



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:16 PM GMT

PDB ID : 3WPH
Title : Crystal structure of mouse TLR9 in complex with inhibitory DNA4084 (form 2)
Authors : Ohto, U.; Shimizu, T.
Deposited on : 2014-01-11
Resolution : 2.33 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

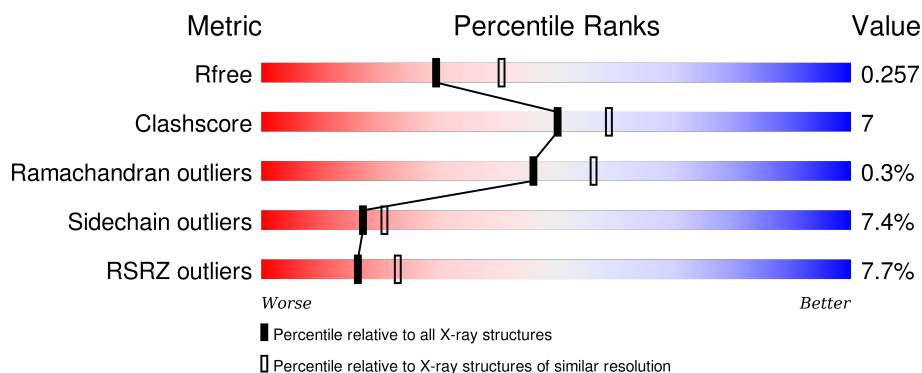
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.33 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	4425 (2.34-2.30)
Clashscore	102246	5057 (2.34-2.30)
Ramachandran outliers	100387	5008 (2.34-2.30)
Sidechain outliers	100360	5007 (2.34-2.30)
RSRZ outliers	91569	4432 (2.34-2.30)

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	803	 7% 71% 17% 10%
2	B	12	 58% 42%

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
4	SO4	A	904	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6169 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 Toll-like receptor 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	725	Total	C	N	O	S	11	0	0
			5728	3659	1007	1033	29			

There are 17 discrepancies between the modelled and reference sequences:

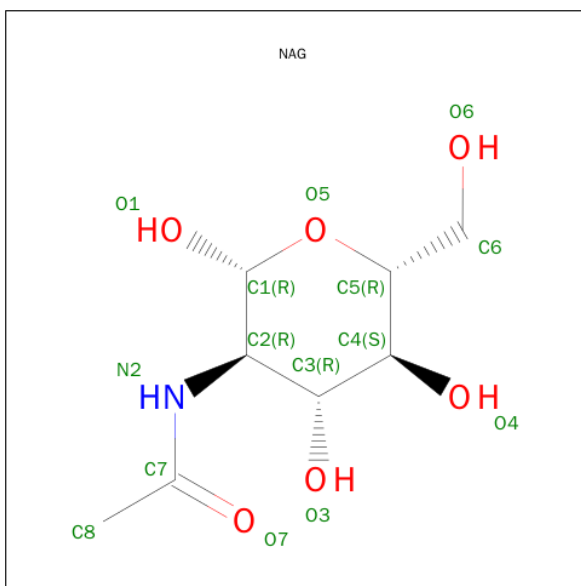
Chain	Residue	Modelled	Actual	Comment	Reference
A	22	ARG	-	EXPRESSION TAG	UNP Q9EQU3
A	23	SER	-	EXPRESSION TAG	UNP Q9EQU3
A	24	PRO	-	EXPRESSION TAG	UNP Q9EQU3
A	25	TRP	-	EXPRESSION TAG	UNP Q9EQU3
A	200	GLN	ASN	ENGINEERED MUTATION	UNP Q9EQU3
A	242	GLN	ASN	ENGINEERED MUTATION	UNP Q9EQU3
A	309	GLN	ASN	ENGINEERED MUTATION	UNP Q9EQU3
A	495	GLN	ASN	ENGINEERED MUTATION	UNP Q9EQU3
A	568	GLN	ASN	ENGINEERED MUTATION	UNP Q9EQU3
A	695	GLN	ASN	ENGINEERED MUTATION	UNP Q9EQU3
A	752	GLN	ASN	ENGINEERED MUTATION	UNP Q9EQU3
A	819	GLU	-	EXPRESSION TAG	UNP Q9EQU3
A	820	PHE	-	EXPRESSION TAG	UNP Q9EQU3
A	821	LEU	-	EXPRESSION TAG	UNP Q9EQU3
A	822	VAL	-	EXPRESSION TAG	UNP Q9EQU3
A	823	PRO	-	EXPRESSION TAG	UNP Q9EQU3
A	824	ARG	-	EXPRESSION TAG	UNP Q9EQU3

