O	2.07	0.54
1:A:303:LEU:HD11	1:A:307:ARG:NE	2.16	0.54
1:A:424:LYS:HG2	5:A:701:HOH:O	2.07	0.54
1:A:125:ARG:HD3	1:A:147:ASN:HA	1.90	0.54
1:A:427:TYR:CB	3:A:602:SO4:O4	2.55	0.54
1:A:536:VAL:HB	1:A:542:ILE:HD13	1.90	0.54
2:B:181:TYR:HA	5:B:628:HOH:O	2.08	0.54
1:A:543:GLY:HA3	2:B:283:LEU:C	2.26	0.53
2:B:263:LYS:NZ	5:B:607:HOH:O	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:360:ALA:CB	2:B:363:ASN:HB3	2.37	0.53
1:A:11:LYS:HA	1:A:11:LYS:HE2	1.91	0.53
1:A:11:LYS:CD	1:A:12:LEU:H	2.22	0.53
2:B:16:MET:HA	5:B:609:HOH:O	2.07	0.53
2:B:107:THR:HG22	2:B:233:GLU:HA	1.89	0.53
1:A:182:GLN:HG3	2:B:140:PRO:HD3	1.89	0.52
2:B:278:GLN:HB3	2:B:299:ALA:HA	1.91	0.52
1:A:244:ILE:HD11	5:A:731:HOH:O	2.10	0.52
1:A:259:LYS:HG3	1:A:259:LYS:O	2.09	0.52
2:B:58:THR:CG2	2:B:76:ASP:O	2.57	0.52
1:A:257:ILE:HG22	1:A:261:VAL:HG13	1.92	0.52
1:A:19:PRO:HG3	1:A:80:LEU:HB2	1.92	0.52
1:A:191:SER:OG	1:A:198:HIS:ND1	2.34	0.51
1:A:82:LYS:CD	5:A:723:HOH:O	2.58	0.51
1:A:108:VAL:CG1	1:A:223:LYS:O	2.58	0.51
1:A:399:GLU:HB2	5:A:768:HOH:O	2.10	0.51
2:B:213:GLY:HA2	5:B:640:HOH:O	2.10	0.51
1:A:46:LYS:HE3	1:A:116:PHE:CE1	2.46	0.51
1:A:101:LYS:HD3	1:A:102:LYS:N	2.26	0.51
2:B:331:LYS:HB2	2:B:337:TRP:CZ3	2.46	0.51
1:A:202:ILE:O	1:A:206:ARG:HG3	2.11	0.51
1:A:244:ILE:HG22	5:A:729:HOH:O	2.11	0.51
1:A:385:LYS:HE3	5:A:738:HOH:O	2.10	0.51
2:B:206:ARG:CG	5:B:612:HOH:O	2.58	0.51
1:A:80:LEU:O	1:A:84:THR:HG23	2.11	0.51
1:A:175:ASN:O	1:A:178:ILE:HG13	2.11	0.51
1:A:108:VAL:HG21	4:A:603:YB7:C8	2.40	0.50
1:A:182:GLN:HG2	5:A:727:HOH:O	2.10	0.50
2:B:337:TRP:CD1	2:B:354:TYR:HD2	2.29	0.50
2:B:395:LYS:O	2:B:399:GLU:HG2	2.11	0.50
1:A:88:TRP:CZ3	5:B:624:HOH:O	2.58	0.50
1:A:90:VAL:CG1	5:B:613:HOH:O	2.60	0.50
1:A:300:GLU:O	1:A:300:GLU:OE1	2.29	0.50
1:A:110:ASP:OD2	4:A:603:YB7:N3	2.45	0.50
