



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:30 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 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

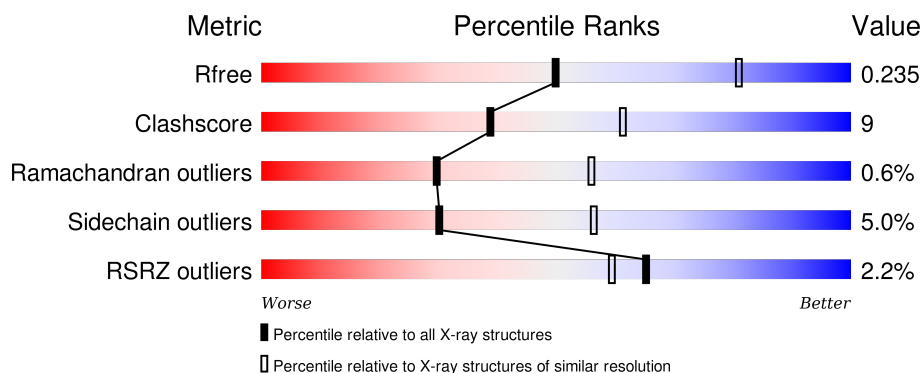
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (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>76%</div> <div>12%</div> <div>•</div> <div>10%</div> </div>
1	B	588	<div> <div>2%</div> <div>77%</div> <div>13%</div> <div>••</div> <div>8%</div> </div>
2	C	179	<div> <div>2%</div> <div>81%</div> <div>17%</div> <div>••</div> </div>
2	D	179	<div> <div>5%</div> <div>80%</div> <div>17%</div> <div>••</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	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 [i](#)

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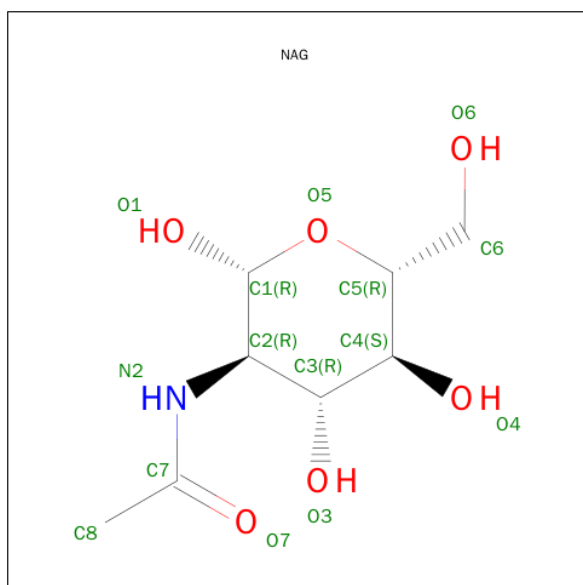
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Chain	Residue	Modelled	Actual	Comment	Reference
B	561	ARG	LYS	CLONING ARTIFACT	UNP Q8N0W4

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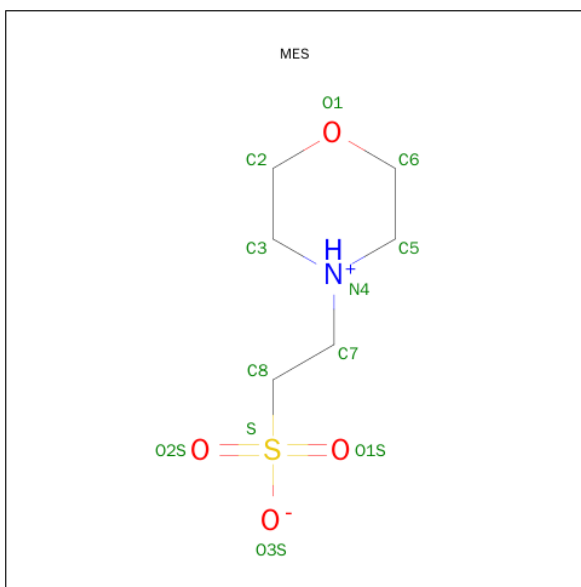
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0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

