



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:15 AM GMT

PDB ID : 2WGH
Title : HUMAN RIBONUCLEOTIDE REDUCTASE R1 SUBUNIT (RRM1) IN COMPLEX WITH DATP AND MG.
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Deposited on : 2009-04-19
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (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

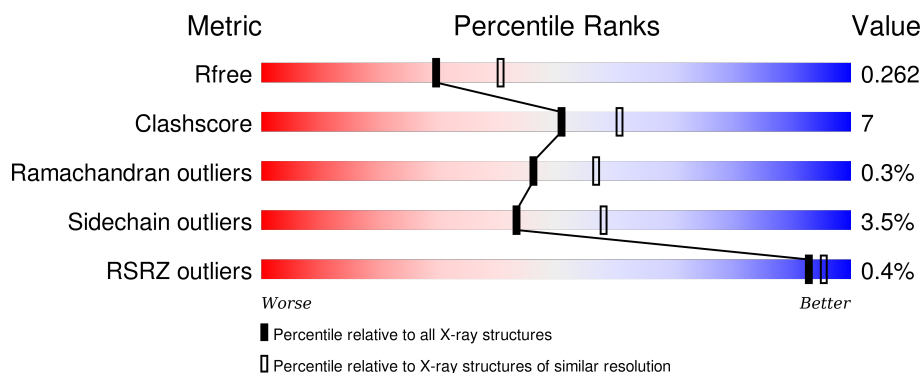
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	676	 78% 16% 5%
1	B	676	 81% 15% . .

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
2	GOL	A	1743	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10661 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 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	644	Total	C	N	O	S	0	0	0
			5132	3275	866	964	27			
1	B	657	Total	C	N	O	S	0	1	0
			5230	3336	885	980	29			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	74	MET	-	EXPRESSION TAG	UNP P23921
A	743	ALA	-	EXPRESSION TAG	UNP P23921
A	744	HIS	-	EXPRESSION TAG	UNP P23921
A	745	HIS	-	EXPRESSION TAG	UNP P23921
A	746	HIS	-	EXPRESSION TAG	UNP P23921
A	747	HIS	-	EXPRESSION TAG	UNP P23921
A	748	HIS	-	EXPRESSION TAG	UNP P23921
A	749	HIS	-	EXPRESSION TAG	UNP P23921
B	74	MET	-	EXPRESSION TAG	UNP P23921
B	743	ALA	-	EXPRESSION TAG	UNP P23921
B	744	HIS	-	EXPRESSION TAG	UNP P23921
B	745	HIS	-	EXPRESSION TAG	UNP P23921
B	746	HIS	-	EXPRESSION TAG	UNP P23921
B	747	HIS	-	EXPRESSION TAG	UNP P23921
B	748	HIS	-	EXPRESSION TAG	UNP P23921
B	749	HIS	-	EXPRESSION TAG	UNP P23921

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).

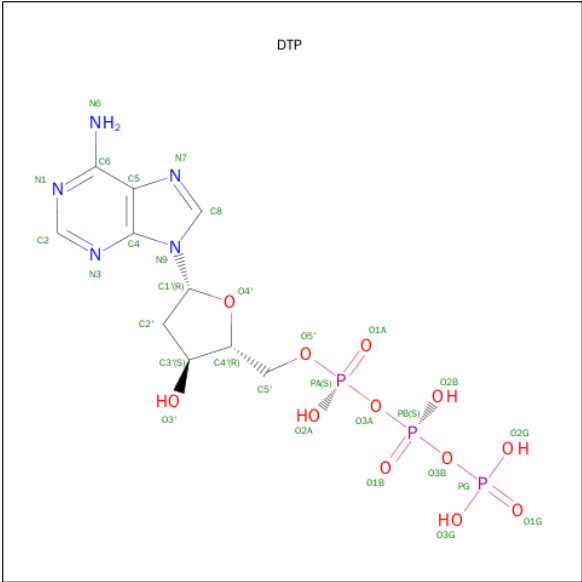


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (three-letter code: DTP) (formula: C₁₀H₁₆N₅O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		
4	B	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

