



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:55 AM GMT

PDB ID : 3NKM  
Title : Crystal structure of mouse autotaxin  
Authors : Nishimasu, H.; Ishitani, R.; Mihara, E.; Takagi, J.; Aoki, J.; Nureki, O.  
Deposited on : 2010-06-20  
Resolution : 2.00 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

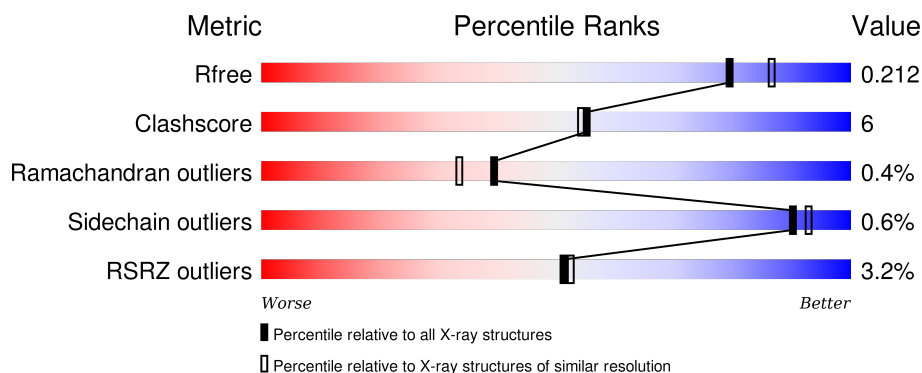
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	831	<div> <div>3%</div> <div>85%</div> <div>12%</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
10	SCN	A	1009	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	EDO	A	1010	-	-	-	X
11	EDO	A	1011	-	-	-	X
11	EDO	A	1018	-	-	-	X
11	EDO	A	1021	-	-	-	X
11	EDO	A	1023	-	-	-	X
11	EDO	A	1025	-	-	-	X
11	EDO	A	1026	-	-	X	X
3	MAN	A	904	-	-	-	X
9	NKP	A	1007	-	-	-	X

## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 7391 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 Ectonucleotide pyrophosphatase/phosphodiesterase family member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	805	Total	C	N	O	S	0	4	0
			6461	4104	1104	1203	50			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LYS	SEE REMARK 999	UNP Q9R1E6
A	?	-	VAL	SEE REMARK 999	UNP Q9R1E6
A	?	-	GLU	SEE REMARK 999	UNP Q9R1E6
A	?	-	PRO	SEE REMARK 999	UNP Q9R1E6
A	859	SER	-	EXPRESSION TAG	UNP Q9R1E6
A	860	ARG	-	EXPRESSION TAG	UNP Q9R1E6
A	861	GLU	-	EXPRESSION TAG	UNP Q9R1E6
A	862	ASN	-	EXPRESSION TAG	UNP Q9R1E6
A	863	LEU	-	EXPRESSION TAG	UNP Q9R1E6
A	864	TYR	-	EXPRESSION TAG	UNP Q9R1E6
A	865	PHE	-	EXPRESSION TAG	UNP Q9R1E6
A	866	GLN	-	EXPRESSION TAG	UNP Q9R1E6

- Molecule 2 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	2	Total	C	N	O	0	0
			28	16	2	10		
2	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Zn	0	0
			2	2		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		

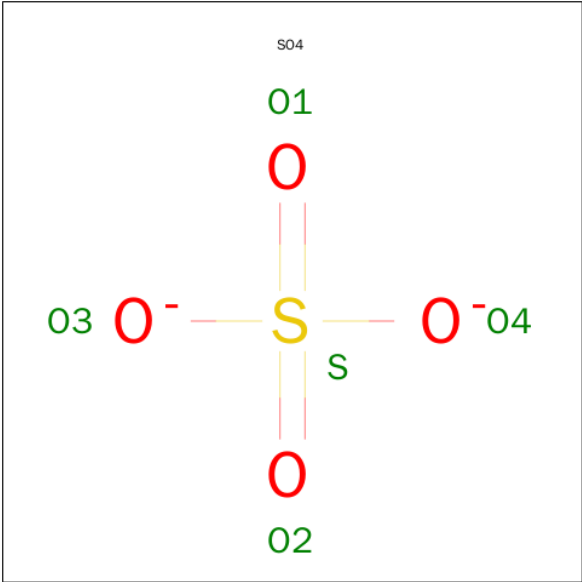
- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Na	0	0
			1	1		

- Molecule 7 is POTASSIUM ION (three-letter code: K) (formula: K).