1:A:405:TYR:C	5:A:715:HOH:O	2.49	0.49
1:A:79:GLU:OE2	1:A:83:ARG:NH2	2.45	0.49
1:A:396:GLU:O	1:A:400:THR:HG23	2.12	0.49
2:B:106:VAL:HG22	2:B:190:GLY:HA3	1.94	0.49
2:B:356:ARG:O	2:B:357:MET:HG2	2.12	0.49
2:B:301:LEU:O	2:B:305:GLU:HG3	2.13	0.49
1:A:107:THR:HG22	1:A:109:LEU:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:LEU:HG	1:A:124:PHE:CE1	2.48	0.49
1:A:171:PHE:O	1:A:175:ASN:ND2	2.37	0.49
2:B:360:ALA:C	2:B:362:THR:N	2.66	0.49
2:B:421:PRO:HB2	2:B:423:VAL:HG22	1.95	0.49
1:A:257:ILE:O	1:A:261:VAL:HG22	2.12	0.48
2:B:296:THR:HG22	2:B:298:GLU:HG2	1.95	0.48
1:A:88:TRP:CD1	1:A:90:VAL:CG2	2.96	0.48
2:B:409:THR:CG2	5:B:619:HOH:O	2.60	0.48
1:A:303:LEU:CD1	1:A:307:ARG:CZ	2.92	0.48
1:A:178:ILE:HG22	1:A:191:SER:HB3	1.96	0.48
1:A:424:LYS:CG	5:A:701:HOH:O	2.61	0.48
2:B:205:LEU:O	2:B:209:LEU:HD23	2.13	0.48
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.95	0.48
1:A:60:VAL:HG23	1:A:75:VAL:HG12	1.96	0.48
1:A:109:LEU:HD23	1:A:216:THR:HG22	1.95	0.48
1:A:370:GLU:HB3	5:A:737:HOH:O	2.13	0.48
1:A:408:ALA:O	2:B:393:ILE:HG13	2.13	0.48
1:A:541:GLY:O	1:A:546:GLU:HB2	2.13	0.48
1:A:426:TRP:HB3	1:A:526:ILE:HG12	1.95	0.47
2:B:64:LYS:HE2	2:B:71:TRP:CE2	2.49	0.47
1:A:196:GLY:O	1:A:200:THR:HG23	2.14	0.47
1:A:416:PHE:N	5:A:712:HOH:O	2.47	0.47
2:B:202:ILE:O	2:B:205:LEU:HB3	2.14	0.47
2:B:84:THR:HB	2:B:154:LYS:HE2	1.97	0.47
1:A:536:VAL:CG2	1:A:542:ILE:CD1	2.84	0.47
1:A:417:VAL:HG22	1:A:419:THR:HG23	1.95	0.47
1:A:516:GLU:O	1:A:520:GLN:HG3	2.15	0.47
2:B:296:THR:CG2	2:B:298:GLU:HG2	2.45	0.47
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.14	0.47
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.50	0.47
1:A:111:VAL:C	1:A:113:ASP:H	2.16	0.47
2:B:101:LYS:HD3	2:B:382:ILE:HG23	1.97	0.46
2:B:161:GLN:O	2:B:165:THR:HG23	2.15	0.46