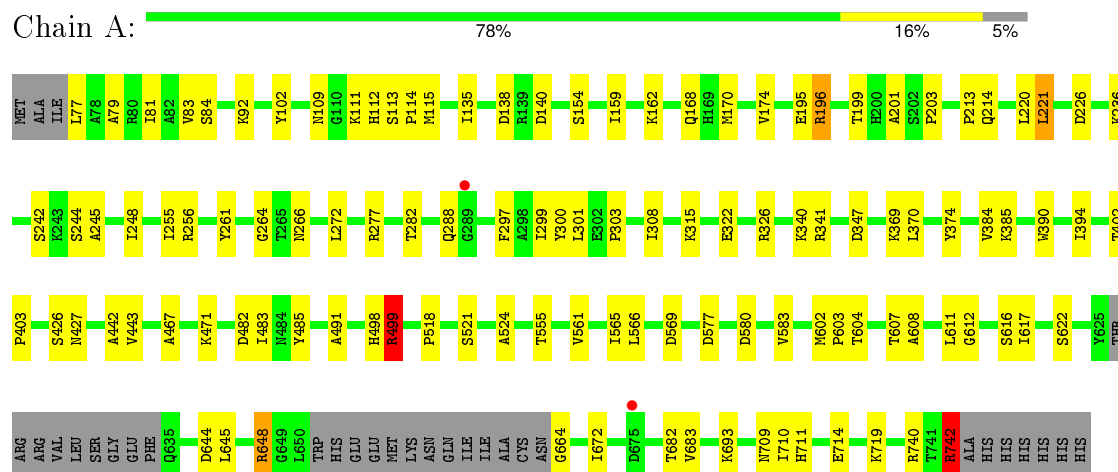
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	118	Total	O	0	0
			118	118		
5	B	113	Total	O	0	0
			113	113		

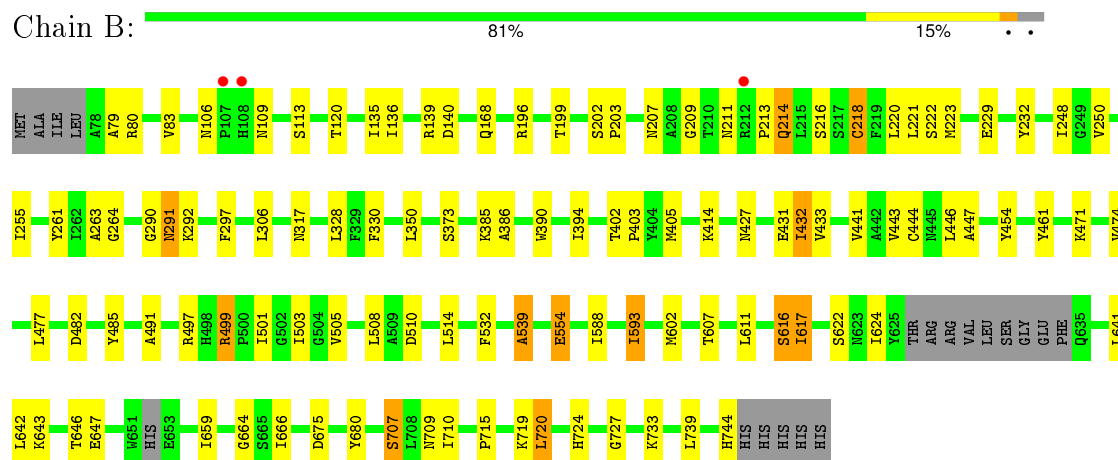
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE SUBUNIT



• Molecule 1: RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE SUBUNIT



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.95Å 129.31Å 76.67Å 90.00° 95.50° 90.00°	Depositor
Resolution (Å)	48.85 – 2.30 48.85 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.85-2.30) 98.4 (48.85-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.51 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.192 , 0.258 0.198 , 0.262	Depositor DCC
R_{free} test set	2837 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 30.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 56722 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10661	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 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, MG, DTP

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	0.84	0/5244	0.82	7/7102 (0.1%)
1	B	0.83	2/5347 (0.0%)	0.80	2/7242 (0.0%)
All	All	0.83	2/10591 (0.0%)	0.81	9/14344 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	218	CYS	CB-SG	-5.87	1.72	1.81
1	B	539	ALA	CA-CB	-5.50	1.40	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	499	ARG	NE-CZ-NH2	-7.67	116.46	120.30
1	A	742	ARG	NE-CZ-NH1	7.40	124.00	120.30
1	B	499	ARG	NE-CZ-NH2	-6.65	116.97	120.30
1	A	277	ARG	NE-CZ-NH1	6.23	123.41	120.30
1	A	499	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	A	221	LEU	CA-CB-CG	5.72	128.45	115.30
1	A	138	ASP	CB-CG-OD1	5.71	123.44	118.30
1	A	138	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	B	499	ARG	NE-CZ-NH1	5.21	122.91	120.30

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	5132	0	5095	67	0
1	B	5230	0	5186	76	0
2	A	6	0	8	3	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	30	0	12	1	0
4	B	30	0	12	2	0
5	A	118	0	0	1	0
5	B	113	0	0	2	0
All	All	10661	0	10313	142	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 7.