- Molecule 2 is a DNA chain called DNA (5'-D(*CP*CP*TP*GP*GP*AP*TP*GP*GP*GP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	12	Total	C	N	O	P	0	0	0
			248	118	50	69	11			

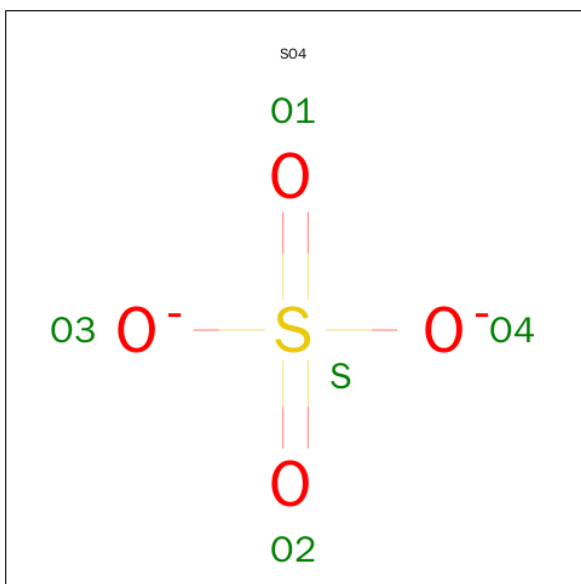
- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:

C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



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

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

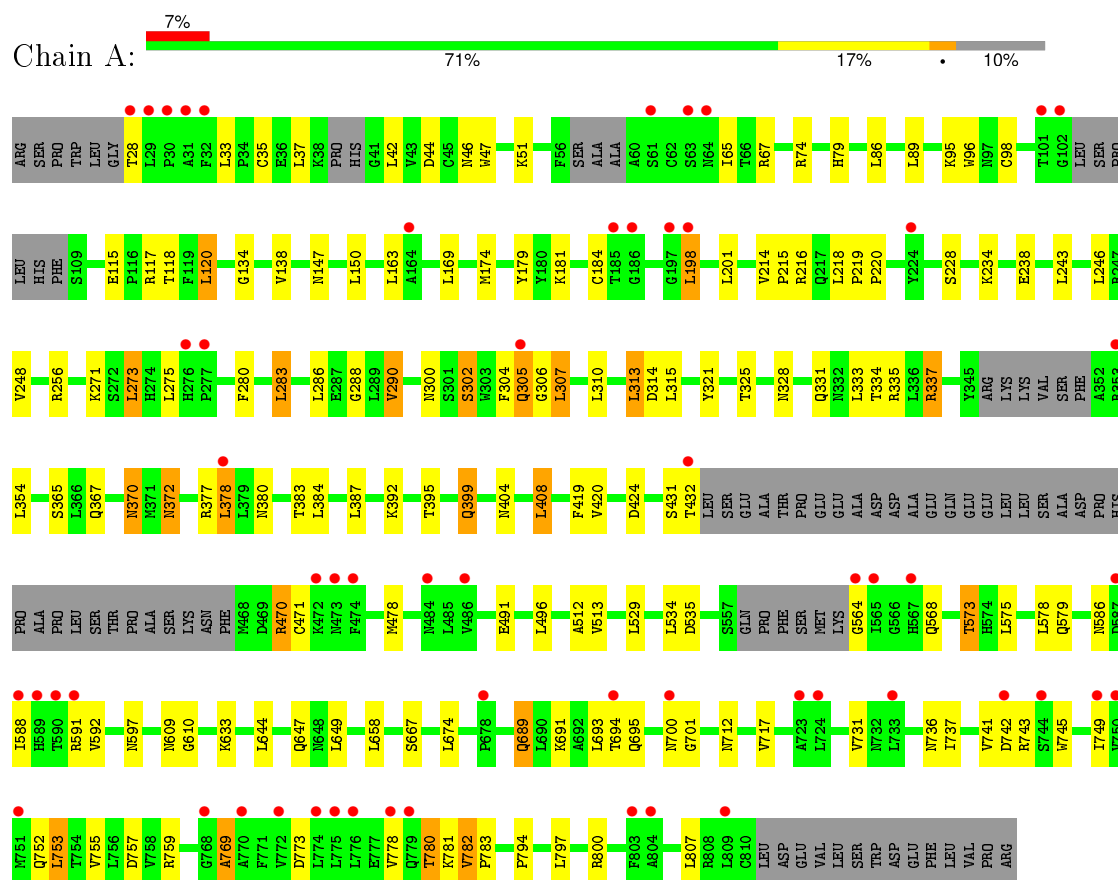
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	136	Total	O	0	0
			136	136		
5	B	14	Total	O	0	0
			14	14		