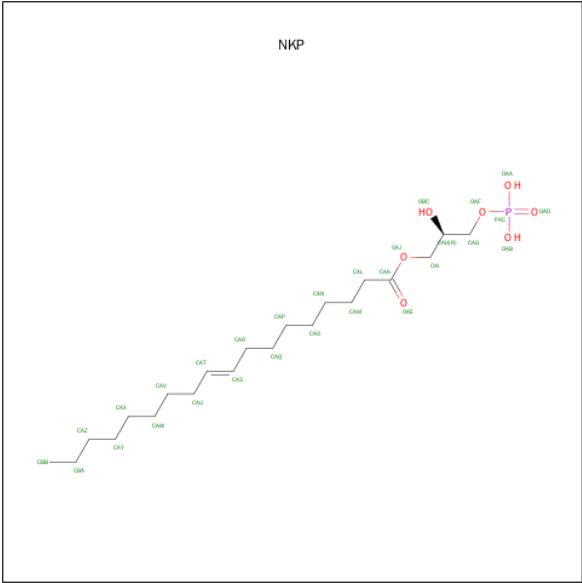
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	K	0	0
			1	1		

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



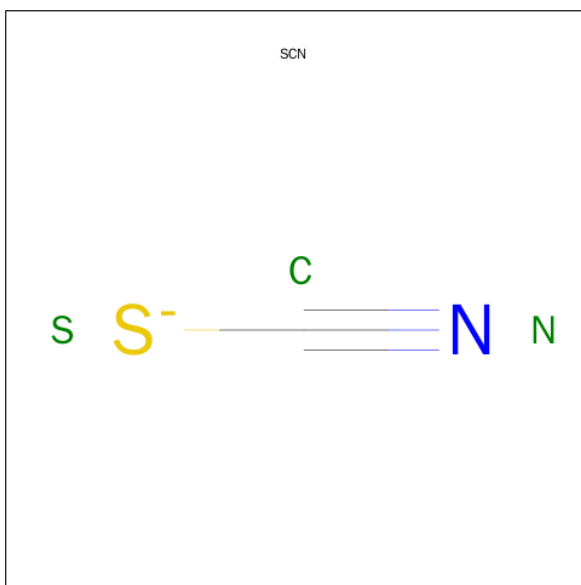
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 9 is (2R)-2-HYDROXY-3-(PHOSPHONOOXY)PROPYL (9E)-OCTADEC-9-EN OATE (three-letter code: NKP) (formula: C<sub>21</sub>H<sub>41</sub>O<sub>7</sub>P).



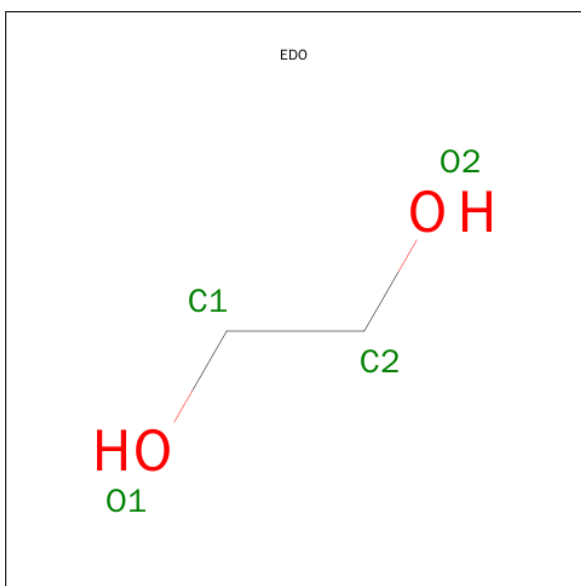
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	C	0	0
			6	6		

- Molecule 10 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	N	S	0	0
			3	1	1	1		
10	A	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 11 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		
11	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 12 is water.