1:A:54:ASN:HB3	1:A:143:ARG:HH21	1.80	0.46
1:A:113:ASP:N	5:A:711:HOH:O	2.47	0.46
1:A:31:ILE:HG12	1:A:133:PRO:O	2.15	0.46
1:A:77:PHE:CE2	1:A:150:PRO:HB2	2.50	0.46
1:A:357:MET:HE3	5:A:737:HOH:O	2.12	0.46
1:A:206:ARG:HH22	1:A:218:ASP:CB	2.26	0.46
2:B:278:GLN:HB2	2:B:302:GLU:CD	2.36	0.46
1:A:229:TRP:CE2	1:A:230:MET:HG2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:212:TRP:CD1	2:B:212:TRP:N	2.84	0.46
2:B:278:GLN:HB2	2:B:302:GLU:OE1	2.16	0.46
1:A:245:VAL:HB	5:A:759:HOH:O	2.16	0.46
1:A:443:ASP:OD2	1:A:549:ASP:HA	2.16	0.46
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.97	0.45
1:A:543:GLY:H	2:B:283:LEU:C	2.19	0.45
1:A:296:THR:HG22	1:A:299:ALA:HB2	1.99	0.45
1:A:186:ASP:OD2	4:A:603:YB7:N7	2.50	0.45
2:B:240:THR:O	2:B:242:GLN:NE2	2.50	0.45
1:A:257:ILE:CG2	1:A:261:VAL:HG13	2.47	0.45
1:A:541:GLY:CA	1:A:546:GLU:HB2	2.46	0.45
1:A:34:LEU:HD21	1:A:62:ALA:HB2	1.98	0.45
1:A:237:ASP:OD1	1:A:237:ASP:N	2.47	0.45
2:B:170:PRO:O	2:B:174:GLN:HG2	2.16	0.45
1:A:317:VAL:HG12	1:A:318:TYR:O	2.16	0.45
2:B:297:GLU:HG3	2:B:298:GLU:N	2.32	0.45
1:A:27:THR:O	1:A:31:ILE:HD12	2.16	0.44
1:A:32:LYS:O	1:A:35:VAL:HG12	2.17	0.44
1:A:90:VAL:HG22	5:B:613:HOH:O	2.07	0.44
2:B:82:LYS:NZ	5:B:615:HOH:O	2.49	0.44
2:B:263:LYS:HB2	2:B:426:TRP:CE3	2.53	0.44
1:A:12:LEU:HD21	1:A:80:LEU:HD11	1.98	0.44
1:A:259:LYS:NZ	1:A:263:LYS:HD2	2.32	0.44
1:A:330:GLN:HB2	1:A:338:THR:HG22	1.99	0.44
2:B:97:PRO:HG3	2:B:181:TYR:HB2	2.00	0.44
1:A:412:PRO:HB2	5:A:744:HOH:O	2.17	0.44
1:A:11:LYS:O	1:A:85:GLN:HG2	2.17	0.44
1:A:203:GLU:HG2	5:A:736:HOH:O	2.17	0.44
2:B:103:LYS:O	2:B:236:PRO:HG2	2.17	0.44
2:B:390:LYS:NZ	2:B:415:GLU:OE2	2.47	0.44
1:A:5:ILE:HG13	5:A:719:HOH:O	2.18	0.44
1:A:82:LYS:HD3	5:A:723:HOH:O	2.17	0.44
2:B:422:LEU:HD23	2:B:422:LEU:HA	1.88	0.44