All (142) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:616:SER:OG	1:B:617:ILE:N	2.04	0.90
1:B:624:ILE:HD11	1:B:659:ILE:HG22	1.55	0.89
4:B:1745:DTP:H8	4:B:1745:DTP:O5'	1.79	0.82
1:B:720:LEU:HD21	1:B:739:LEU:HD22	1.64	0.80
1:B:624:ILE:HD11	1:B:659:ILE:CG2	2.12	0.78
1:B:624:ILE:CD1	1:B:659:ILE:HG22	2.14	0.76
1:B:290:GLY:O	1:B:292:LYS:N	2.18	0.76
1:A:604:THR:HA	2:A:1743:GOL:H11	1.73	0.71
1:A:644:ASP:O	1:A:648:ARG:HG2	1.91	0.70
1:B:532:PHE:CZ	1:B:617:ILE:HD11	2.27	0.69
1:B:532:PHE:HZ	1:B:617:ILE:HD11	1.57	0.68
1:A:220:LEU:HB2	1:A:442:ALA:HB3	1.76	0.67
1:B:616:SER:HG	1:B:617:ILE:H	1.41	0.66
1:B:709:ASN:O	1:B:710:ILE:HD12	1.95	0.65
1:A:580:ASP:OD2	1:A:583:VAL:HG23	1.97	0.64
1:B:218:CYS:HB3	1:B:432[A]:ILE:HD11	1.81	0.61
1:A:248:ILE:HD12	1:A:297:PHE:CE2	2.36	0.61
1:B:202:SER:HB2	1:B:203:PRO:HD3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:709:ASN:C	1:B:710:ILE:HD12	2.21	0.60
1:A:264:GLY:HA3	4:A:1745:DTP:O1B	2.02	0.59
1:A:742:ARG:HG3	1:A:742:ARG:HH11	1.68	0.59
1:B:643:LYS:O	1:B:647:GLU:HG3	2.03	0.59
1:B:264:GLY:HA3	4:B:1745:DTP:O1B	2.02	0.58
1:B:79:ALA:O	1:B:83:VAL:HG23	2.03	0.58
1:A:443:VAL:CG2	1:A:491:ALA:HB1	2.35	0.57
1:A:261:TYR:OH	1:A:266:ASN:OD1	2.18	0.56
1:B:622:SER:OG	1:B:664:GLY:HA3	2.05	0.56
1:A:714:GLU:O	1:A:719:LYS:NZ	2.39	0.56
1:A:482:ASP:OD2	1:A:499:ARG:NH2	2.39	0.56
1:B:220:LEU:HD11	1:B:432[A]:ILE:HG13	1.88	0.55
1:B:497:ARG:O	1:B:554:GLU:HB3	2.07	0.55
1:B:120:THR:HG21	1:B:209:GLY:HA2	1.90	0.54
1:B:617:ILE:O	1:B:617:ILE:HG23	2.07	0.54
1:B:248:ILE:HG22	1:B:250:VAL:HG23	1.90	0.54
1:A:170:MET:O	1:A:174:VAL:HG23	2.08	0.54
1:B:218:CYS:SG	1:B:432[B]:ILE:CD1	2.95	0.54
1:B:642:LEU:O	1:B:646:THR:HG23	2.07	0.54
1:A:315:LYS:NZ	1:A:326:ARG:O	2.39	0.54
1:A:482:ASP:CG	1:A:499:ARG:HH22	2.12	0.53
1:B:715:PRO:HB2	1:B:720:LEU:HD11	1.89	0.53
1:B:402:THR:HB	1:B:403:PRO:HA	1.89	0.53
1:B:443:VAL:HG21	1:B:491:ALA:HB1	1.91	0.52
1:B:223:MET:HG2	1:B:255:ILE:HD11	1.90	0.52
1:B:427:ASN:ND2	1:B:432[B]:ILE:HD12	2.24	0.52
1:A:709:ASN:O	1:A:710:ILE:HD12	2.10	0.52
1:B:433:VAL:HG13	5:B:2049:HOH:O	2.08	0.52
1:B:443:VAL:CG2	1:B:491:ALA:HB1	2.40	0.51
1:A:303:PRO:HA	1:A:308:ILE:HD13	1.92	0.51