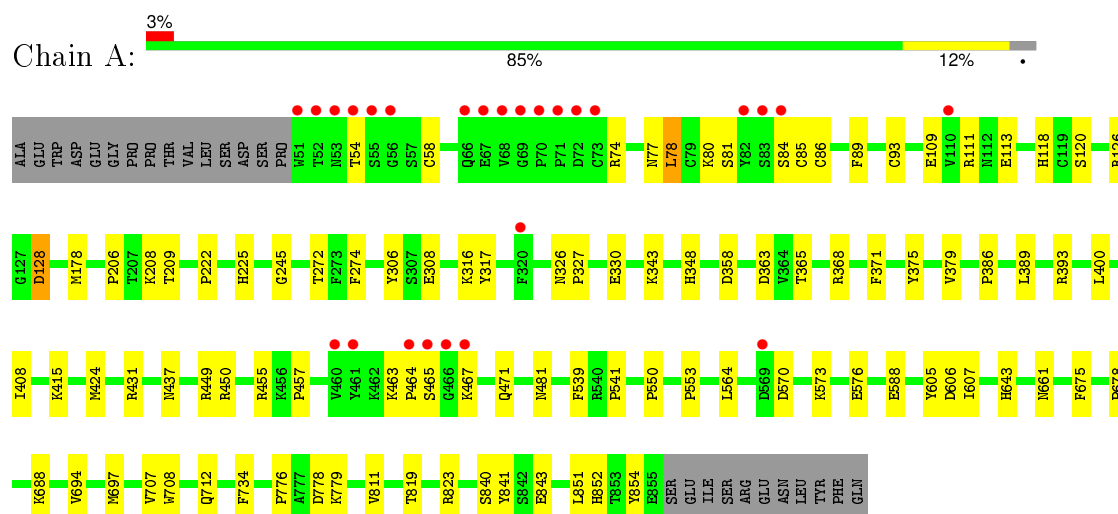
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	712	Total	O	0	0
			712	712		



### 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: Ectonucleotide pyrophosphatase/phosphodiesterase family member 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.59Å 94.73Å 75.65Å 90.00° 94.05° 90.00°	Depositor
Resolution (Å)	34.18 – 2.00 34.18 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.3 (34.18-2.00) 97.3 (34.18-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.44 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6 _289)	Depositor
R, $R_{free}$	0.163 , 0.213 0.163 , 0.212	Depositor DCC
$R_{free}$ test set	2875 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.6	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 52.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 56809 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7391	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% 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, 0.375 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: ZN, BMA, NAG, NA, K, EDO, NKP, SCN, SO4, CA, MAN

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	0.36	0/6659	0.51	0/9049

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	6461	0	6168	81	0
2	A	56	0	50	0	0
3	A	72	0	61	0	0
4	A	2	0	0	0	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	1	0	0	0	0
8	A	5	0	0	0	0
9	A	6	0	11	0	0
10	A	6	0	0	1	0
11	A	68	0	102	19	0
12	A	712	0	0	6	0
All	All	7391	0	6392	82	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 6.