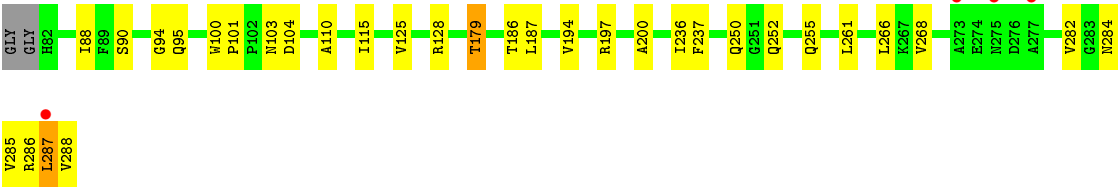
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	1	Total	Ca	0	0
			1	1		
7	C	1	Total	Ca	0	0
			1	1		

- Molecule 8 is water.

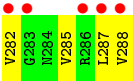
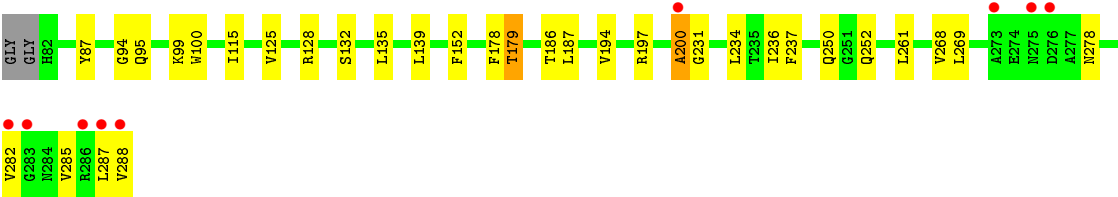
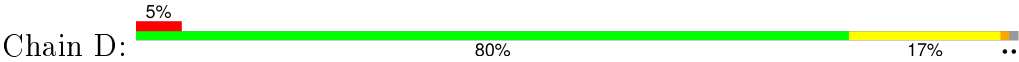
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	129	Total	O	0	0
			129	129		
8	B	162	Total	O	0	0
			162	162		
8	C	38	Total	O	0	0
			38	38		
8	D	20	Total	O	0	0
			20	20		







● 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
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 72486 reflections	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, 0.375 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: 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%)

All (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
1	B	238	VAL	CB-CG2	-9.28	1.33	1.52
1	A	238	VAL	CB-CG1	-8.14	1.35	1.52
1	A	238	VAL	CB-CG2	-7.73	1.36	1.52
1	A	-1	ALA	C-N	6.76	1.49	1.34

All (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
1	A	501	MET	CB-CG-SD	10.07	142.61	112.40
1	B	440	LEU	CB-CG-CD1	7.59	123.90	111.00
1	A	231	LEU	CB-CG-CD1	6.09	121.35	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	352	ASP	CB-CG-OD2	5.38	123.15	118.30
1	B	436	ARG	NE-CZ-NH2	-5.04	117.78	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	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.

