



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 7, 2024 – 09:04 am GMT

PDB ID : 5O0O
Title : Deglycosylated Nogo Receptor with native disulfide structure 5
Authors : Pronker, M.F.; Janssen, B.J.C.
Deposited on : 2017-05-16
Resolution : 2.20 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

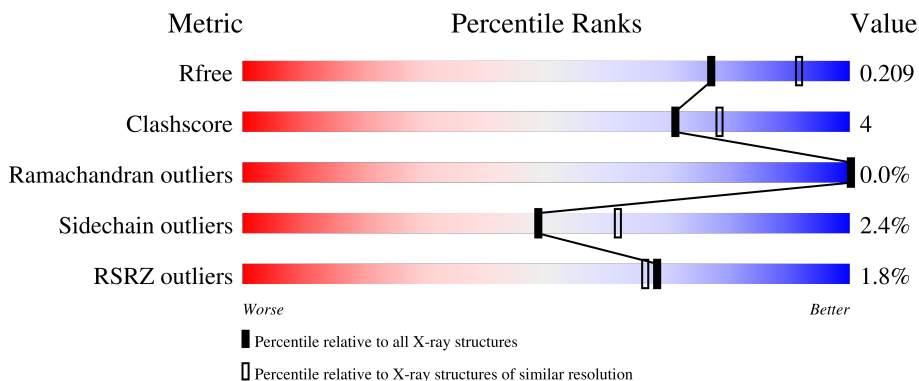
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	323	
1	B	323	
1	C	323	
1	D	323	
1	E	323	

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Mol	Chain	Length	Quality of chain
1	F	323	
1	G	323	
1	H	323	

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	CL	A	417	-	-	X	-
4	CL	C	407	-	-	X	-
4	CL	C	414	-	-	X	-
4	CL	D	406	-	-	X	-
4	CL	D	412	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 21913 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 Reticulon-4 receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	316	Total 2465	C 1553	N 459	O 438	S 15	0	0	0
1	B	317	Total 2491	C 1571	N 466	O 439	S 15	0	1	0
1	C	313	Total 2447	C 1542	N 456	O 434	S 15	0	0	0
1	D	315	Total 2470	C 1557	N 460	O 438	S 15	0	1	0
1	E	315	Total 2479	C 1560	N 465	O 439	S 15	0	2	0
1	F	311	Total 2453	C 1546	N 459	O 433	S 15	0	2	0
1	G	312	Total 2442	C 1540	N 455	O 432	S 15	0	0	0
1	H	308	Total 2429	C 1530	N 454	O 430	S 15	0	2	0

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLY	-	expression tag	UNP Q99PI8
A	25	SER	-	expression tag	UNP Q99PI8
A	26	PRO	-	expression tag	UNP Q99PI8
A	338	ALA	-	expression tag	UNP Q99PI8
A	339	ALA	-	expression tag	UNP Q99PI8
A	340	ALA	-	expression tag	UNP Q99PI8
A	341	HIS	-	expression tag	UNP Q99PI8
A	342	HIS	-	expression tag	UNP Q99PI8
A	343	HIS	-	expression tag	UNP Q99PI8
A	344	HIS	-	expression tag	UNP Q99PI8
A	345	HIS	-	expression tag	UNP Q99PI8
A	346	HIS	-	expression tag	UNP Q99PI8
B	24	GLY	-	expression tag	UNP Q99PI8