All (82) 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:675:PHE:H	11:A:1012:EDO:H11	1.10	1.11
1:A:118:HIS:HD2	1:A:128:ASP:HB3	1.40	0.84
1:A:675:PHE:N	11:A:1012:EDO:H11	1.94	0.78
1:A:424:MET:HG3	12:A:1560:HOH:O	1.84	0.77
1:A:368:ARG:HH22	11:A:1026:EDO:C2	2.00	0.73
1:A:77:ASN:HD21	1:A:272:THR:HB	1.53	0.73
1:A:365:THR:HG23	11:A:1026:EDO:H21	1.70	0.72
1:A:363:ASP:HB3	11:A:1026:EDO:H22	1.72	0.71
1:A:570:ASP:HB2	1:A:643:HIS:HD2	1.56	0.70
1:A:118:HIS:CD2	1:A:128:ASP:HB3	2.29	0.66
1:A:78:LEU:HD21	1:A:274:PHE:CB	2.25	0.66
1:A:368:ARG:HH22	11:A:1026:EDO:H22	1.61	0.66
1:A:363:ASP:OD1	11:A:1026:EDO:H11	1.97	0.63
1:A:852:HIS:HD2	1:A:854:TYR:CZ	2.17	0.62
1:A:437:ASN:ND2	11:A:1025:EDO:H22	2.15	0.62
1:A:437:ASN:HD21	11:A:1025:EDO:H22	1.64	0.61
1:A:209:THR:OG1	1:A:358:ASP:OD2	2.20	0.60
1:A:678:PRO:HB3	1:A:712:GLN:HB3	1.83	0.60
1:A:734:PHE:CD2	11:A:1013:EDO:H11	2.38	0.59
1:A:570:ASP:HB2	1:A:643:HIS:CD2	2.38	0.58
1:A:326:ASN:HB3	1:A:327:PRO:HD3	1.86	0.57
1:A:363:ASP:HB3	11:A:1026:EDO:C2	2.36	0.56
1:A:776:PRO:HG2	1:A:779:LYS:HB2	1.87	0.56
1:A:694:VAL:HG23	1:A:697:MET:HE2	1.88	0.55
11:A:1026:EDO:H12	12:A:954:HOH:O	2.06	0.55
1:A:74:ARG:HD3	1:A:84:SER:OG	2.08	0.54
1:A:272:THR:HG22	1:A:274:PHE:H	1.71	0.54
1:A:840:SER:OG	1:A:843:GLU:HG3	2.08	0.54
1:A:408[A]:ILE:HD11	1:A:424:MET:SD	2.48	0.53
1:A:694:VAL:HG23	1:A:697:MET:CE	2.39	0.53
1:A:463:LYS:HB3	1:A:464:PRO:HD2	1.90	0.52
1:A:708:TRP:CD1	11:A:1012:EDO:H12	2.44	0.51
1:A:437:ASN:HD21	11:A:1025:EDO:C2	2.23	0.51
1:A:550:PRO:HB3	1:A:605:TYR:CE1	2.46	0.51
1:A:306:TYR:CE2	1:A:308:GLU:HG3	2.45	0.51
1:A:588:GLU:HB3	12:A:1542:HOH:O	2.12	0.50
1:A:222:PRO:HA	1:A:225:HIS:CE1	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:THR:HG22	1:A:54:THR:O	2.12	0.49
1:A:89:PHE:O	1:A:93:CYS:HB2	2.13	0.49
1:A:564:LEU:O	1:A:661:ASN:HB2	2.13	0.49
1:A:316:LYS:HE3	1:A:317:TYR:OH	2.13	0.48
1:A:316:LYS:HE3	1:A:317:TYR:CZ	2.49	0.48
1:A:389:LEU:HD23	1:A:389:LEU:N	2.28	0.48
1:A:58:CYS:SG	1:A:86:CYS:HB2	2.53	0.48
1:A:120:SER:HB2	12:A:1565:HOH:O	2.13	0.48
1:A:77:ASN:HD21	1:A:272:THR:CB	2.25	0.47
1:A:573:LYS:HD2	1:A:576:GLU:OE2	2.15	0.46
1:A:178:MET:HE3	12:A:1082:HOH:O	2.15	0.46
1:A:539:PHE:O	1:A:541:PRO:HD3	2.16	0.46
1:A:245:GLY:HA3	12:A:1265:HOH:O	2.15	0.45
1:A:78:LEU:HD12	1:A:81:SER:HB2	1.98	0.45
1:A:77:ASN:OD1	1:A:272:THR:HG21	2.17	0.45
1:A:708:TRP:O	1:A:712:GLN:HG2	2.17	0.45
1:A:375:TYR:OH	1:A:415:LYS:HE2	2.16	0.45
1:A:111:ARG:CZ	1:A:126:ARG:HD3	2.47	0.44
1:A:550:PRO:HB3	1:A:605:TYR:CZ	2.52	0.44
1:A:389:LEU:H	1:A:389:LEU:HD23	1.83	0.44
1:A:379:VAL:HB	1:A:455:ARG:HG2	2.00	0.44
1:A:449:ARG:O	1:A:450:ARG:HB2	2.17	0.44
1:A:208:LYS:HG3	10:A:1009:SCN:S	2.58	0.43
1:A:688:LYS:HE2	1:A:688:LYS:HB2	1.86	0.43
1:A:206:PRO:HB3	1:A:389:LEU:HD13	1.99	0.43
1:A:471:GLN:HB3	11:A:1026:EDO:O1	2.19	0.43
1:A:326:ASN:O	1:A:330:GLU:HG3	2.19	0.43
1:A:80:LYS:HG2	1:A:85:CYS:SG	2.58	0.43
1:A:553:PRO:CD	1:A:606:ASP:HB3	2.49	0.43
1:A:365:THR:CG2	11:A:1026:EDO:H21	2.44	0.42
1:A:778:ASP:OD1	1:A:779:LYS:HG3	2.20	0.42
1:A:707:VAL:HG13	1:A:811:VAL:HG13	2.01	0.42
1:A:343:LYS:HA	1:A:348:HIS:CD2	2.55	0.42
1:A:471:GLN:O	11:A:1026:EDO:O1	2.36	0.42
1:A:77:ASN:ND2	1:A:272:THR:HB	2.26	0.42
1:A:371:PHE:CE1	1:A:457:PRO:HA	2.55	0.42
1:A:550:PRO:HB2	1:A:607:ILE:HG12	2.02	0.41
1:A:465:SER:C	1:A:467:LYS:H	2.24	0.41
1:A:393:ARG:HA	11:A:1017:EDO:H22	2.02	0.41
1:A:819:THR:HG23	1:A:851:LEU:HD11	2.02	0.41
1:A:431:ARG:HD3	1:A:819:THR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:852:HIS:HD2	1:A:854:TYR:CE1	2.38	0.41
1:A:463:LYS:HB3	1:A:464:PRO:CD	2.50	0.40
1:A:541:PRO:HG2	1:A:841:TYR:CD2	2.56	0.40
1:A:823:ARG:CZ	11:A:1010:EDO:H11	2.51	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	807/831 (97%)	779 (96%)	25 (3%)	3 (0%)	39	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	113	GLU
1	A	109	GLU
1	A	386	PRO