1:A:498:HIS:CE1	1:A:555:THR:HG21	2.46	0.51
1:B:290:GLY:C	1:B:292:LYS:H	2.13	0.51
1:A:602:MET:HG3	2:A:1743:GOL:H31	1.93	0.51
1:B:641:LEU:HD13	1:B:680:TYR:CD1	2.45	0.51
1:A:467:ALA:O	1:A:471:LYS:HG3	2.10	0.50
1:A:201:ALA:HB1	1:A:203:PRO:HD2	1.92	0.50
1:B:588:ILE:HG12	1:B:593:ILE:CD1	2.41	0.50
1:A:370:LEU:HD11	1:A:374:TYR:CZ	2.47	0.50
1:B:140:ASP:OD2	1:B:168:GLN:HG2	2.11	0.50
1:A:196:ARG:HG2	1:A:611:LEU:HD22	1.92	0.49
1:A:742:ARG:HH11	1:A:742:ARG:CG	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:HIS:CE1	1:A:114:PRO:HG3	2.47	0.49
1:B:441:VAL:O	1:B:491:ALA:HA	2.13	0.49
1:B:199:THR:HG21	1:B:607:THR:HB	1.95	0.49
1:A:622:SER:HA	1:A:682:THR:HG22	1.95	0.48
1:A:443:VAL:HG21	1:A:491:ALA:HB1	1.95	0.48
1:B:727:GLY:HA3	5:B:2108:HOH:O	2.12	0.48
1:A:622:SER:HB2	1:A:664:GLY:N	2.27	0.48
1:A:81:ILE:O	1:A:84:SER:OG	2.28	0.48
1:B:508:LEU:HD22	1:B:617:ILE:HG13	1.95	0.48
1:A:709:ASN:C	1:A:710:ILE:HD12	2.34	0.48
1:A:199:THR:HG21	1:A:607:THR:HB	1.94	0.48
1:B:715:PRO:CB	1:B:720:LEU:HD11	2.44	0.48
1:B:196:ARG:HG2	1:B:611:LEU:HD22	1.96	0.48
1:A:255:ILE:HB	1:A:272:LEU:HD21	1.96	0.47
1:B:290:GLY:C	1:B:292:LYS:N	2.67	0.47
1:A:602:MET:HB2	1:A:603:PRO:CD	2.44	0.47
1:B:220:LEU:HD12	1:B:220:LEU:N	2.29	0.47
1:A:645:LEU:HD21	1:A:672:ILE:HG12	1.96	0.47
1:B:330:PHE:O	1:B:403:PRO:HA	2.14	0.47
1:B:446:LEU:HB3	1:B:602:MET:HE2	1.97	0.47
1:B:248:ILE:CG2	1:B:250:VAL:CG2	2.92	0.47
1:B:390:TRP:NE1	1:B:394:ILE:HD11	2.30	0.47
1:A:402:THR:HB	1:A:403:PRO:HA	1.97	0.47
1:B:106:ASN:HB3	1:B:109:ASN:HB2	1.97	0.46
1:B:211:ASN:O	1:B:213:PRO:HD3	2.15	0.46
1:B:641:LEU:HD21	1:B:666:ILE:HG21	1.96	0.46
1:A:140:ASP:OD2	1:A:168:GLN:HG2	2.16	0.46
1:A:604:THR:O	1:A:608:ALA:HB3	2.16	0.46
1:A:341:ARG:HD2	1:A:347:ASP:O	2.16	0.46
1:A:521:SER:O	1:A:524:ALA:HB3	2.16	0.46
1:A:683:VAL:HG21	1:A:711:HIS:CE1	2.52	0.45
1:B:297:PHE:HB2	1:B:328:LEU:HD22	1.97	0.45
1:A:109:ASN:HB3	1:A:111:LYS:H	1.81	0.45
1:A:195:GLU:O	1:A:196:ARG:HB2	2.17	0.45
1:A:604:THR:O	1:A:608:ALA:CB	2.65	0.45
1:A:213:PRO:HD2	1:A:485:TYR:CD1	2.52	0.45
1:B:505:VAL:O	1:B:616:SER:HA	2.17	0.45
1:A:301:LEU:HD23	1:A:308:ILE:HD12	1.99	0.45
1:B:474:VAL:HG21	1:B:539:ALA:HA	1.98	0.44