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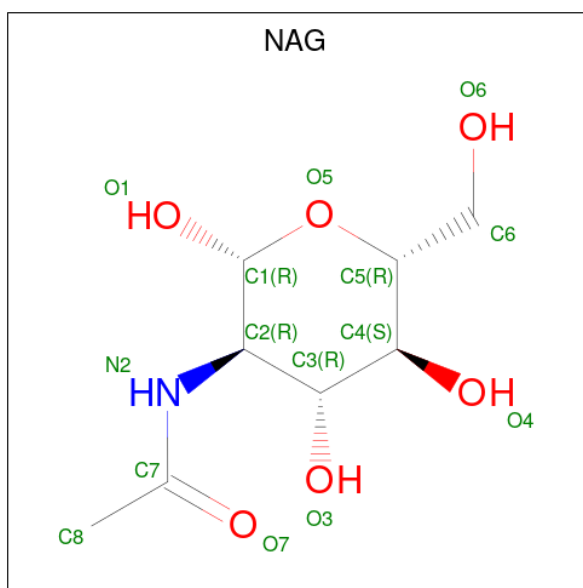
Chain	Residue	Modelled	Actual	Comment	Reference
B	25	SER	-	expression tag	UNP Q99PI8
B	26	PRO	-	expression tag	UNP Q99PI8
B	338	ALA	-	expression tag	UNP Q99PI8
B	339	ALA	-	expression tag	UNP Q99PI8
B	340	ALA	-	expression tag	UNP Q99PI8
B	341	HIS	-	expression tag	UNP Q99PI8
B	342	HIS	-	expression tag	UNP Q99PI8
B	343	HIS	-	expression tag	UNP Q99PI8
B	344	HIS	-	expression tag	UNP Q99PI8
B	345	HIS	-	expression tag	UNP Q99PI8
B	346	HIS	-	expression tag	UNP Q99PI8
C	24	GLY	-	expression tag	UNP Q99PI8
C	25	SER	-	expression tag	UNP Q99PI8
C	26	PRO	-	expression tag	UNP Q99PI8
C	338	ALA	-	expression tag	UNP Q99PI8
C	339	ALA	-	expression tag	UNP Q99PI8
C	340	ALA	-	expression tag	UNP Q99PI8
C	341	HIS	-	expression tag	UNP Q99PI8
C	342	HIS	-	expression tag	UNP Q99PI8
C	343	HIS	-	expression tag	UNP Q99PI8
C	344	HIS	-	expression tag	UNP Q99PI8
C	345	HIS	-	expression tag	UNP Q99PI8
C	346	HIS	-	expression tag	UNP Q99PI8
D	24	GLY	-	expression tag	UNP Q99PI8
D	25	SER	-	expression tag	UNP Q99PI8
D	26	PRO	-	expression tag	UNP Q99PI8
D	338	ALA	-	expression tag	UNP Q99PI8
D	339	ALA	-	expression tag	UNP Q99PI8
D	340	ALA	-	expression tag	UNP Q99PI8
D	341	HIS	-	expression tag	UNP Q99PI8
D	342	HIS	-	expression tag	UNP Q99PI8
D	343	HIS	-	expression tag	UNP Q99PI8
D	344	HIS	-	expression tag	UNP Q99PI8
D	345	HIS	-	expression tag	UNP Q99PI8
D	346	HIS	-	expression tag	UNP Q99PI8
E	24	GLY	-	expression tag	UNP Q99PI8
E	25	SER	-	expression tag	UNP Q99PI8
E	26	PRO	-	expression tag	UNP Q99PI8
E	338	ALA	-	expression tag	UNP Q99PI8
E	339	ALA	-	expression tag	UNP Q99PI8
E	340	ALA	-	expression tag	UNP Q99PI8
E	341	HIS	-	expression tag	UNP Q99PI8