### 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	721/756 (95%)	717 (99%)	4 (1%)	90	93

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	LEU
1	A	128	ASP
1	A	400	LEU
1	A	481	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	HIS
1	A	257	GLN
1	A	337	GLN
1	A	348	HIS
1	A	374	ASN
1	A	667	ASN
1	A	802	ASN
1	A	827	HIS

### 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 ⓘ

10 carbohydrates 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	NAG	A	898	1,2	14,14,15	0.48	0	15,19,21	1.07	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	A	899	2	14,14,15	0.52	0	15,19,21	0.75	0
3	NAG	A	900	1,3	14,14,15	0.68	0	15,19,21	1.05	1 (6%)
3	NAG	A	901	3	14,14,15	0.56	0	15,19,21	0.78	0
3	BMA	A	902	3	11,11,12	0.61	0	14,15,17	0.74	0
3	MAN	A	903	3	11,11,12	0.68	0	14,15,17	0.99	1 (7%)
3	MAN	A	904	3	11,11,12	0.57	0	14,15,17	0.89	1 (7%)
3	MAN	A	905	3	11,11,12	0.54	0	14,15,17	0.81	1 (7%)
2	NAG	A	907	1,2	14,14,15	0.63	0	15,19,21	0.82	0
2	NAG	A	908	2	14,14,15	0.51	0	15,19,21	0.69	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	NAG	A	898	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	899	2	-	0/6/23/26	0/1/1/1
3	NAG	A	900	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	901	3	-	0/6/23/26	0/1/1/1
3	BMA	A	902	3	-	0/2/19/22	0/1/1/1
3	MAN	A	903	3	-	0/2/19/22	0/1/1/1
3	MAN	A	904	3	-	0/2/19/22	0/1/1/1
3	MAN	A	905	3	-	0/2/19/22	0/1/1/1
2	NAG	A	907	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	908	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	904	MAN	O5-C1-C2	-2.22	107.26	110.86
3	A	905	MAN	C2-C3-C4	-2.11	107.46	111.04
2	A	898	NAG	C2-N2-C7	-2.03	120.44	123.04
3	A	900	NAG	C3-C4-C5	2.46	114.49	110.20
3	A	903	MAN	C1-C2-C3	2.47	112.47	109.54
2	A	898	NAG	C1-O5-C5	2.97	116.02	112.25