All (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
1:B:189:ILE:HD11	1:B:502:ILE:HG12	1.54	0.89
1:B:308:MET:H	1:B:308:MET:CE	1.91	0.84
1:A:308:MET:H	1:A:308:MET:CE	1.91	0.84
1:A:128:PHE:CD1	1:A:135:LEU:HD11	2.12	0.83
1:B:189:ILE:HD11	1:B:502:ILE:CG1	2.08	0.83
2:C:186:THR:HG23	2:C:194:VAL:CG1	2.08	0.82
2:D:186:THR:HG23	2:D:194:VAL:CG1	2.14	0.78
2:C:186:THR:CG2	2:C:194:VAL:CG1	2.64	0.76
1:B:596:HIS:O	1:B:597:LEU:HB2	1.86	0.75
1:B:395:PHE:CD1	1:B:440:LEU:HD13	2.23	0.74
1:B:189:ILE:CD1	1:B:502:ILE:HG12	2.18	0.73
1:A:480:MET:HE2	4:A:1605:EDO:H21	1.69	0.73
2:D:186:THR:CG2	2:D:194:VAL:HG13	2.21	0.70
1:B:306:CYS:C	1:B:308:MET:HE3	2.12	0.69
1:B:58:LEU:HD21	1:B:104:THR:HB	1.74	0.69
2:D:186:THR:CG2	2:D:194:VAL:CG1	2.71	0.68
2:C:287:LEU:HD13	2:C:287:LEU:O	1.94	0.68
1:A:306:CYS:C	1:A:308:MET:HE3	2.14	0.67
1:A:189:ILE:HD11	1:A:502:ILE:CG1	2.25	0.67
1:A:128:PHE:CD1	1:A:135:LEU:CD1	2.78	0.67
1:B:49:ASN:HD22	1:B:54:LYS:HG2	1.60	0.67
2:D:135:LEU:O	8:D:2005:HOH:O	2.13	0.66
1:B:365:TYR:HB2	1:B:367:ILE:HD11	1.78	0.66
1:A:308:MET:H	1:A:308:MET:HE3	1.61	0.65
1:A:414:ASP:N	1:A:414:ASP:OD1	2.26	0.65
1:B:308:MET:HE2	1:B:308:MET:H	1.61	0.65
1:A:107:ALA:HB3	4:A:1601:EDO:H22	1.79	0.64
1:A:308:MET:H	1:A:308:MET:HE2	1.62	0.64
2:C:186:THR:CG2	2:C:194:VAL:HG13	2.26	0.64
1:A:365:TYR:O	1:A:367:ILE:HD13	1.96	0.64
1:B:275:LYS:HG2	1:B:366:ASP:HB2	1.80	0.64
1:A:202:ASN:CG	4:A:1601:EDO:H12	2.19	0.64
1:B:593:LEU:O	1:B:596:HIS:O	2.14	0.63
1:A:365:TYR:HB2	1:A:367:ILE:HD11	1.80	0.63
2:D:288:VAL:HG12	2:D:288:VAL:O	1.97	0.63
2:D:115:ILE:HD12	2:D:261:LEU:HD13	1.79	0.63
1:B:498:GLY:O	1:B:501:MET:HB2	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:94:GLY:HA3	2:C:285:VAL:HG23	1.81	0.62
1:B:308:MET:HE3	1:B:308:MET:H	1.63	0.62
1:B:155:THR:O	1:B:156:GLU:HG2	1.99	0.61
1:B:596:HIS:O	1:B:597:LEU:CB	2.48	0.61
1:A:593:LEU:O	1:A:596:HIS:O	2.18	0.61
1:B:395:PHE:CD1	1:B:440:LEU:CD1	2.83	0.60
1:B:306:CYS:HA	1:B:308:MET:HE1	1.83	0.60
1:B:411:GLU:HG3	1:B:412:GLY:H	1.66	0.60
1:A:306:CYS:HA	1:A:308:MET:HE1	1.84	0.60
1:A:480:MET:HE2	4:A:1605:EDO:C2	2.31	0.59
1:B:234:ILE:O	1:B:238:VAL:HG22	2.02	0.59