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Chain	Residue	Modelled	Actual	Comment	Reference
E	342	HIS	-	expression tag	UNP Q99PI8
E	343	HIS	-	expression tag	UNP Q99PI8
E	344	HIS	-	expression tag	UNP Q99PI8
E	345	HIS	-	expression tag	UNP Q99PI8
E	346	HIS	-	expression tag	UNP Q99PI8
F	24	GLY	-	expression tag	UNP Q99PI8
F	25	SER	-	expression tag	UNP Q99PI8
F	26	PRO	-	expression tag	UNP Q99PI8
F	338	ALA	-	expression tag	UNP Q99PI8
F	339	ALA	-	expression tag	UNP Q99PI8
F	340	ALA	-	expression tag	UNP Q99PI8
F	341	HIS	-	expression tag	UNP Q99PI8
F	342	HIS	-	expression tag	UNP Q99PI8
F	343	HIS	-	expression tag	UNP Q99PI8
F	344	HIS	-	expression tag	UNP Q99PI8
F	345	HIS	-	expression tag	UNP Q99PI8
F	346	HIS	-	expression tag	UNP Q99PI8
G	24	GLY	-	expression tag	UNP Q99PI8
G	25	SER	-	expression tag	UNP Q99PI8
G	26	PRO	-	expression tag	UNP Q99PI8
G	338	ALA	-	expression tag	UNP Q99PI8
G	339	ALA	-	expression tag	UNP Q99PI8
G	340	ALA	-	expression tag	UNP Q99PI8
G	341	HIS	-	expression tag	UNP Q99PI8
G	342	HIS	-	expression tag	UNP Q99PI8
G	343	HIS	-	expression tag	UNP Q99PI8
G	344	HIS	-	expression tag	UNP Q99PI8
G	345	HIS	-	expression tag	UNP Q99PI8
G	346	HIS	-	expression tag	UNP Q99PI8
H	24	GLY	-	expression tag	UNP Q99PI8
H	25	SER	-	expression tag	UNP Q99PI8
H	26	PRO	-	expression tag	UNP Q99PI8
H	338	ALA	-	expression tag	UNP Q99PI8
H	339	ALA	-	expression tag	UNP Q99PI8
H	340	ALA	-	expression tag	UNP Q99PI8
H	341	HIS	-	expression tag	UNP Q99PI8
H	342	HIS	-	expression tag	UNP Q99PI8
H	343	HIS	-	expression tag	UNP Q99PI8
H	344	HIS	-	expression tag	UNP Q99PI8
H	345	HIS	-	expression tag	UNP Q99PI8
H	346	HIS	-	expression tag	UNP Q99PI8

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:

C₈H₁₅NO₆).

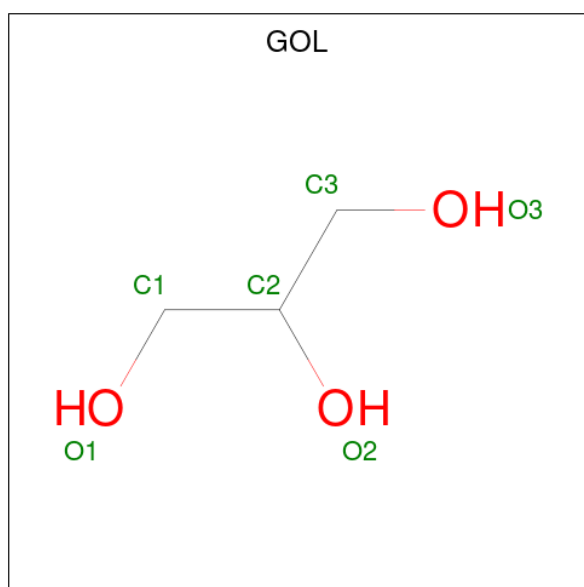
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	E	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	E	1	Total	C	N	O	0	0
			14	8	1	5		
2	E	1	Total	C	N	O	0	0
			14	8	1	5		
2	F	1	Total	C	N	O	0	0
			14	8	1	5		
2	F	1	Total	C	N	O	0	0
			14	8	1	5		
2	F	1	Total	C	N	O	0	0
			14	8	1	5		
2	G	1	Total	C	N	O	0	0
			14	8	1	5		
2	G	1	Total	C	N	O	0	0
			14	8	1	5		
2	G	1	Total	C	N	O	0	0
			14	8	1	5		
2	H	1	Total	C	N	O	0	0
			14	8	1	5		
2	H	1	Total	C	N	O	0	0
			14	8	1	5		
2	H	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	12	Total	Cl	0	0
			12	12		
4	B	13	Total	Cl	0	0
			13	13		
4	C	14	Total	Cl	0	0
			14	14		
4	D	9	Total	Cl	0	0
			9	9		
4	E	11	Total	Cl	0	0
			11	11		
4	F	13	Total	Cl	0	0
			13	13		
4	G	12	Total	Cl	0	0
			12	12		
4	H	10	Total	Cl	0	0
			10	10		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	243	Total	O	0	0
			243	243		
5	B	230	Total	O	0	0
			230	230		
5	C	204	Total	O	0	0
			204	204		

