



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 01:09 am GMT

PDB ID : 2XB6  
Title : REVISITED CRYSTAL STRUCTURE OF NEUREXIN1BETA-NEUROLIGIN4 COMPLEX  
Authors : Leone, P.; Comoletti, D.; Ferracci, G.; Conrod, S.; Garcia, S.U.; Taylor, P.; Bourne, Y.; Marchot, P.  
Deposited on : 2010-04-07  
Resolution : 2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

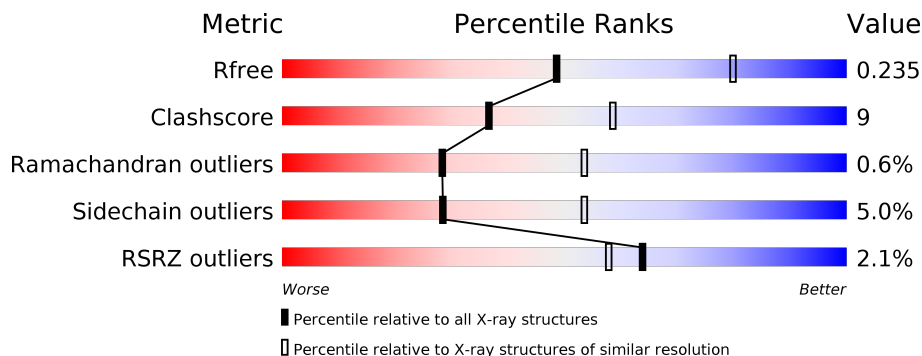
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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	588	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>12%</div> <div>•</div> <div>10%</div> </div> </div>
1	B	588	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>13%</div> <div>••</div> <div>8%</div> </div> </div>
2	C	179	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>17%</div> <div>••</div> </div> </div>
2	D	179	<div> <div>4%</div> <div> <div></div> <div>80%</div> <div>17%</div> <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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	A	700	-	-	-	X
4	EDO	A	1599	-	-	-	X
4	EDO	A	1601	-	-	X	X
4	EDO	A	1604	-	-	-	X
4	EDO	A	1605	-	-	X	X
4	EDO	A	1606	-	-	-	X
4	EDO	A	1608	-	-	-	X
4	EDO	B	1600	-	-	-	X
4	EDO	B	1601	-	-	-	X
4	EDO	B	1602	-	-	-	X
4	EDO	B	1604	-	-	-	X
4	EDO	B	1606	-	-	-	X
4	EDO	B	1607	-	-	-	X
4	EDO	B	1608	-	-	-	X
4	EDO	B	1610	-	-	-	X
4	EDO	B	1611	-	-	-	X
4	EDO	B	1612	-	-	-	X
4	EDO	C	1290	-	-	-	X
4	EDO	C	1291	-	-	-	X
4	EDO	C	1293	-	-	-	X
5	CL	A	1610	-	-	-	X
5	CL	B	1614	-	-	-	X
5	CL	B	1615	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11720 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 NEUROLIGIN-4, X-LINKED.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	529	Total	C	N	O	S	0	0	0
			4182	2681	692	788	21			
1	B	541	Total	C	N	O	S	0	0	0
			4276	2738	707	810	21			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	ASP	-	EXPRESSION TAG	UNP Q8N0W4
A	-11	TYR	-	EXPRESSION TAG	UNP Q8N0W4
A	-10	LYS	-	EXPRESSION TAG	UNP Q8N0W4
A	-9	ASP	-	EXPRESSION TAG	UNP Q8N0W4
A	-8	ASP	-	EXPRESSION TAG	UNP Q8N0W4
A	-7	ASP	-	EXPRESSION TAG	UNP Q8N0W4
A	-6	ASP	-	EXPRESSION TAG	UNP Q8N0W4
A	-5	LYS	-	EXPRESSION TAG	UNP Q8N0W4
A	-4	LEU	-	EXPRESSION TAG	UNP Q8N0W4
A	-3	ALA	-	EXPRESSION TAG	UNP Q8N0W4
A	-2	ALA	-	EXPRESSION TAG	UNP Q8N0W4
A	-1	ALA	-	EXPRESSION TAG	UNP Q8N0W4
B	-12	ASP	-	EXPRESSION TAG	UNP Q8N0W4
B	-11	TYR	-	EXPRESSION TAG	UNP Q8N0W4
B	-10	LYS	-	EXPRESSION TAG	UNP Q8N0W4
B	-9	ASP	-	EXPRESSION TAG	UNP Q8N0W4
B	-8	ASP	-	EXPRESSION TAG	UNP Q8N0W4
B	-7	ASP	-	EXPRESSION TAG	UNP Q8N0W4
B	-6	ASP	-	EXPRESSION TAG	UNP Q8N0W4
B	-5	LYS	-	EXPRESSION TAG	UNP Q8N0W4
B	-4	LEU	-	EXPRESSION TAG	UNP Q8N0W4
B	-3	ALA	-	EXPRESSION TAG	UNP Q8N0W4
B	-2	ALA	-	EXPRESSION TAG	UNP Q8N0W4
B	-1	ALA	-	EXPRESSION TAG	UNP Q8N0W4
A	561	ARG	LYS	CLONING ARTIFACT	UNP Q8N0W4