1:A:189:ILE:HD11	1:A:502:ILE:HG12	1.82	0.59
2:C:115:ILE:HD12	2:C:261:LEU:HD13	1.83	0.59
1:B:567:GLN:HB3	4:B:1600:EDO:H12	1.85	0.59
1:B:116:GLU:HA	1:B:119:LEU:HD12	1.84	0.58
1:B:414:ASP:N	1:B:414:ASP:OD1	2.35	0.58
1:B:181:THR:HG22	1:B:184:MET:CE	2.34	0.58
2:C:179:THR:HB	2:C:186:THR:HB	1.84	0.58
1:A:596:HIS:O	1:A:597:LEU:CB	2.43	0.58
1:B:234:ILE:HG23	1:B:238:VAL:HG13	1.86	0.58
1:A:49:ASN:HD22	1:A:54:LYS:HG2	1.69	0.58
1:A:338:ILE:HD12	1:A:341:GLY:HA3	1.86	0.57
1:B:365:TYR:O	1:B:367:ILE:HD13	2.04	0.57
1:B:411:GLU:OE1	1:B:411:GLU:HA	2.05	0.57
1:A:275:LYS:HG2	1:A:366:ASP:HB2	1.87	0.57
2:D:179:THR:HB	2:D:186:THR:HB	1.86	0.56
1:A:58:LEU:HD21	1:A:104:THR:HB	1.88	0.56
3:A:700:NAG:C6	8:A:2124:HOH:O	2.50	0.56
1:A:181:THR:CG2	1:A:184:MET:HE3	2.36	0.55
2:D:139:LEU:HD11	2:D:178:PHE:CE2	2.41	0.55
1:B:365:TYR:HB2	1:B:367:ILE:CD1	2.37	0.55
1:A:386:ASN:ND2	4:A:1602:EDO:O2	2.39	0.55
2:D:287:LEU:HG	2:D:287:LEU:O	2.06	0.54
1:B:62:LEU:O	4:B:1611:EDO:O2	2.20	0.54
1:B:181:THR:HG22	1:B:184:MET:HE3	1.88	0.54
1:B:284:LEU:HD21	1:B:357:MET:CE	2.38	0.54
1:B:361:GLU:CG	2:D:234:LEU:HD22	2.38	0.53
2:D:287:LEU:O	2:D:288:VAL:C	2.45	0.53
1:B:181:THR:CG2	1:B:184:MET:HE2	2.39	0.53
1:A:411:GLU:HA	1:A:411:GLU:OE1	2.09	0.53
2:D:261:LEU:HD23	2:D:268:VAL:HB	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:261:LEU:HD23	2:C:268:VAL:HB	1.91	0.53
1:A:101:ARG:NH2	8:A:2006:HOH:O	2.43	0.52
3:A:700:NAG:O6	8:A:2124:HOH:O	1.94	0.52
2:D:95:GLN:HB3	2:D:282:VAL:HG12	1.91	0.52
2:C:88:ILE:HG23	2:C:286:ARG:HB3	1.90	0.52
1:B:63:PRO:HG2	1:B:502:ILE:HD12	1.92	0.52
1:B:338:ILE:HD12	1:B:341:GLY:HA3	1.92	0.52
1:A:406:LEU:HD13	1:A:447:HIS:CE1	2.45	0.51
1:B:306:CYS:HA	1:B:308:MET:CE	2.41	0.51
1:B:155:THR:O	1:B:156:GLU:CG	2.58	0.51
2:C:95:GLN:HB3	2:C:282:VAL:HG12	1.92	0.51
2:C:287:LEU:O	2:C:288:VAL:C	2.49	0.51
1:A:189:ILE:CD1	1:A:502:ILE:HG12	2.41	0.51
1:A:306:CYS:HA	1:A:308:MET:CE	2.41	0.51
1:B:395:PHE:CE1	1:B:440:LEU:HD13	2.46	0.51
2:C:88:ILE:CG2	2:C:286:ARG:HB3	2.40	0.51
1:A:155:THR:O	1:A:156:GLU:HG2	2.09	0.51
1:B:181:THR:HG23	1:B:184:MET:HE2	1.92	0.51
1:B:582:TYR:N	4:B:1600:EDO:H21	2.26	0.50