There are no chirality outliers.

There are no torsion outliers.



There are no ring outliers.

No monomer is involved in short contacts.

## 5.6 Ligand geometry

Of 26 ligands modelled in this entry, 5 are monoatomic - leaving 21 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
8	SO4	A	1006	4	4,4,4	0.13	0	6,6,6	0.25	0
9	NKP	A	1007	-	5,5,28	0.37	0	4,4,32	0.47	0
10	SCN	A	1008	-	2,2,2	1.84	1 (50%)	1,1,1	0.25	0
10	SCN	A	1009	-	2,2,2	1.60	1 (50%)	1,1,1	0.22	0
11	EDO	A	1010	-	3,3,3	0.52	0	2,2,2	0.52	0
11	EDO	A	1011	-	3,3,3	0.66	0	2,2,2	0.05	0
11	EDO	A	1012	-	3,3,3	0.37	0	2,2,2	0.54	0
11	EDO	A	1013	-	3,3,3	0.47	0	2,2,2	0.57	0
11	EDO	A	1014	-	3,3,3	0.57	0	2,2,2	0.08	0
11	EDO	A	1015	-	3,3,3	0.49	0	2,2,2	0.48	0
11	EDO	A	1016	-	3,3,3	0.53	0	2,2,2	0.37	0
11	EDO	A	1017	-	3,3,3	0.45	0	2,2,2	0.37	0
11	EDO	A	1018	-	3,3,3	0.55	0	2,2,2	0.16	0
11	EDO	A	1019	-	3,3,3	0.50	0	2,2,2	0.34	0
11	EDO	A	1020	-	3,3,3	0.48	0	2,2,2	0.48	0
11	EDO	A	1021	-	3,3,3	0.52	0	2,2,2	0.37	0
11	EDO	A	1022	-	3,3,3	0.53	0	2,2,2	0.40	0
11	EDO	A	1023	-	3,3,3	0.54	0	2,2,2	0.45	0
11	EDO	A	1024	-	3,3,3	0.63	0	2,2,2	0.34	0
11	EDO	A	1025	-	3,3,3	0.50	0	2,2,2	0.25	0
11	EDO	A	1026	-	3,3,3	0.44	0	2,2,2	0.53	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
8	SO4	A	1006	4	-	0/0/0/0	0/0/0/0
9	NKP	A	1007	-	-	0/3/3/28	0/0/0/0
10	SCN	A	1008	-	-	0/0/0/0	0/0/0/0
10	SCN	A	1009	-	-	0/0/0/0	0/0/0/0
11	EDO	A	1010	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1011	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1012	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1013	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1014	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1015	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1016	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1017	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1018	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1019	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1020	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1021	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1022	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1023	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1024	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1025	-	-	0/1/1/1	0/0/0/0
11	EDO	A	1026	-	-	0/1/1/1	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	1009	SCN	C-S	2.23	1.78	1.63
10	A	1008	SCN	C-S	2.55	1.80	1.63