1:A:395:LYS:NZ	5:A:717:HOH:O	2.50	0.44
2:B:238:LYS:HD2	2:B:238:LYS:HA	1.49	0.44
1:A:541:GLY:C	1:A:546:GLU:CB	2.75	0.43
1:A:335:GLY:HA3	1:A:356:ARG:HG2	2.00	0.43
1:A:544:GLY:O	1:A:548:VAL:HG12	2.18	0.43
2:B:13:LYS:HD3	2:B:14:PRO:CD	2.48	0.43
2:B:88:TRP:HB3	2:B:92:LEU:HA	2.01	0.43
2:B:281:LYS:HD3	5:B:636:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:LEU:O	1:A:260:LEU:HG	2.18	0.43
1:A:115:TYR:OH	1:A:151:GLN:HB3	2.19	0.43
2:B:202:ILE:HD13	2:B:202:ILE:HA	1.63	0.43
2:B:168:LEU:O	2:B:172:LYS:HG2	2.18	0.43
1:A:206:ARG:NH2	1:A:218:ASP:CB	2.81	0.43
1:A:94:ILE:O	1:A:94:ILE:HG13	2.19	0.43
1:A:66:LYS:HA	1:A:66:LYS:NZ	2.34	0.42
1:A:260:LEU:O	1:A:264:LEU:CG	2.65	0.42
1:A:541:GLY:HA2	1:A:546:GLU:CB	2.49	0.42
2:B:89:GLU:HG3	2:B:90:VAL:H	1.84	0.42
2:B:116:PHE:C	2:B:148:VAL:HG21	2.39	0.42
2:B:336:GLN:HA	2:B:354:TYR:O	2.19	0.42
2:B:404:GLU:CG	3:B:502:SO4:O1	2.50	0.42
2:B:399:GLU:HA	2:B:399:GLU:OE1	2.19	0.42
1:A:220:LYS:HB3	1:A:221:HIS:H	1.57	0.42
1:A:11:LYS:CD	1:A:12:LEU:N	2.78	0.42
1:A:541:GLY:CA	1:A:546:GLU:HG3	2.48	0.42
2:B:61:PHE:CZ	2:B:74:LEU:HD13	2.53	0.42
2:B:166:LYS:HG2	2:B:212:TRP:HZ3	1.84	0.42
1:A:88:TRP:HB2	2:B:54:ASN:O	2.20	0.42
1:A:217:PRO:HB3	1:A:221:HIS:HB3	2.02	0.42
1:A:253:THR:HA	1:A:292:VAL:HA	2.01	0.42
1:A:293:ILE:HG13	1:A:294:PRO:HD2	2.02	0.42
1:A:26:LEU:HB2	1:A:31:ILE:HD11	2.01	0.42
1:A:429:LEU:HD11	1:A:506:ILE:HG22	2.00	0.42
1:A:379:SER:CB	1:A:387:PRO:HD3	2.50	0.42
2:B:116:PHE:O	2:B:148:VAL:HG21	2.19	0.42
1:A:63:ILE:HD13	1:A:63:ILE:HA	1.88	0.42
1:A:115:TYR:CD1	5:A:711:HOH:O	2.42	0.41
1:A:259:LYS:O	1:A:263:LYS:HG3	2.19	0.41
1:A:206:ARG:HG2	1:A:216:THR:HG21	2.02	0.41
2:B:141:GLY:N	5:B:613:HOH:O	2.46	0.41
1:A:229:TRP:CE3	1:A:234:LEU:HD11	2.56	0.41
2:B:394:GLN:HG3	5:B:614:HOH:O	2.20	0.41