1:B:181:THR:CG2	1:B:184:MET:CE	2.89	0.50
1:B:494:PRO:HG3	1:B:508:PHE:CD2	2.46	0.50
1:B:-8:ASP:O	1:B:-7:ASP:HB2	2.11	0.50
2:C:186:THR:HG22	2:C:187:LEU:N	2.27	0.50
1:B:409:TYR:O	1:B:410:PRO:C	2.48	0.49
1:A:155:THR:O	1:A:156:GLU:CG	2.60	0.49
1:A:253:SER:HA	1:A:279:GLN:O	2.11	0.49
1:A:447:HIS:ND1	1:A:448:GLN:NE2	2.57	0.49
1:A:168:VAL:HG21	1:A:238:VAL:HG21	1.94	0.49
1:B:124:LEU:HD23	1:B:175:GLY:HA3	1.94	0.49
1:B:115:ASP:O	1:B:116:GLU:CB	2.40	0.48
1:A:128:PHE:CE1	1:A:135:LEU:CD1	2.87	0.48
1:B:-9:ASP:O	1:B:-7:ASP:N	2.47	0.48
1:B:128:PHE:CE1	1:B:135:LEU:HD22	2.48	0.48
1:A:494:PRO:HG3	1:A:508:PHE:CD2	2.49	0.48
1:A:443:LEU:HD23	1:A:443:LEU:C	2.34	0.48
1:B:65:GLU:HA	4:B:1611:EDO:H12	1.96	0.48
1:A:307:ASN:N	1:A:308:MET:HE3	2.29	0.47
1:A:499:ILE:N	1:A:500:PRO:CD	2.77	0.47
1:A:135:LEU:C	1:A:135:LEU:HD23	2.35	0.47
2:C:90:SER:HB2	2:C:284:ASN:ND2	2.29	0.47
3:B:700:NAG:H62	4:B:1609:EDO:H11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:186:THR:CG2	2:C:194:VAL:HG11	2.45	0.47
1:B:388:ASP:OD2	8:B:2106:HOH:O	2.20	0.47
1:A:202:ASN:CG	4:A:1601:EDO:C1	2.83	0.47
1:A:132:LEU:HA	1:A:135:LEU:HB3	1.96	0.47
1:A:411:GLU:OE2	1:A:414:ASP:OD1	2.32	0.47
2:D:125:VAL:HG23	2:D:252:GLN:HE21	1.79	0.47
2:D:139:LEU:HD12	2:D:152:PHE:HB3	1.97	0.46
1:B:499:ILE:N	1:B:500:PRO:CD	2.78	0.46
1:A:392:PRO:HD3	4:A:1603:EDO:H22	1.96	0.46
1:A:365:TYR:HB2	1:A:367:ILE:CD1	2.44	0.46
2:C:101:PRO:HB2	2:C:103:ASN:OD1	2.15	0.46
2:D:200:ALA:C	2:D:231:GLY:CA	2.77	0.46
1:B:63:PRO:HD2	1:B:502:ILE:HD12	1.98	0.46
1:A:181:THR:HG22	1:A:184:MET:HE3	1.97	0.46
2:C:255:GLN:OE1	8:C:2037:HOH:O	2.21	0.46
1:B:307:ASN:N	1:B:308:MET:HE3	2.30	0.46
1:A:58:LEU:N	1:A:58:LEU:HD23	2.31	0.46
1:B:499:ILE:HD13	1:B:508:PHE:CD1	2.51	0.46
2:D:94:GLY:HA3	2:D:285:VAL:CG2	2.46	0.45
1:B:234:ILE:HG23	1:B:238:VAL:CG1	2.46	0.45
1:B:294:ALA:CB	4:B:1599:EDO:H11	2.46	0.45
1:A:476:CYS:SG	4:A:1605:EDO:H11	2.56	0.45
2:D:128:ARG:HD3	2:D:250:GLN:NE2	2.31	0.45
1:B:395:PHE:HD1	1:B:440:LEU:HD13	1.80	0.45
2:D:125:VAL:HG23	2:D:252:GLN:NE2	2.32	0.45
1:A:116:GLU:O	1:A:117:ARG:CB	2.65	0.45
1:A:181:THR:HG22	1:A:184:MET:CE	2.46	0.45
1:A:181:THR:HG23	1:A:184:MET:HE3	1.97	0.45