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 ($\text{RSRZ} > 2$). 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: Toll-like receptor 9



• Molecule 2: DNA (5'-D(*CP*CP*TP*GP*GP*AP*TP*GP*GP*GP*AP*A)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	136.41Å 130.10Å 71.33Å 90.00° 91.54° 90.00°	Depositor
Resolution (Å)	38.95 – 2.33 38.95 – 2.33	Depositor EDS
% Data completeness (in resolution range)	99.6 (38.95-2.33) 99.7 (38.95-2.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 2.31Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.213 , 0.247 0.225 , 0.257	Depositor DCC
R_{free} test set	2704 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.909	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.4	EDS
Estimated twinning fraction	0.000 for k,h,-l 0.000 for -k,-h,-l 0.038 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 53149 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6169	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, 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	0.30	0/5849	0.50	0/7935
2	B	0.58	0/279	1.19	1/430 (0.2%)
All	All	0.32	0/6128	0.55	1/8365 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4	DG	O4'-C1'-N9	6.16	112.31	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5728	0	5776	82	1
2	B	248	0	136	3	0
3	A	28	0	26	0	0
4	A	10	0	0	1	0
4	B	5	0	0	0	0
5	A	136	0	0	2	1
5	B	14	0	0	1	0
All	All	6169	0	5938	84	1