1:A:91:GLN:CD	1:A:91:GLN:N	2.72	0.41
2:B:236:PRO:HA	2:B:239:TRP:CZ3	2.54	0.41
1:A:73:LYS:NZ	1:A:146:TYR:OH	2.51	0.41
1:A:34:LEU:HD22	1:A:73:LYS:HG3	2.02	0.41
1:A:61:PHE:CD1	1:A:62:ALA:N	2.86	0.41
1:A:343:GLN:HG3	1:A:349:LEU:HD11	2.03	0.41
2:B:151:GLN:HB3	2:B:185:ASP:OD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:VAL:C	1:A:113:ASP:N	2.73	0.41
2:B:202:ILE:O	2:B:205:LEU:N	2.54	0.40
2:B:393:ILE:HD13	2:B:398:TRP:HB2	2.03	0.40
1:A:342:TYR:HB3	1:A:348:ASN:HA	2.03	0.40
1:A:543:GLY:N	2:B:283:LEU:O	2.54	0.40
2:B:281:LYS:HD3	5:B:604:HOH:O	2.21	0.40
2:B:360:ALA:HB2	2:B:363:ASN:HB3	2.03	0.40
1:A:541:GLY:O	1:A:542:ILE:C	2.57	0.40
1:A:363:ASN:ND2	1:A:366:LYS:HE3	2.36	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	554/557 (100%)	527 (95%)	27 (5%)	0	100	100
2	B	408/429 (95%)	388 (95%)	20 (5%)	0	100	100
All	All	962/986 (98%)	915 (95%)	47 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	495/495 (100%)	477 (96%)	18 (4%)	35	46
2	B	374/390 (96%)	362 (97%)	12 (3%)	39	50
All	All	869/885 (98%)	839 (96%)	30 (4%)	36	47

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LYS
1	A	24	TRP
1	A	61	PHE
1	A	65	LYS
1	A	66	LYS
1	A	113	ASP
1	A	116	PHE
1	A	182	GLN
1	A	193	LEU
1	A	220	LYS
1	A	251	SER
1	A	277	ARG
1	A	300	GLU
1	A	306	ASN
1	A	353	LYS
1	A	373	GLN
1	A	516	GLU
1	A	545	ASN
2	B	13	LYS
2	B	101	LYS
2	B	113	ASP
2	B	173	LYS
2	B	193	LEU
2	B	211	ARG
2	B	237	ASP
2	B	238	LYS
2	B	239	TRP
2	B	240	THR
2	B	356	ARG
2	B	361	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides 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$
3	SO4	B	501	-	4,4,4	0.18	0	6,6,6	0.47	0
3	SO4	B	502	-	4,4,4	0.32	0	6,6,6	0.05	0
3	SO4	A	602	-	4,4,4	0.29	0	6,6,6	0.38	0
3	SO4	A	601	-	4,4,4	0.27	0	6,6,6	0.78	0