1:B:482:ASP:CG	1:B:499:ARG:HH22	2.20	0.44
1:B:405:MET:HG3	1:B:724:HIS:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:VAL:HG12	1:A:385:LYS:N	2.33	0.44
1:A:248:ILE:HD12	1:A:297:PHE:CD2	2.52	0.44
1:B:474:VAL:CG2	1:B:503:ILE:HD11	2.47	0.44
1:A:612:GLY:HA3	5:A:2009:HOH:O	2.17	0.44
1:B:385:LYS:O	1:B:386:ALA:C	2.55	0.44
1:B:248:ILE:CG2	1:B:250:VAL:HG23	2.47	0.44
1:A:226:ASP:OD1	1:A:256:ARG:HB3	2.18	0.44
1:A:201:ALA:CB	1:A:203:PRO:HD2	2.48	0.43
1:A:604:THR:HA	2:A:1743:GOL:C1	2.43	0.43
1:A:79:ALA:O	1:A:83:VAL:HG23	2.19	0.43
1:B:474:VAL:HG23	1:B:503:ILE:HD11	2.01	0.42
1:B:431:GLU:HB3	1:B:707:SER:OG	2.20	0.42
1:B:715:PRO:HB2	1:B:720:LEU:CD1	2.48	0.42
1:B:588:ILE:HG12	1:B:593:ILE:HD13	2.01	0.42
1:A:242:SER:O	1:A:288:GLN:HA	2.20	0.42
1:B:454:TYR:HB2	1:B:461:TYR:CZ	2.54	0.42
1:A:300:TYR:OH	1:A:426:SER:HB3	2.19	0.42
1:A:244:SER:O	1:A:245:ALA:HB3	2.20	0.42
1:B:290:GLY:O	1:B:291:ASN:C	2.59	0.42
1:A:616:SER:OG	1:A:617:ILE:N	2.52	0.42
1:A:236:LYS:NZ	1:B:229:GLU:HG3	2.34	0.42
1:A:566:LEU:O	1:A:569:ASP:HB2	2.19	0.42
1:B:136:ILE:CD1	1:B:139:ARG:NH2	2.83	0.41
1:B:218:CYS:CB	1:B:432[A]:ILE:HD11	2.49	0.41
1:A:742:ARG:HG3	1:A:742:ARG:NH1	2.33	0.41
1:A:300:TYR:OH	1:A:427:ASN:O	2.31	0.41
1:B:447:ALA:HB2	1:B:477:LEU:HD21	2.01	0.41
1:A:518:PRO:O	1:A:524:ALA:HB2	2.20	0.41
1:B:214:GLN:HG2	1:B:485:TYR:O	2.20	0.41
1:B:414:LYS:HB2	1:B:733:LYS:HE2	2.02	0.41
1:A:282:THR:HG23	1:B:232:TYR:OH	2.20	0.41
1:B:624:ILE:CD1	1:B:659:ILE:CG2	2.86	0.41
1:B:477:LEU:HD12	1:B:501:ILE:HD12	2.02	0.41
1:A:483:ILE:HD13	1:A:483:ILE:HG21	1.66	0.41
1:B:261:TYR:CE1	1:B:263:ALA:HA	2.56	0.41
1:A:561:VAL:HA	1:A:565:ILE:O	2.21	0.41
1:A:390:TRP:NE1	1:A:394:ILE:HD12	2.36	0.41
1:A:102:TYR:CD1	1:A:114:PRO:HB3	2.56	0.41
1:A:714:GLU:O	1:A:719:LYS:CE	2.70	0.40
1:B:207:ASN:HB3	1:B:213:PRO:HA	2.03	0.40
1:B:306:LEU:HA	1:B:350:LEU:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:MET:CE	1:A:159:ILE:HG12	2.52	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	638/676 (94%)	614 (96%)	23 (4%)	1 (0%)	52 64
1	B	652/676 (96%)	624 (96%)	25 (4%)	3 (0%)	34 41
All	All	1290/1352 (95%)	1238 (96%)	48 (4%)	4 (0%)	46 57