1:B:114:LEU:HD22	1:B:139:VAL:HG21	1.98	0.45
1:A:181:THR:CG2	1:A:184:MET:CE	2.95	0.45
1:B:597:LEU:O	1:B:598:HIS:HB2	2.17	0.44
2:C:186:THR:HG23	2:C:194:VAL:HG11	1.97	0.44
1:B:253:SER:HA	1:B:279:GLN:O	2.17	0.44
1:B:222:TYR:OH	4:B:1605:EDO:H22	2.18	0.44
1:A:107:ALA:C	4:A:1601:EDO:H22	2.38	0.44
1:B:294:ALA:HB3	4:B:1599:EDO:H11	1.98	0.44
1:A:597:LEU:O	1:A:598:HIS:HB2	2.18	0.44
1:B:58:LEU:HD21	1:B:104:THR:CB	2.44	0.44
1:B:443:LEU:HD23	1:B:443:LEU:C	2.38	0.44
2:C:128:ARG:HD3	2:C:250:GLN:NE2	2.33	0.44
1:A:480:MET:HE1	4:A:1605:EDO:O1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:LEU:HD11	1:A:188:SER:HB3	1.99	0.43
1:A:366:ASP:C	1:A:367:ILE:HD12	2.38	0.43
1:A:58:LEU:HD23	1:A:104:THR:HG22	1.99	0.43
1:A:499:ILE:HD13	1:A:508:PHE:CD1	2.53	0.43
1:A:58:LEU:HD21	1:A:104:THR:CB	2.48	0.43
2:D:87:TYR:CD1	2:D:269:LEU:HD22	2.54	0.43
2:D:186:THR:HG22	2:D:187:LEU:N	2.34	0.43
1:A:183:ASN:HD21	4:A:1601:EDO:H21	1.84	0.42
2:D:186:THR:HG22	8:D:2012:HOH:O	2.17	0.42
1:A:402:PHE:CE1	1:A:406:LEU:HD12	2.54	0.42
1:B:-9:ASP:OD1	1:B:-8:ASP:N	2.52	0.42
1:A:238:VAL:HG22	1:A:243:GLY:HA3	2.02	0.42
1:A:284:LEU:HD21	1:A:357:MET:CE	2.50	0.42
1:A:581:HIS:HB3	1:A:584:ALA:HB2	2.00	0.42
1:B:58:LEU:HD23	1:B:104:THR:HG22	2.01	0.42
1:B:499:ILE:CD1	1:B:508:PHE:CD1	3.03	0.42
1:B:277:ILE:HA	1:B:368:MET:O	2.19	0.42
1:B:135:LEU:HG	1:B:507:LEU:HD21	2.01	0.42
1:B:447:HIS:ND1	1:B:448:GLN:NE2	2.64	0.42
1:B:125:PRO:HG2	1:B:128:PHE:HB2	2.00	0.42
2:C:110:ALA:HB1	4:C:1293:EDO:H22	2.01	0.41
2:D:99:LYS:O	2:D:278:ASN:HB3	2.20	0.41
1:A:369:LEU:N	1:A:369:LEU:HD23	2.34	0.41
2:C:125:VAL:HG23	2:C:252:GLN:HE21	1.85	0.41
2:D:94:GLY:HA3	2:D:285:VAL:HG22	2.02	0.41
1:A:202:ASN:ND2	4:A:1601:EDO:H12	2.36	0.41
1:B:62:LEU:HD11	1:B:188:SER:HB3	2.02	0.41
1:B:435:THR:O	1:B:439:THR:HG23	2.20	0.41
1:A:491:ASP:OD2	4:A:1605:EDO:H12	2.21	0.41
1:A:369:LEU:H	1:A:369:LEU:HD23	1.86	0.41
1:B:189:ILE:HD11	1:B:502:ILE:HG13	1.94	0.40
1:B:185:ILE:HG21	1:B:497:PHE:CZ	2.57	0.40
1:A:232:ARG:NH1	4:A:1599:EDO:O2	2.54	0.40
1:B:376:GLY:HA2	4:B:1607:EDO:H11	2.04	0.40
1:A:410:PRO:HA	1:A:411:GLU:HA	1.83	0.40
1:B:149:LEU:HD12	1:B:149:LEU:C	2.42	0.40