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 (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:A:256:ARG:NH1	4:A:904:SO4:O4	2.20	0.71
1:A:564:GLY:O	1:A:591:ARG:NH1	2.28	0.67
1:A:689:GLN:HB2	1:A:691:LYS:HE3	1.80	0.65
1:A:712:ASN:O	1:A:736:ASN:ND2	2.31	0.64
1:A:147:ASN:ND2	5:A:1038:HOH:O	2.29	0.63
1:A:305:GLN:OE1	1:A:306:GLY:N	2.34	0.60
1:A:95:LYS:HG2	1:A:96:TRP:CD1	2.37	0.60
1:A:304:PHE:HA	1:A:307:LEU:HD22	1.82	0.60
1:A:717:VAL:HB	1:A:745:TRP:CE2	2.37	0.59
1:A:337:ARG:HD3	1:A:367:GLN:HE21	1.66	0.59
1:A:568:GLN:HB2	1:A:592:VAL:HA	1.85	0.59
1:A:378:LEU:HD23	1:A:380:ASN:HD22	1.68	0.58
1:A:115:GLU:O	1:A:118:THR:HG23	2.04	0.58
1:A:273:LEU:HD13	1:A:275:LEU:HG	1.86	0.57
1:A:588:ILE:HD11	1:A:610:GLY:H	1.69	0.57
1:A:150:LEU:HB2	1:A:174:MET:HG3	1.85	0.57
1:A:328:ASN:HB2	1:A:331:GLN:HE21	1.70	0.57
1:A:753:LEU:O	1:A:781:LYS:HD2	2.05	0.57
1:A:408:LEU:HB3	1:A:496:LEU:HD11	1.88	0.56
1:A:780:THR:HG23	1:A:781:LYS:HE2	1.86	0.56
1:A:42:LEU:HA	1:A:67:ARG:HB2	1.89	0.55
1:A:46:ASN:HB3	1:A:47:TRP:CE3	2.42	0.55
1:A:328:ASN:HB2	1:A:331:GLN:NE2	2.22	0.54
1:A:377:ARG:HE	1:A:404:ASN:HD21	1.55	0.53
1:A:384:LEU:HG	1:A:387:LEU:HD12	1.90	0.53
1:A:512:ALA:HA	1:A:535:ASP:HB3	1.90	0.53
1:A:283:LEU:HB3	1:A:286:LEU:HB2	1.90	0.52
1:A:215:PRO:HB2	1:A:218:LEU:HD21	1.91	0.52
1:A:304:PHE:HB3	1:A:333:LEU:HD21	1.91	0.51
1:A:214:VAL:O	1:A:216:ARG:NH1	2.44	0.50
1:A:96:TRP:NE1	5:A:1074:HOH:O	2.34	0.50
1:A:313:LEU:HD22	1:A:315:LEU:HG	1.93	0.50
1:A:757:ASP:OD1	1:A:759:ARG:HD3	2.12	0.50
1:A:377:ARG:NE	1:A:404:ASN:HD21	2.11	0.48
1:A:288:GLY:HA3	2:B:1:DC:H5'	1.94	0.48
1:A:117:ARG:HA	1:A:120:LEU:HD23	1.96	0.48
1:A:633:LYS:HG2	1:A:658:LEU:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:LEU:HG	1:A:478:MET:CE	2.45	0.47
1:A:742:ASP:OD1	1:A:743:ARG:N	2.48	0.46
1:A:575:LEU:HD12	1:A:578:LEU:HD22	1.97	0.46
1:A:694:THR:OG1	1:A:695:GLN:N	2.49	0.46
1:A:782:VAL:HA	1:A:783:PRO:HD3	1.76	0.46
1:A:769:ALA:HB3	1:A:807:LEU:HD23	1.97	0.46
1:A:588:ILE:HD13	1:A:609:ASN:HB3	1.97	0.45
1:A:79:HIS:C	1:A:118:THR:HG22	2.37	0.45
1:A:300:ASN:OD1	1:A:302:SER:OG	2.35	0.45
1:A:378:LEU:CD2	1:A:380:ASN:HD22	2.30	0.45
1:A:529:LEU:HD22	1:A:534:LEU:HD11	1.99	0.45
1:A:238:GLU:H	1:A:238:GLU:CD	2.19	0.45
1:A:86:LEU:HB3	1:A:89:LEU:HG	1.99	0.45
1:A:644:LEU:HA	1:A:644:LEU:HD12	1.80	0.45
1:A:395:THR:HG23	1:A:419:PHE:HD2	1.82	0.44
1:A:95:LYS:HG2	1:A:96:TRP:HD1	1.82	0.44
1:A:337:ARG:NH1	1:A:365:SER:O	2.51	0.44
1:A:778:VAL:O	1:A:782:VAL:HG12	2.17	0.44
1:A:408:LEU:HG	1:A:478:MET:HE1	1.99	0.44
1:A:35:CYS:HB3	1:A:44:ASP:O	2.18	0.44
1:A:370:ASN:N	1:A:370:ASN:OD1	2.51	0.44
1:A:337:ARG:HH22	1:A:392:LYS:NZ	2.16	0.43
1:A:470:ARG:N	1:A:471:CYS:HB2	2.33	0.43
1:A:372:ASN:OD1	1:A:399:GLN:NE2	2.52	0.43
1:A:163:LEU:HD13	1:A:198:LEU:HD21	2.01	0.43
1:A:749:ILE:HG23	1:A:752:GLN:HE21	1.84	0.43
2:B:2:DC:H2'	2:B:3:DT:O4'	2.19	0.43
1:A:337:ARG:HD3	1:A:367:GLN:NE2	2.32	0.42
1:A:700:ASN:HA	1:A:701:GLY:HA2	1.65	0.42
1:A:573:THR:HB	1:A:597:ASN:HB2	2.00	0.42
1:A:51:LYS:HE2	1:A:74:ARG:CZ	2.49	0.42
1:A:431:SER:OG	1:A:432:THR:N	2.52	0.42
1:A:321:TYR:CZ	1:A:354:LEU:HD23	2.55	0.42
1:A:198:LEU:HB3	1:A:201:LEU:HB2	2.02	0.42
1:A:238:GLU:N	1:A:238:GLU:OE1	2.44	0.41
1:A:310:LEU:HA	1:A:310:LEU:HD12	1.79	0.41
1:A:280:PHE:HA	1:A:283:LEU:HD22	2.02	0.41
1:A:219:PRO:HA	1:A:220:PRO:HD3	1.88	0.41
1:A:179:TYR:CZ	1:A:181:LYS:HB2	2.56	0.41
2:B:11:DA:N6	5:B:206:HOH:O	2.52	0.41
1:A:383:THR:HG22	1:A:384:LEU:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:CYS:O	1:A:134:GLY:N	2.52	0.41
1:A:800:ARG:HD2	1:A:800:ARG:HA	1.87	0.41
1:A:759:ARG:HD2	1:A:783:PRO:O	2.21	0.41
1:A:290:VAL:HB	1:A:314:ASP:HB3	2.03	0.40
1:A:243:LEU:HB3	1:A:246:LEU:HG	2.03	0.40
1:A:794:PRO:HD2	1:A:797:LEU:HD22	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:647:GLN:OE1	5:A:1002:HOH:O[4_555]	2.15	0.05