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	291	ASN
1	B	675	ASP
1	A	196	ARG
1	B	707	SER

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	558/590 (95%)	540 (97%)	18 (3%)	46 62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	567/590 (96%)	545 (96%)	22 (4%)	39	53
All	All	1125/1180 (95%)	1085 (96%)	40 (4%)	43	57

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	77	LEU
1	A	92	LYS
1	A	113	SER
1	A	135	ILE
1	A	154	SER
1	A	162	LYS
1	A	214	GLN
1	A	221	LEU
1	A	299	ILE
1	A	322	GLU
1	A	340	LYS
1	A	369	LYS
1	A	499	ARG
1	A	577	ASP
1	A	648	ARG
1	A	693	LYS
1	A	740	ARG
1	A	742	ARG
1	B	80	ARG
1	B	113	SER
1	B	135	ILE
1	B	214	GLN
1	B	216	SER
1	B	221	LEU
1	B	222	SER
1	B	317	ASN
1	B	373	SER
1	B	432[A]	ILE
1	B	432[B]	ILE
1	B	444	CYS
1	B	471	LYS
1	B	510	ASP
1	B	514	LEU
1	B	554	GLU
1	B	593	ILE
1	B	616	SER

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Mol	Chain	Res	Type
1	B	617	ILE
1	B	719	LYS
1	B	720	LEU
1	B	744	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	237	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 ⓘ

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 for Mogul analysis.

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	GOL	A	1743	-	5,5,5	0.75	0	5,5,5	0.79	0
4	DTP	A	1745	3	24,32,32	1.28	1 (4%)	32,50,50	2.27	4 (12%)
4	DTP	B	1745	3	24,32,32	1.37	4 (16%)	32,50,50	2.29	6 (18%)

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	GOL	A	1743	-	-	0/4/4/4	0/0/0/0
4	DTP	A	1745	3	-	0/18/34/34	0/3/3/3
4	DTP	B	1745	3	-	0/18/34/34	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1745	DTP	PG-O2G	2.25	1.62	1.54
4	A	1745	DTP	PA-O1A	2.28	1.59	1.51
4	B	1745	DTP	PB-O1B	2.28	1.59	1.51
4	B	1745	DTP	PA-O1A	2.35	1.59	1.51
4	B	1745	DTP	PG-O1G	2.83	1.60	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1745	DTP	N3-C2-N1	-9.71	121.46	128.89
4	B	1745	DTP	N3-C2-N1	-9.58	121.56	128.89
4	A	1745	DTP	PB-O3B-PG	-4.65	117.08	132.67
4	B	1745	DTP	PB-O3B-PG	-4.44	117.77	132.67
4	A	1745	DTP	C4-C5-N7	-3.57	106.20	109.48
4	A	1745	DTP	PA-O3A-PB	-3.52	122.84	132.73
4	B	1745	DTP	C2'-C1'-N9	-3.49	105.67	114.16
4	B	1745	DTP	C4-C5-N7	-2.40	107.27	109.48
4	B	1745	DTP	PA-O3A-PB	-2.17	126.63	132.73
4	B	1745	DTP	O2B-PB-O3A	2.23	115.21	105.09

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1743	GOL	3	0
4	A	1745	DTP	1	0
4	B	1745	DTP	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	644/676 (95%)	-0.37	2 (0%) 94 96	12, 25, 43, 51	0
1	B	657/676 (97%)	-0.33	3 (0%) 91 94	12, 24, 43, 60	0
All	All	1301/1352 (96%)	-0.35	5 (0%) 93 95	12, 25, 43, 60	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	107	PRO	3.2
1	B	212	ARG	2.8
1	B	108	HIS	2.3
1	A	675	ASP	2.1
1	A	289	GLY	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	GOL	A	1743	6/6	0.89	0.17	3.58	30,32,34,36	0
4	DTP	B	1745	30/30	0.97	0.09	-0.61	17,20,25,27	0
4	DTP	A	1745	30/30	0.98	0.10	-0.75	13,20,29,30	0
3	MG	B	1746	1/1	0.99	0.06	-	18,18,18,18	0
3	MG	A	1744	1/1	0.97	0.06	-	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.