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%)	39	65
1	B	535/588 (91%)	511 (96%)	19 (4%)	5 (1%)	21	42
2	C	175/179 (98%)	170 (97%)	5 (3%)	0	100	100
2	D	175/179 (98%)	168 (96%)	6 (3%)	1 (1%)	30	56
All	All	1406/1534 (92%)	1342 (95%)	56 (4%)	8 (1%)	30	56

All (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
1	A	117	ARG
1	A	597	LEU
2	D	132	SER

### 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%)	27	51
1	B	463/510 (91%)	439 (95%)	24 (5%)	29	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	143/143 (100%)	136 (95%)	7 (5%)	31	57
2	D	143/143 (100%)	139 (97%)	4 (3%)	51	78
All	All	1202/1306 (92%)	1142 (95%)	60 (5%)	30	56

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	LEU
1	A	109	VAL
1	A	124	LEU
1	A	131	ASN
1	A	137	THR
1	A	156	GLU
1	A	179	GLU
1	A	181	THR
1	A	189	ILE
1	A	208	LEU
1	A	231	LEU
1	A	251	PHE
1	A	287	TRP
1	A	307	ASN
1	A	308	MET
1	A	309	LEU
1	A	393	ASN
1	A	414	ASP
1	A	415	THR
1	A	501	MET
1	A	518	MET
1	A	527	TRP
1	A	561	ARG
1	A	565	LYS
1	A	566	ASP
1	B	-10	LYS
1	B	58	LEU
1	B	116	GLU
1	B	135	LEU
1	B	156	GLU
1	B	179	GLU
1	B	181	THR
1	B	208	LEU
1	B	238	VAL

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Mol	Chain	Res	Type
1	B	251	PHE
1	B	287	TRP
1	B	308	MET
1	B	309	LEU
1	B	393	ASN
1	B	414	ASP
1	B	415	THR
1	B	440	LEU
1	B	501	MET
1	B	518	MET
1	B	527	TRP
1	B	561	ARG
1	B	565	LYS
1	B	566	ASP
1	B	596	HIS
2	C	100	TRP
2	C	104	ASP
2	C	179	THR
2	C	236	ILE
2	C	237	PHE
2	C	266	LEU
2	C	287	LEU
2	D	100	TRP
2	D	179	THR
2	D	236	ILE
2	D	237	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	51	ASN
1	A	89	GLN
1	A	202	ASN
1	A	292	GLN
1	A	322	ASN
1	A	386	ASN
1	A	405	ASN
1	A	448	GLN
1	A	515	ASN
1	A	529	ASN
1	B	49	ASN