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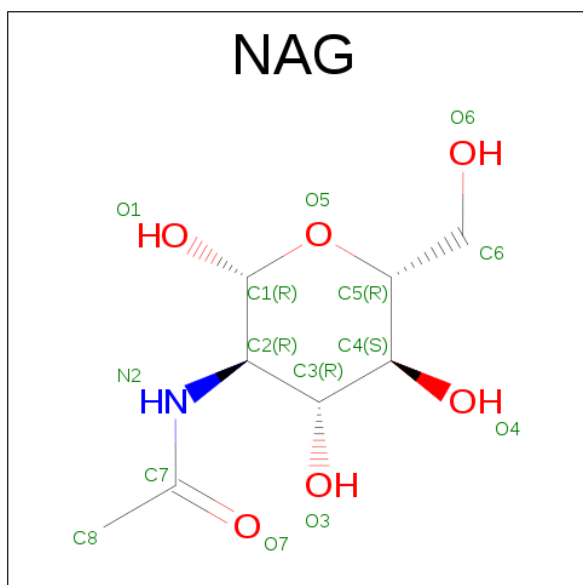
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Chain	Residue	Modelled	Actual	Comment	Reference
B	561	ARG	LYS	CLONING ARTIFACT	UNP Q8N0W4

- Molecule 2 is a protein called NEUREXIN-1-BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	177	Total	C	N	O	S	0	0	0
			1359	857	243	258	1			
2	D	177	Total	C	N	O	S	0	0	0
			1359	857	243	258	1			

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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			
3	B	1	Total	C	N	O		0	0
			14	8	1	5			
3	B	1	Total	C	N	O		0	0
			14	8	1	5			

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

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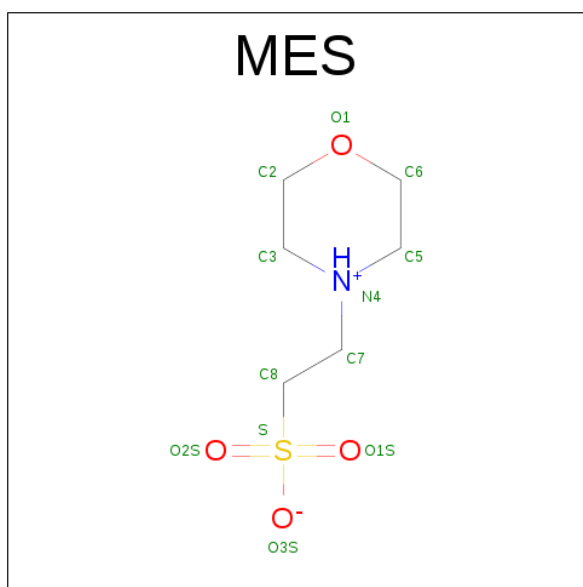
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0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

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	3	Total Cl 3 3	0	0
5	A	2	Total Cl 2 2	0	0

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	1	Total	Ca	0	0
			1	1		
7	C	1	Total	Ca	0	0
			1	1		

- Molecule 8 is water.