4	YB7	A	603	-	27,31,31	3.80	7 (25%)	26,45,45	1.84	6 (23%)

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
4	YB7	A	603	-	-	1/13/26/26	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	YB7	C14-N2	15.93	1.59	1.36
4	A	603	YB7	C15-S1	-6.53	1.60	1.73
4	A	603	YB7	C6-N1	5.27	1.45	1.34
4	A	603	YB7	C13-S1	-4.20	1.60	1.73
4	A	603	YB7	C14-C15	3.89	1.47	1.37
4	A	603	YB7	C16-C15	2.20	1.53	1.50
4	A	603	YB7	O6-C6	-2.16	1.18	1.23

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	YB7	C14-C15-S1	-4.84	107.19	112.00
4	A	603	YB7	C4'-C18-N9	-3.39	120.11	123.34
4	A	603	YB7	C18-N9-C1'	3.13	122.02	117.90
4	A	603	YB7	C7-CAA-C1'	-2.84	125.18	129.32
4	A	603	YB7	C2'-C1'-N9	-2.33	118.78	122.26
4	A	603	YB7	CAA-C1'-N9	2.15	120.58	116.77

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	603	YB7	N1-C12-C17-N3

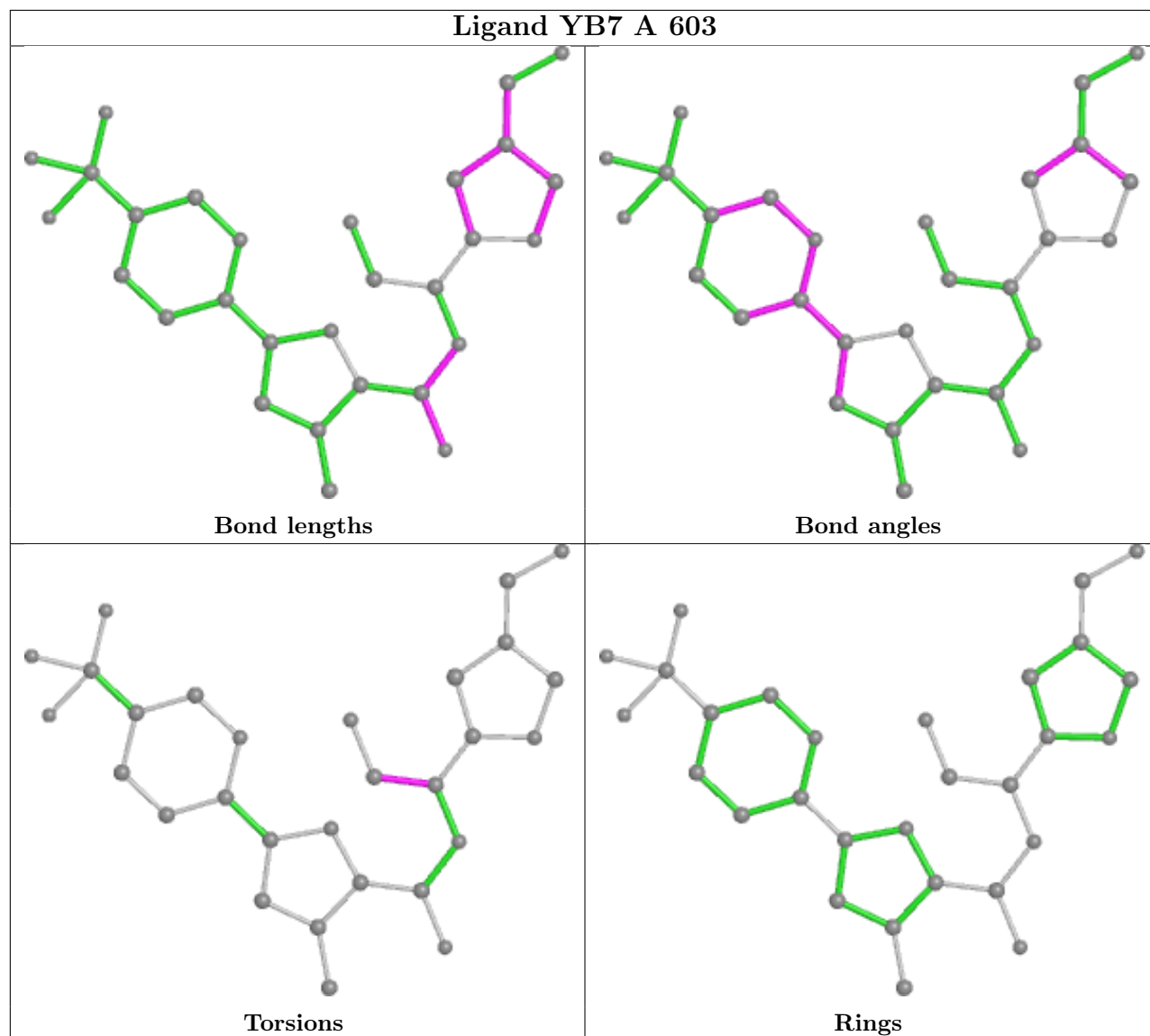
There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	SO4	3	0
3	B	502	SO4	2	0
3	A	602	SO4	2	0
4	A	603	YB7	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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	556/557 (99%)	0.45	53 (9%) 8 5	52, 97, 180, 284	0
2	B	412/429 (96%)	0.56	48 (11%) 4 3	51, 90, 174, 269	0
All	All	968/986 (98%)	0.50	101 (10%) 6 4	51, 93, 178, 284	0

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	90	VAL	12.5
2	B	230	MET	10.7
1	A	289	LEU	10.1
2	B	92	LEU	10.0
2	B	89	GLU	9.6
1	A	554	ALA	9.0
2	B	214	LEU	8.6
1	A	247	PRO	7.9
2	B	231	GLY	7.8
2	B	66	LYS	7.6
2	B	93	GLY	7.6
2	B	358	ARG	6.7
1	A	67	ASP	6.7
1	A	92	LEU	6.4
1	A	290	THR	6.1
1	A	283	LEU	5.7
2	B	91	GLN	5.5
2	B	357	MET	5.4
2	B	241	VAL	5.4
1	A	254	VAL	5.2
1	A	552	VAL	5.0
2	B	173	LYS	4.9
2	B	229	TRP	4.8
2	B	94	ILE	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	282	LEU	4.5
1	A	249	LYS	4.5
2	B	87	PHE	4.4