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	711/803 (88%)	655 (92%)	54 (8%)	2 (0%)	46 56

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	470	ARG
1	A	769	ALA

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	659/728 (90%)	610 (93%)	49 (7%)	17	21

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	THR
1	A	33	LEU
1	A	37	LEU
1	A	65	ILE
1	A	120	LEU
1	A	138	VAL
1	A	169	LEU
1	A	184	CYS
1	A	198	LEU
1	A	228	SER
1	A	234	LYS
1	A	248	VAL
1	A	271	LYS
1	A	273	LEU
1	A	283	LEU
1	A	290	VAL
1	A	302	SER
1	A	305	GLN
1	A	307	LEU
1	A	313	LEU
1	A	325	THR
1	A	334	THR
1	A	335	ARG
1	A	337	ARG
1	A	370	ASN
1	A	372	ASN
1	A	378	LEU
1	A	399	GLN
1	A	408	LEU
1	A	420	VAL
1	A	424	ASP
1	A	491	GLU
1	A	513	VAL
1	A	573	THR
1	A	579	GLN
1	A	586	ASN

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Mol	Chain	Res	Type
1	A	649	LEU
1	A	667	SER
1	A	674	LEU
1	A	689	GLN
1	A	693	LEU
1	A	731	VAL
1	A	737	ILE
1	A	741	VAL
1	A	753	LEU
1	A	755	VAL
1	A	773	ASP
1	A	780	THR
1	A	782	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	270	GLN
1	A	331	GLN
1	A	367	GLN
1	A	399	GLN
1	A	595	HIS
1	A	736	ASN