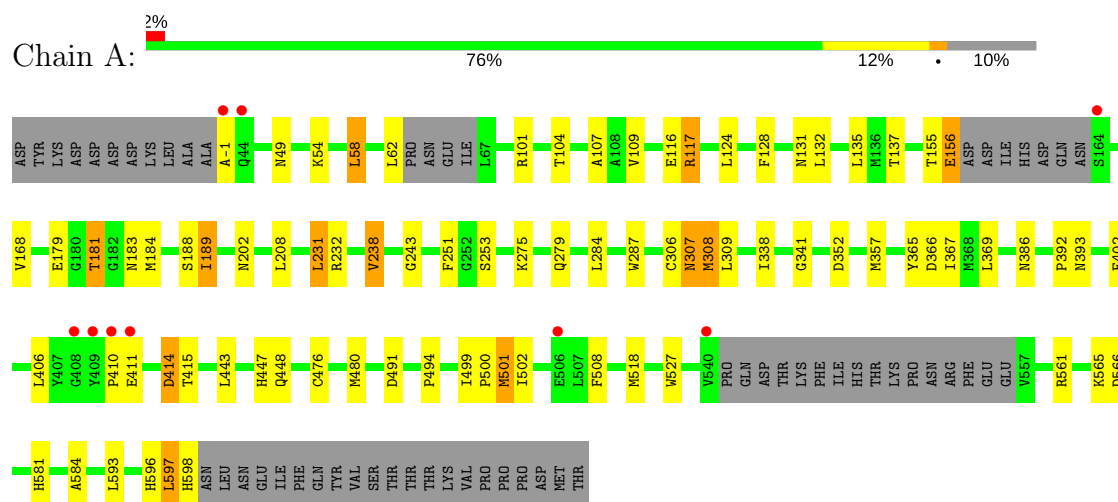
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	129	Total	O	0	0
			129	129		
8	B	162	Total	O	0	0
			162	162		
8	C	38	Total	O	0	0
			38	38		
8	D	20	Total	O	0	0
			20	20		



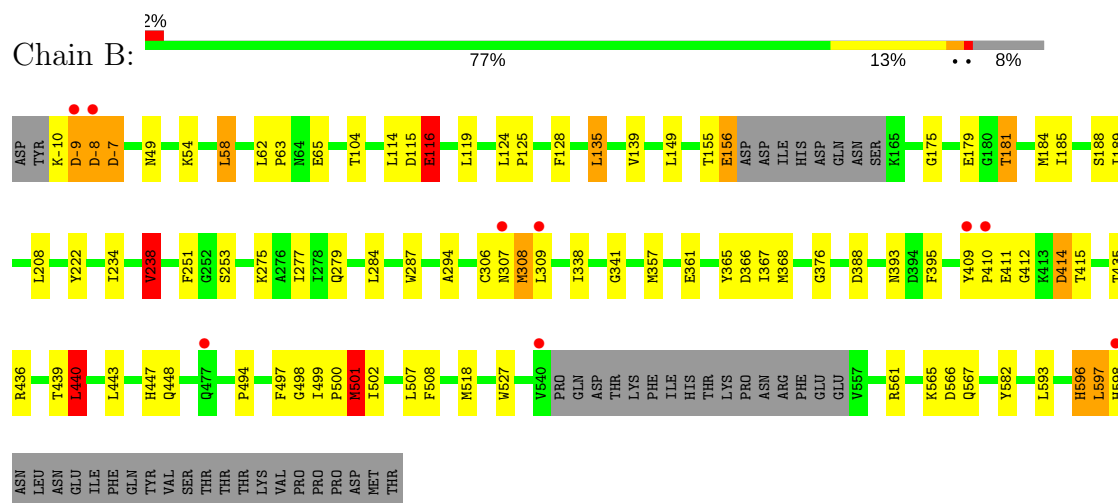
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