2	B	354	TYR	4.4
1	A	66	LYS	4.4
2	B	232	TYR	4.3
1	A	261	VAL	4.3
2	B	240	THR	4.2
1	A	284	ARG	4.1
2	B	168	LEU	4.1
2	B	67	ASP	4.0
2	B	15	GLY	4.0
2	B	195	ILE	3.9
2	B	172	LYS	3.8
1	A	246	LEU	3.8
1	A	115	TYR	3.8
1	A	297	GLU	3.7
1	A	287	LYS	3.6
1	A	252	TRP	3.6
2	B	5	ILE	3.5
1	A	70	LYS	3.4
1	A	546	GLU	3.3
1	A	251	SER	3.3
2	B	212	TRP	3.3
1	A	221	HIS	3.2
1	A	288	ALA	3.2
2	B	14	PRO	3.1
1	A	244	ILE	3.1
1	A	315	HIS	3.1
1	A	227	PHE	3.0
2	B	239	TRP	3.0
1	A	295	LEU	3.0
1	A	358	ARG	3.0
1	A	551	LEU	2.9
1	A	301	LEU	2.9
1	A	548	VAL	2.8
1	A	281	LYS	2.8
1	A	544	GLY	2.8
2	B	170	PRO	2.8
2	B	215	THR	2.8
2	B	16	MET	2.7
1	A	220	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	174	GLN	2.7
1	A	304	ALA	2.6
1	A	250	ASP	2.6
2	B	237	ASP	2.6
1	A	278	GLN	2.6
2	B	11	LYS	2.6
2	B	171	PHE	2.5
1	A	68	SER	2.5
1	A	89	GLU	2.5
1	A	224	GLU	2.4
1	A	291	GLU	2.4
2	B	206	ARG	2.4
1	A	65	LYS	2.3
1	A	69	THR	2.3
1	A	219	LYS	2.3
2	B	186	ASP	2.3
2	B	360	ALA	2.3
1	A	545	ASN	2.2
2	B	184	MET	2.2
2	B	183	TYR	2.2
2	B	110	ASP	2.2
1	A	292	VAL	2.2
2	B	409	THR	2.2
1	A	311	LYS	2.2
1	A	248	GLU	2.1
2	B	88	TRP	2.1
2	B	238	LYS	2.1
1	A	313	PRO	2.1
1	A	187	LEU	2.1
2	B	208	HIS	2.1
2	B	75	VAL	2.1
1	A	553	SER	2.1
2	B	209	LEU	2.0
2	B	112	GLY	2.0
1	A	346	PHE	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

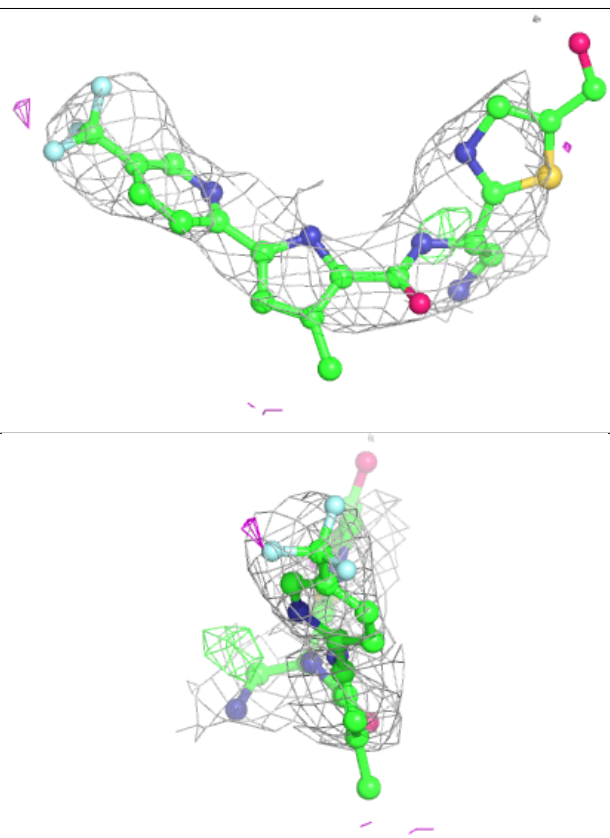
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	SO4	A	601	5/5	0.70	0.21	147,148,151,153	0
4	YB7	A	603	29/29	0.73	0.30	130,150,170,173	0
3	SO4	B	501	5/5	0.76	0.20	169,169,172,174	0
3	SO4	A	602	5/5	0.85	0.28	138,138,140,141	0
3	SO4	B	502	5/5	0.94	0.29	126,127,131,131	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

### Electron density around YB7 A 603:

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.