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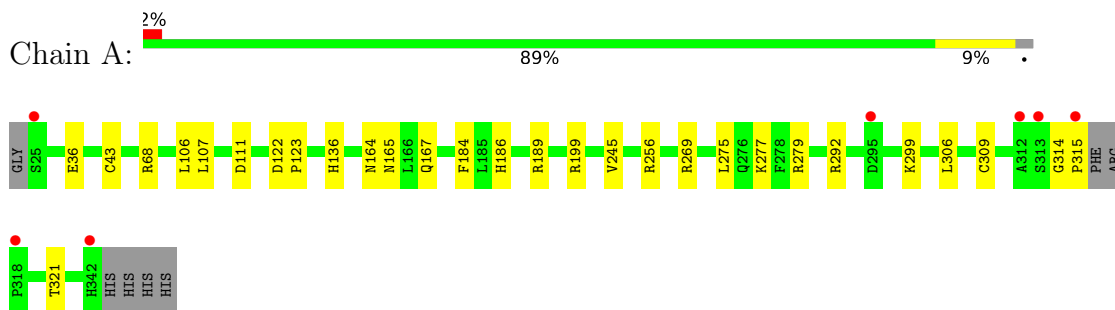
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	249	Total 249	O 249	0	0
5	E	200	Total 200	O 200	0	0
5	F	258	Total 258	O 258	0	0
5	G	194	Total 194	O 194	0	0
5	H	187	Total 187	O 187	0	0

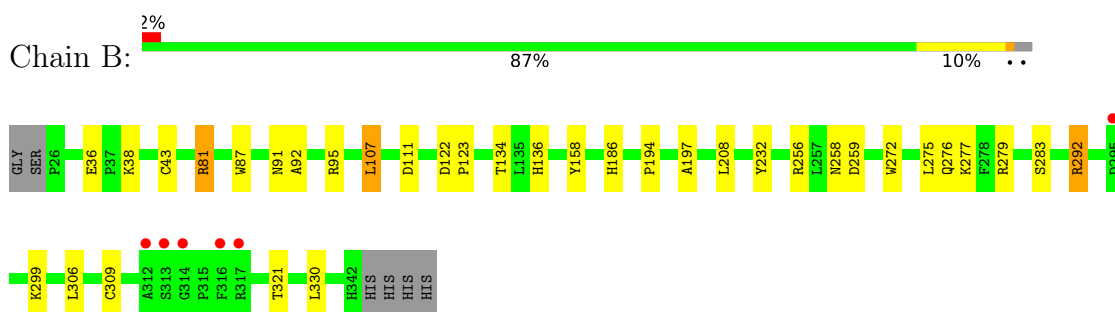
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