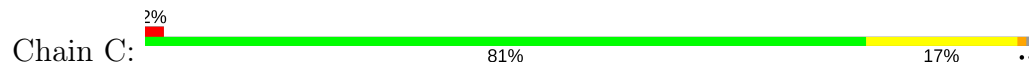
#### • Molecule 1: NEUROLIGIN-4, X-LINKED

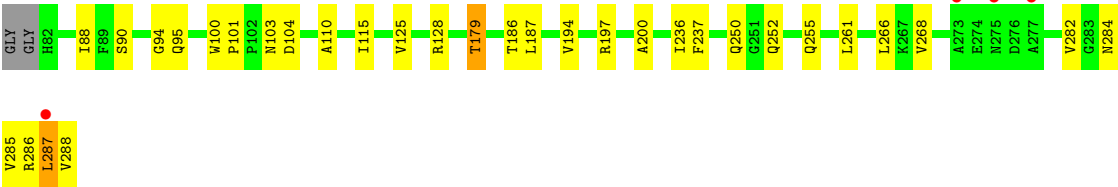


#### • Molecule 1: NEUROLIGIN-4, X-LINKED

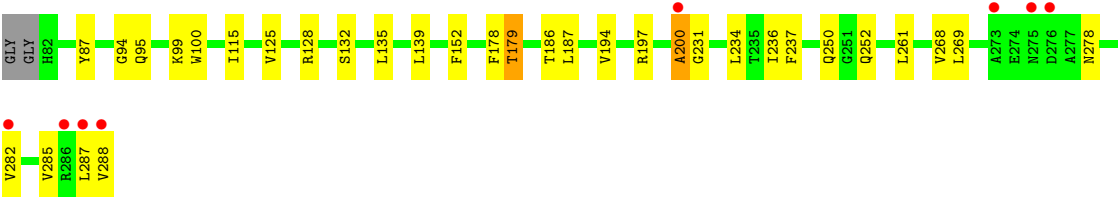
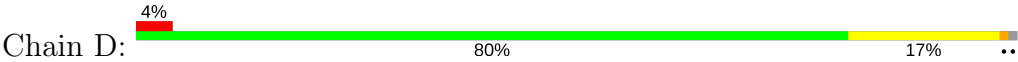


#### • Molecule 2: NEUREXIN-1-BETA





● Molecule 2: NEUREXIN-1-BETA



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.31Å 198.78Å 85.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 29.92 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-2.60) 100.0 (29.92-2.60)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.43 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.204 , 0.236 0.202 , 0.235	Depositor DCC
$R_{free}$ test set	3656 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	44.8	Xtriage
Anisotropy	0.541	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 43.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11720	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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: CA, EDO, NAG, MES, CL

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	0.69	3/4298 (0.1%)	0.74	3/5860 (0.1%)
1	B	0.72	2/4394 (0.0%)	0.74	3/5992 (0.1%)
2	C	0.96	2/1385 (0.1%)	1.04	2/1877 (0.1%)
2	D	1.10	2/1385 (0.1%)	1.02	2/1877 (0.1%)
All	All	0.79	9/11462 (0.1%)	0.82	10/15606 (0.1%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	200	ALA	C-N	29.93	1.86	1.33
2	C	200	ALA	C-N	18.41	1.66	1.33
2	C	197	ARG	CZ-NH1	-16.43	1.11	1.33
2	D	197	ARG	CZ-NH1	-15.89	1.12	1.33
1	B	238	VAL	CB-CG1	-9.30	1.33	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	197	ARG	NE-CZ-NH2	26.47	133.54	120.30
2	C	197	ARG	NE-CZ-NH2	26.09	133.34	120.30
2	C	197	ARG	NE-CZ-NH1	-17.54	111.53	120.30
2	D	197	ARG	NE-CZ-NH1	-17.24	111.68	120.30
1	B	501	MET	CB-CG-SD	10.58	144.15	112.40

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	4182	0	4027	73	0
1	B	4276	0	4116	80	0
2	C	1359	0	1347	21	0
2	D	1359	0	1346	25	0
3	A	28	0	26	2	0
3	B	28	0	26	1	0
4	A	40	0	60	14	0
4	B	56	0	84	9	0
4	C	24	0	36	1	0
5	A	2	0	0	0	0
5	B	3	0	0	0	0
6	C	12	0	12	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	129	0	0	3	0
8	B	162	0	0	1	0
8	C	38	0	0	1	0
8	D	20	0	0	2	0
All	All	11720	0	11080	201	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 9.