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	$\# Z > 2$
3	NAG	A	901	1	14,14,15	0.47	0	15,19,21	1.10	1 (6%)
3	NAG	A	902	1	14,14,15	0.39	0	15,19,21	1.18	2 (13%)
4	SO4	A	903	-	4,4,4	0.29	0	6,6,6	0.09	0
4	SO4	A	904	-	4,4,4	0.28	0	6,6,6	0.08	0
4	SO4	B	101	-	4,4,4	0.26	0	6,6,6	0.07	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
3	NAG	A	901	1	-	0/6/23/26	0/1/1/1
3	NAG	A	902	1	-	0/6/23/26	0/1/1/1
4	SO4	A	903	-	-	0/0/0/0	0/0/0/0
4	SO4	A	904	-	-	0/0/0/0	0/0/0/0
4	SO4	B	101	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	902	NAG	C2-N2-C7	-2.14	120.29	123.04
3	A	902	NAG	C1-O5-C5	3.42	116.59	112.25
3	A	901	NAG	C1-O5-C5	3.65	116.89	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	904	SO4	1	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, 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	725/803 (90%)	0.73	57 (7%) 15 22	17, 45, 86, 125	2 (0%)
2	B	12/12 (100%)	-0.05	0 100 100	23, 31, 63, 72	0
All	All	737/815 (90%)	0.72	57 (7%) 16 23	17, 45, 86, 125	2 (0%)

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	565	ILE	7.8
1	A	102	GLY	7.4
1	A	473	ASN	6.8
1	A	744	SER	6.5
1	A	474	PHE	6.4
1	A	29	LEU	6.3
1	A	750	VAL	6.3
1	A	587	ASP	6.2
1	A	749	ILE	5.5
1	A	590	THR	4.9
1	A	31	ALA	4.7
1	A	772	VAL	4.3
1	A	305	GLN	4.2
1	A	185	THR	4.2
1	A	63	SER	4.2
1	A	776	LEU	4.1
1	A	588	ILE	4.1
1	A	564	GLY	4.0
1	A	751	MET	4.0
1	A	589	HIS	3.8
1	A	804	ALA	3.7
1	A	432	THR	3.5
1	A	61	SER	3.5
1	A	591	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	276	HIS	3.4
1	A	724	LEU	3.4
1	A	803	PHE	3.1
1	A	472	LYS	3.1
1	A	30	PRO	3.1
1	A	779	GLN	3.1
1	A	224	TYR	3.0
1	A	378	LEU	2.9
1	A	809	LEU	2.9
1	A	700	ASN	2.9
1	A	694	THR	2.9
1	A	486	VAL	2.9
1	A	198	LEU	2.9
1	A	32	PHE	2.8
1	A	778	VAL	2.8
1	A	774	LEU	2.7
1	A	353	ARG	2.6
1	A	28	THR	2.6
1	A	277	PRO	2.5
1	A	567	HIS	2.5
1	A	164	ALA	2.4
1	A	64	ASN	2.3
1	A	101	THR	2.3
1	A	742	ASP	2.3
1	A	197	GLY	2.2
1	A	775	LEU	2.2
1	A	770	ALA	2.2
1	A	768	GLY	2.1
1	A	733	LEU	2.1
1	A	186	GLY	2.1
1	A	678	PRO	2.1
1	A	723	ALA	2.0
1	A	484	ASN	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 ⓘ

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(Å ²)	Q<0.9
4	SO4	A	904	5/5	0.86	0.46	14.87	106,107,108,110	0
3	NAG	A	901	14/15	0.85	0.18	1.11	34,42,46,49	0
4	SO4	B	101	5/5	0.94	0.16	-0.21	71,79,80,82	0
3	NAG	A	902	14/15	0.88	0.13	-0.99	69,82,94,94	0
4	SO4	A	903	5/5	0.84	0.24	-	105,107,111,113	0

6.5 Other polymers [i](#)

There are no such residues in this entry.