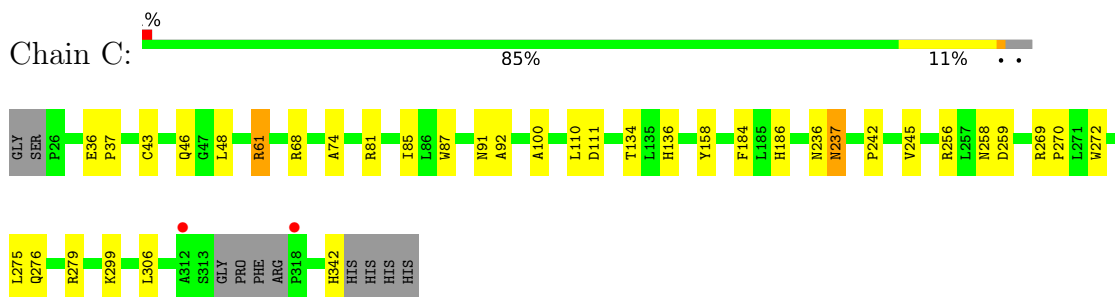
- Molecule 1: Reticulon-4 receptor



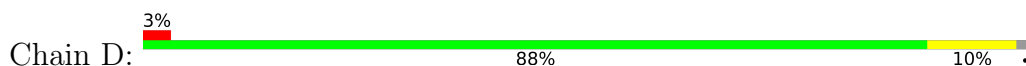
- Molecule 1: Reticulon-4 receptor

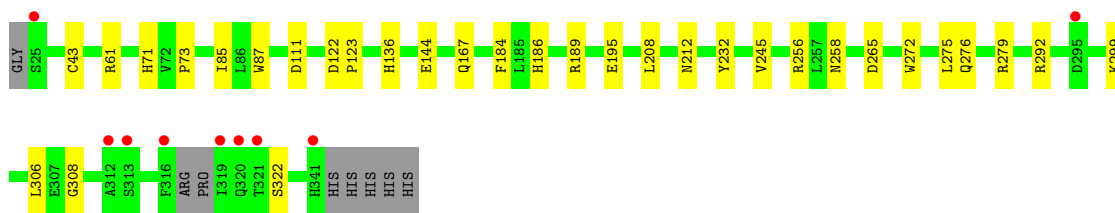


- Molecule 1: Reticulon-4 receptor

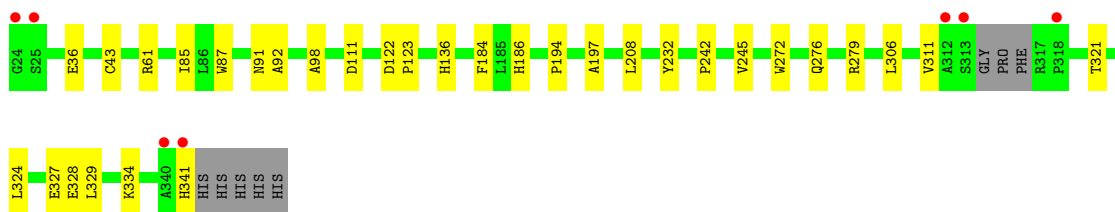
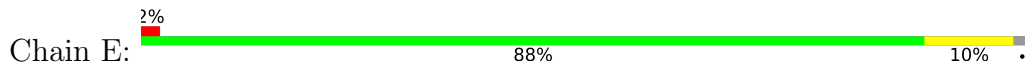


- Molecule 1: Reticulon-4 receptor

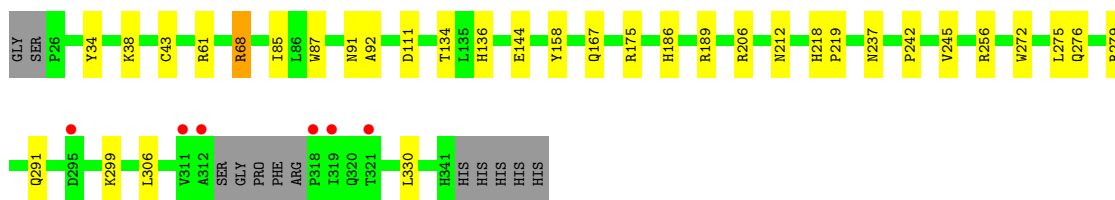
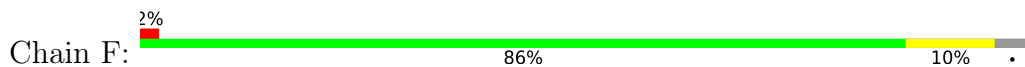




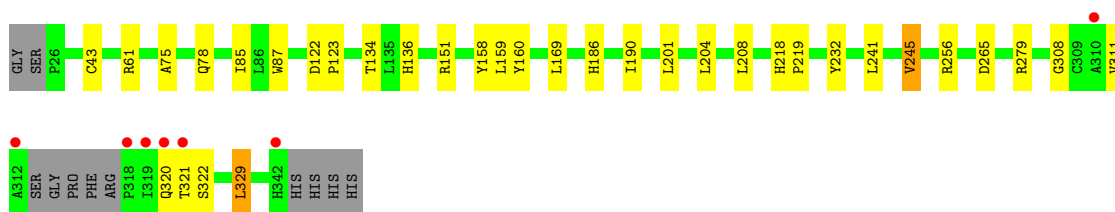
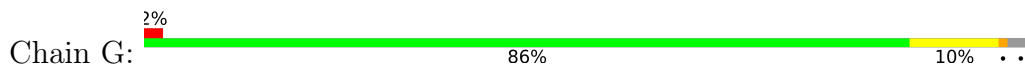
• Molecule 1: Reticulon-4 receptor