The worst 5 of 201 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)
2:D:200:ALA:C	2:D:231:GLY:N	1.86	1.28
1:B:115:ASP:O	1:B:116:GLU:HB3	1.56	1.05
1:A:596:HIS:O	1:A:597:LEU:HB2	1.64	0.94
1:B:411:GLU:OE2	1:B:414:ASP:OD1	1.86	0.94
1:A:128:PHE:CE1	1:A:135:LEU:HD11	2.04	0.92

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	521/588 (89%)	493 (95%)	26 (5%)	2 (0%)	38	63
1	B	535/588 (91%)	511 (96%)	19 (4%)	5 (1%)	20	40
2	C	175/179 (98%)	170 (97%)	5 (3%)	0	100	100
2	D	175/179 (98%)	168 (96%)	6 (3%)	1 (1%)	28	53
All	All	1406/1534 (92%)	1342 (95%)	56 (4%)	8 (1%)	28	53

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	-8	ASP
1	B	-9	ASP
1	B	-7	ASP
1	B	116	GLU
1	B	597	LEU

### 5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	453/510 (89%)	428 (94%)	25 (6%)	25	49
1	B	463/510 (91%)	439 (95%)	24 (5%)	27	52
2	C	143/143 (100%)	136 (95%)	7 (5%)	29	54
2	D	143/143 (100%)	139 (97%)	4 (3%)	49	76
All	All	1202/1306 (92%)	1142 (95%)	60 (5%)	28	53

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	116	GLU
1	B	238	VAL
2	C	287	LEU
1	B	179	GLU
1	B	287	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	89	GLN
1	B	292	GLN
2	C	270	ASN
1	B	131	ASN
1	B	322	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](#)