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	1009	SCN	1	0
11	A	1010	EDO	1	0
11	A	1012	EDO	3	0
11	A	1013	EDO	1	0
11	A	1017	EDO	1	0
11	A	1025	EDO	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	1026	EDO	10	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	805/831 (96%)	-0.13	26 (3%) 51 52	9, 22, 47, 69	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	51	TRP	6.6
1	A	71	PRO	5.9
1	A	465	SER	5.2
1	A	464	PRO	4.9
1	A	70	PRO	4.5
1	A	52	THR	4.3
1	A	68	VAL	4.1
1	A	69	GLY	4.1
1	A	466	GLY	3.9
1	A	66	GLN	3.5
1	A	55	SER	3.3
1	A	54	THR	3.1
1	A	467	LYS	3.0
1	A	72	ASP	3.0
1	A	320	PHE	2.7
1	A	56	GLY	2.6
1	A	569	ASP	2.4
1	A	110	VAL	2.4
1	A	73	CYS	2.4
1	A	67	GLU	2.4
1	A	53	ASN	2.4
1	A	83	SER	2.3
1	A	461	TYR	2.2
1	A	82	TYR	2.2
1	A	84	SER	2.2
1	A	460	VAL	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](#)

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(Å <sup>2</sup> )	Q<0.9
3	MAN	A	904	11/12	0.90	0.31	6.48	33,35,40,50	0
2	NAG	A	898	14/15	0.86	0.30	0.50	49,54,58,62	0
2	NAG	A	907	14/15	0.95	0.09	0.10	17,26,37,41	0
3	NAG	A	900	14/15	0.97	0.09	-0.06	9,14,19,20	0
3	MAN	A	905	11/12	0.94	0.19	-	23,31,36,36	0
2	NAG	A	899	14/15	0.86	0.31	-	60,67,70,71	0
3	NAG	A	901	14/15	0.97	0.09	-	19,24,29,37	0
3	MAN	A	903	11/12	0.90	0.20	-	36,38,43,51	0
2	NAG	A	908	14/15	0.89	0.26	-	44,53,61,62	0
3	BMA	A	902	11/12	0.87	0.19	-	37,41,45,47	0

## 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(Å <sup>2</sup> )	Q<0.9
11	EDO	A	1025	4/4	0.96	0.22	16.37	22,25,29,41	0
11	EDO	A	1018	4/4	0.95	0.15	9.14	18,25,28,36	0
10	SCN	A	1009	3/3	0.90	0.20	4.50	11,11,34,36	0
11	EDO	A	1026	4/4	0.92	0.23	4.32	24,24,25,28	0
9	NKP	A	1007	6/29	0.79	0.17	2.60	32,34,37,38	0
11	EDO	A	1011	4/4	0.91	0.15	2.60	19,22,26,28	0
11	EDO	A	1023	4/4	0.98	0.13	2.53	13,14,15,16	0
11	EDO	A	1010	4/4	0.96	0.15	2.44	21,27,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
11	EDO	A	1021	4/4	0.94	0.14	2.23	30,30,33,41	0
11	EDO	A	1017	4/4	0.96	0.12	1.95	13,25,25,26	0
11	EDO	A	1020	4/4	0.96	0.13	1.89	17,23,28,33	0
11	EDO	A	1022	4/4	0.92	0.13	1.85	26,31,35,36	0
10	SCN	A	1008	3/3	0.98	0.12	1.57	22,22,27,38	0
11	EDO	A	1014	4/4	0.95	0.11	1.55	18,23,24,24	0
11	EDO	A	1012	4/4	0.96	0.14	1.00	19,22,23,27	0
11	EDO	A	1015	4/4	0.99	0.10	0.43	21,22,23,23	0
11	EDO	A	1013	4/4	0.95	0.11	0.33	26,27,27,29	0
7	K	A	1005	1/1	0.85	0.12	0.01	38,38,38,38	0
11	EDO	A	1024	4/4	0.96	0.09	-0.26	13,15,15,26	0
11	EDO	A	1019	4/4	0.95	0.08	-0.74	25,25,32,33	0
11	EDO	A	1016	4/4	0.96	0.06	-0.99	20,26,26,28	0
4	ZN	A	1002	1/1	1.00	0.07	-1.30	13,13,13,13	0
4	ZN	A	1001	1/1	1.00	0.07	-2.16	21,21,21,21	0
8	SO4	A	1006	5/5	0.99	0.06	-2.17	13,18,24,28	0
5	CA	A	1003	1/1	1.00	0.04	-4.98	19,19,19,19	0
6	NA	A	1004	1/1	0.99	0.06	-	21,21,21,21	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.