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Mol	Chain	Res	Type
1	B	51	ASN
1	B	89	GLN
1	B	131	ASN
1	B	202	ASN
1	B	292	GLN
1	B	322	ASN
1	B	405	ASN
1	B	448	GLN
1	B	515	ASN
1	B	529	ASN
1	B	571	HIS
1	B	596	HIS
2	C	252	GLN
2	C	255	GLN
2	C	270	ASN
2	D	252	GLN
2	D	270	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	0.60	0	2,2,2	0.14	0
4	EDO	A	1600	-	3,3,3	0.48	0	2,2,2	0.41	0
4	EDO	A	1601	-	3,3,3	0.74	0	2,2,2	0.56	0
4	EDO	A	1602	-	3,3,3	0.44	0	2,2,2	0.39	0
4	EDO	A	1603	-	3,3,3	0.51	0	2,2,2	0.56	0
4	EDO	A	1604	-	3,3,3	0.65	0	2,2,2	0.44	0
4	EDO	A	1605	-	3,3,3	0.61	0	2,2,2	0.15	0
4	EDO	A	1606	-	3,3,3	0.69	0	2,2,2	0.18	0
4	EDO	A	1607	-	3,3,3	0.61	0	2,2,2	0.11	0
4	EDO	A	1608	-	3,3,3	0.53	0	2,2,2	0.26	0
3	NAG	A	700	1	14,14,15	0.48	0	15,19,21	1.20	1 (6%)
3	NAG	A	701	1	14,14,15	0.51	0	15,19,21	1.07	1 (6%)
4	EDO	B	1599	-	3,3,3	0.53	0	2,2,2	0.23	0
4	EDO	B	1600	-	3,3,3	0.47	0	2,2,2	0.60	0
4	EDO	B	1601	-	3,3,3	0.52	0	2,2,2	0.14	0
4	EDO	B	1602	-	3,3,3	0.85	0	2,2,2	0.53	0
4	EDO	B	1603	-	3,3,3	0.52	0	2,2,2	0.36	0
4	EDO	B	1604	-	3,3,3	0.69	0	2,2,2	0.09	0
4	EDO	B	1605	-	3,3,3	0.64	0	2,2,2	0.23	0
4	EDO	B	1606	-	3,3,3	0.63	0	2,2,2	0.16	0
4	EDO	B	1607	-	3,3,3	0.93	0	2,2,2	1.00	0
4	EDO	B	1608	-	3,3,3	0.56	0	2,2,2	0.34	0
4	EDO	B	1609	-	3,3,3	0.53	0	2,2,2	0.43	0
4	EDO	B	1610	-	3,3,3	0.54	0	2,2,2	0.31	0
4	EDO	B	1611	-	3,3,3	0.45	0	2,2,2	0.37	0
4	EDO	B	1612	-	3,3,3	0.62	0	2,2,2	0.12	0
3	NAG	B	700	1	14,14,15	0.52	0	15,19,21	0.96	0
3	NAG	B	701	1	14,14,15	0.51	0	15,19,21	1.07	1 (6%)
6	MES	C	1289	-	11,12,12	0.52	0	14,16,16	3.63	4 (28%)
4	EDO	C	1290	-	3,3,3	0.65	0	2,2,2	0.43	0
4	EDO	C	1291	-	3,3,3	0.70	0	2,2,2	0.17	0
4	EDO	C	1292	-	3,3,3	0.61	0	2,2,2	0.19	0
4	EDO	C	1293	-	3,3,3	0.58	0	2,2,2	0.05	0
4	EDO	C	1294	-	3,3,3	0.45	0	2,2,2	0.23	0
4	EDO	C	1295	-	3,3,3	0.39	0	2,2,2	0.46	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

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	1289	MES	O1S-S-C8	-2.31	104.94	106.91
3	A	701	NAG	C1-O5-C5	-2.22	109.43	112.25
3	B	701	NAG	C1-O5-C5	2.90	115.92	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	700	NAG	C2-N2-C7	3.16	127.10	123.04
6	C	1289	MES	C7-N4-C3	4.57	122.99	111.27
6	C	1289	MES	C5-N4-C3	5.75	121.34	108.90
6	C	1289	MES	O2S-S-C8	10.54	115.90	106.91

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 ⓘ

### 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	529/588 (89%)	-0.32	9 (1%) 73 68	6, 21, 36, 54	0
1	B	541/588 (92%)	-0.33	9 (1%) 73 68	6, 21, 34, 62	0
2	C	177/179 (98%)	-0.24	4 (2%) 64 57	18, 26, 42, 52	0
2	D	177/179 (98%)	-0.01	9 (5%) 32 25	18, 26, 46, 54	0
All	All	1424/1534 (92%)	-0.28	31 (2%) 65 59	6, 23, 40, 62	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	410	PRO	5.0
1	A	409	TYR	4.9
1	A	410	PRO	4.2
1	B	540	VAL	3.9
1	B	409	TYR	3.9
1	A	44	GLN	3.8
1	B	-9	ASP	3.4
1	A	540	VAL	3.1
2	D	273	ALA	3.0
1	A	408	GLY	2.9
2	D	288	VAL	2.9
1	A	164	SER	2.9
2	D	286	ARG	2.9
1	B	309	LEU	2.8
2	D	275	ASN	2.8
2	D	276	ASP	2.7
2	D	282	VAL	2.6
2	C	275	ASN	2.5
2	C	277	ALA	2.5
2	D	200	ALA	2.4
1	A	-1	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	-8	ASP	2.4
1	B	477	GLN	2.3
2	D	287	LEU	2.3
2	C	273	ALA	2.3
1	B	307	ASN	2.2
1	B	598	HIS	2.2
1	A	411	GLU	2.2
1	A	506	GLU	2.2
2	C	287	LEU	2.1
2	D	283	GLY	2.0

## 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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
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
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

There are no such residues in this entry.