Of 42 ligands modelled in this entry, 7 are monoatomic - leaving 35 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
4	EDO	A	1599	-	3,3,3	0.59	0	2,2,2	0.08	0
4	EDO	A	1600	-	3,3,3	0.47	0	2,2,2	0.35	0
4	EDO	A	1601	-	3,3,3	0.74	0	2,2,2	0.62	0
4	EDO	A	1602	-	3,3,3	0.42	0	2,2,2	0.33	0
4	EDO	A	1603	-	3,3,3	0.49	0	2,2,2	0.56	0
4	EDO	A	1604	-	3,3,3	0.64	0	2,2,2	0.45	0
4	EDO	A	1605	-	3,3,3	0.60	0	2,2,2	0.21	0
4	EDO	A	1606	-	3,3,3	0.68	0	2,2,2	0.23	0
4	EDO	A	1607	-	3,3,3	0.60	0	2,2,2	0.15	0
4	EDO	A	1608	-	3,3,3	0.51	0	2,2,2	0.22	0
3	NAG	A	700	1	14,14,15	0.50	0	15,19,21	1.41	2 (13%)
3	NAG	A	701	1	14,14,15	0.52	0	15,19,21	1.00	0
4	EDO	B	1599	-	3,3,3	0.51	0	2,2,2	0.17	0
4	EDO	B	1600	-	3,3,3	0.46	0	2,2,2	0.61	0
4	EDO	B	1601	-	3,3,3	0.51	0	2,2,2	0.19	0
4	EDO	B	1602	-	3,3,3	0.84	0	2,2,2	0.59	0
4	EDO	B	1603	-	3,3,3	0.51	0	2,2,2	0.33	0
4	EDO	B	1604	-	3,3,3	0.68	0	2,2,2	0.15	0
4	EDO	B	1605	-	3,3,3	0.63	0	2,2,2	0.26	0
4	EDO	B	1606	-	3,3,3	0.62	0	2,2,2	0.20	0
4	EDO	B	1607	-	3,3,3	0.93	0	2,2,2	1.06	0
4	EDO	B	1608	-	3,3,3	0.55	0	2,2,2	0.30	0
4	EDO	B	1609	-	3,3,3	0.52	0	2,2,2	0.41	0
4	EDO	B	1610	-	3,3,3	0.52	0	2,2,2	0.25	0
4	EDO	B	1611	-	3,3,3	0.43	0	2,2,2	0.31	0
4	EDO	B	1612	-	3,3,3	0.61	0	2,2,2	0.05	0
3	NAG	B	700	1	14,14,15	0.54	0	15,19,21	1.01	1 (6%)
3	NAG	B	701	1	14,14,15	0.52	0	15,19,21	1.31	3 (20%)
6	MES	C	1289	-	12,12,12	2.08	1 (8%)	14,16,16	3.61	4 (28%)
4	EDO	C	1290	-	3,3,3	0.64	0	2,2,2	0.45	0
4	EDO	C	1291	-	3,3,3	0.69	0	2,2,2	0.21	0
4	EDO	C	1292	-	3,3,3	0.60	0	2,2,2	0.17	0
4	EDO	C	1293	-	3,3,3	0.57	0	2,2,2	0.11	0
4	EDO	C	1294	-	3,3,3	0.43	0	2,2,2	0.19	0
4	EDO	C	1295	-	3,3,3	0.37	0	2,2,2	0.40	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
4	EDO	A	1599	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1600	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1601	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1602	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1603	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1604	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1605	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1606	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1607	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1608	-	-	0/1/1/1	0/0/0/0
3	NAG	A	700	1	-	0/6/23/26	0/1/1/1
3	NAG	A	701	1	-	0/6/23/26	0/1/1/1
4	EDO	B	1599	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1600	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1601	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1602	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1603	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1604	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1605	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1606	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1607	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1608	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1609	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1610	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1611	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1612	-	-	0/1/1/1	0/0/0/0
3	NAG	B	700	1	-	0/6/23/26	0/1/1/1
3	NAG	B	701	1	-	0/6/23/26	0/1/1/1
6	MES	C	1289	-	-	0/6/14/14	0/1/1/1
4	EDO	C	1290	-	-	0/1/1/1	0/0/0/0
4	EDO	C	1291	-	-	0/1/1/1	0/0/0/0
4	EDO	C	1292	-	-	0/1/1/1	0/0/0/0
4	EDO	C	1293	-	-	0/1/1/1	0/0/0/0
4	EDO	C	1294	-	-	0/1/1/1	0/0/0/0
4	EDO	C	1295	-	-	0/1/1/1	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1289	MES	C8-S	-6.99	1.67	1.77

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	700	NAG	C1-C2-N2	-3.30	104.84	110.49
3	B	701	NAG	O5-C1-C2	-2.33	108.22	111.47
3	B	700	NAG	C1-C2-N2	-2.28	106.59	110.49
6	C	1289	MES	O1S-S-C8	-2.16	104.94	106.79
3	B	701	NAG	C1-C2-N2	-2.15	106.82	110.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1599	EDO	1	0
4	A	1601	EDO	6	0
4	A	1602	EDO	1	0
4	A	1603	EDO	1	0
4	A	1605	EDO	5	0
3	A	700	NAG	2	0
4	B	1599	EDO	2	0
4	B	1600	EDO	2	0
4	B	1605	EDO	1	0
4	B	1607	EDO	1	0
4	B	1609	EDO	1	0
4	B	1611	EDO	2	0
3	B	700	NAG	1	0
4	C	1293	EDO	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 [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, 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	529/588 (89%)	-0.35	9 (1%) 70 65	6, 21, 36, 54	0
1	B	541/588 (92%)	-0.36	9 (1%) 70 65	6, 21, 34, 62	0
2	C	177/179 (98%)	-0.28	4 (2%) 61 54	18, 26, 42, 52	0
2	D	177/179 (98%)	-0.04	8 (4%) 34 26	18, 26, 46, 54	0
All	All	1424/1534 (92%)	-0.31	30 (2%) 64 58	6, 23, 40, 62	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	410	PRO	4.9
1	A	409	TYR	4.8
1	A	410	PRO	4.1
1	B	540	VAL	3.9
1	B	409	TYR	3.8

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	EDO	A	1604	4/4	0.86	0.32	15.94	57,60,60,60	0
4	EDO	B	1600	4/4	0.93	0.38	14.18	48,51,51,54	0
4	EDO	A	1606	4/4	0.66	0.51	11.31	66,68,68,68	0
4	EDO	B	1606	4/4	0.66	0.32	10.70	74,77,77,77	0
4	EDO	C	1293	4/4	0.63	0.46	10.60	86,87,87,87	0
4	EDO	C	1290	4/4	0.80	0.27	8.91	53,55,57,58	0
4	EDO	B	1602	4/4	0.85	0.27	8.50	56,58,58,59	0
4	EDO	A	1599	4/4	0.59	0.38	8.41	77,78,78,79	0
4	EDO	A	1601	4/4	0.73	0.36	8.40	59,61,61,61	0
4	EDO	B	1612	4/4	0.81	0.44	8.06	70,71,72,72	0
4	EDO	B	1607	4/4	0.75	0.35	7.93	50,51,52,53	0
4	EDO	B	1601	4/4	0.89	0.23	6.48	48,48,49,50	0
5	CL	B	1615	1/1	0.89	0.19	5.31	82,82,82,82	0
4	EDO	B	1608	4/4	0.86	0.31	5.28	63,63,64,64	0
4	EDO	C	1291	4/4	0.90	0.41	5.00	59,61,62,62	0
5	CL	A	1610	1/1	0.94	0.29	4.72	68,68,68,68	0
5	CL	B	1614	1/1	0.90	0.23	4.61	60,60,60,60	0
4	EDO	A	1608	4/4	0.91	0.22	3.57	69,70,71,71	0
4	EDO	B	1611	4/4	0.84	0.25	2.96	74,76,77,77	0
4	EDO	B	1604	4/4	0.78	0.26	2.67	66,67,68,69	0
3	NAG	A	700	14/15	0.84	0.31	2.65	62,66,68,69	0
4	EDO	B	1610	4/4	0.87	0.29	2.58	73,74,74,75	0
4	EDO	A	1605	4/4	0.94	0.17	2.08	52,52,53,53	0
4	EDO	A	1600	4/4	0.92	0.18	1.60	58,59,59,59	0
4	EDO	C	1295	4/4	0.94	0.18	1.56	65,65,66,67	0
4	EDO	B	1599	4/4	0.86	0.16	1.04	58,58,60,60	0
4	EDO	C	1294	4/4	0.84	0.21	0.82	87,87,87,87	0
4	EDO	B	1605	4/4	0.86	0.18	0.77	54,55,56,56	0
6	MES	C	1289	12/12	0.96	0.13	-0.14	39,41,51,51	0
7	CA	D	1289	1/1	0.97	0.04	-3.50	32,32,32,32	0
7	CA	C	1296	1/1	0.95	0.05	-3.94	29,29,29,29	0
4	EDO	A	1603	4/4	0.82	0.61	-	58,60,60,60	0
5	CL	A	1609	1/1	0.98	0.17	-	46,46,46,46	0
4	EDO	A	1607	4/4	0.84	0.40	-	73,74,74,74	0
4	EDO	A	1602	4/4	0.92	0.16	-	62,65,65,65	0
4	EDO	C	1292	4/4	0.81	0.42	-	67,68,68,69	0
4	EDO	B	1603	4/4	0.80	0.44	-	73,74,75,75	0
3	NAG	A	701	14/15	0.86	0.51	-	65,70,71,72	0
5	CL	B	1613	1/1	0.99	0.15	-	49,49,49,49	0
4	EDO	B	1609	4/4	0.81	0.30	-	74,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	B	700	14/15	0.91	0.32	-	59,64,65,66	0
3	NAG	B	701	14/15	0.79	0.46	-	66,71,71,72	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.