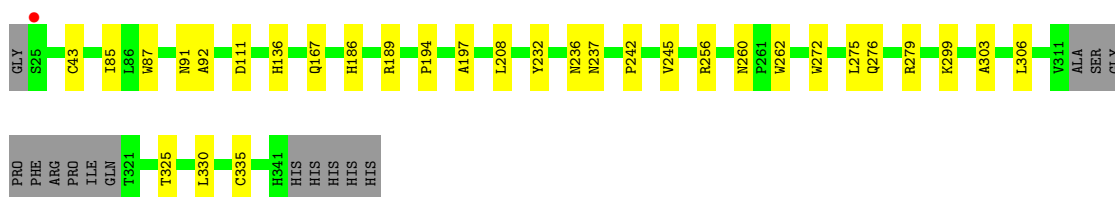
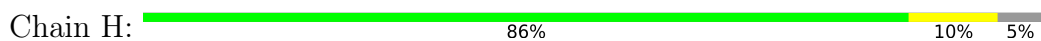
• Molecule 1: Reticulon-4 receptor



• Molecule 1: Reticulon-4 receptor



• Molecule 1: Reticulon-4 receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	168.49Å 168.49Å 256.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.39 – 2.20 70.39 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (70.39-2.20) 99.9 (70.39-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.20Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.167 , 0.207 0.170 , 0.209	Depositor DCC
R_{free} test set	9334 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtrriage
Anisotropy	0.556	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	21913	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.42% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: CL, NAG, GOL

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	0.25	0/2527	0.42	0/3443
1	B	0.25	0/2556	0.42	0/3483
1	C	0.25	0/2508	0.41	0/3415
1	D	0.26	0/2531	0.43	0/3447
1	E	0.25	0/2540	0.42	0/3458
1	F	0.26	0/2514	0.43	0/3423
1	G	0.24	0/2503	0.41	0/3409
1	H	0.24	0/2490	0.40	0/3392
All	All	0.25	0/20169	0.42	0/27470

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 [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	2465	0	2432	17	0
1	B	2491	0	2456	22	0
1	C	2447	0	2414	19	0
1	D	2470	0	2438	18	0
1	E	2479	0	2443	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2453	0	2424	20	0
1	G	2442	0	2413	17	0
1	H	2429	0	2390	17	0
2	A	42	0	39	0	0
2	B	42	0	39	0	0
2	C	42	0	39	0	0
2	D	42	0	39	0	0
2	E	42	0	39	0	0
2	F	42	0	39	2	0
2	G	42	0	39	0	0
2	H	42	0	39	0	0
3	A	18	0	24	3	0
3	B	6	0	8	1	0
3	D	6	0	8	1	0
3	F	6	0	8	2	0
3	H	6	0	8	0	0
4	A	12	0	0	5	0
4	B	13	0	0	5	0
4	C	14	0	0	5	0
4	D	9	0	0	4	0
4	E	11	0	0	1	0
4	F	13	0	0	3	0
4	G	12	0	0	2	0
4	H	10	0	0	2	0
5	A	243	0	0	4	0
5	B	230	0	0	3	0
5	C	204	0	0	1	0
5	D	249	0	0	1	0
5	E	200	0	0	0	0
5	F	258	0	0	3	0
5	G	194	0	0	0	0
5	H	187	0	0	1	0
All	All	21913	0	19778	141	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 4.

The worst 5 of 141 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:H:186:HIS:ND1	4:H:413:CL:CL	2.31	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:186:HIS:ND1	4:E:411:CL:CL	2.33	0.99
1:D:186:HIS:ND1	4:D:412:CL:CL	2.32	0.98
1:C:186:HIS:ND1	4:C:414:CL:CL	2.34	0.98
1:B:186:HIS:ND1	4:B:415:CL:CL	2.40	0.89

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	312/323 (97%)	297 (95%)	15 (5%)	0	100	100
1	B	316/323 (98%)	302 (96%)	14 (4%)	0	100	100
1	C	309/323 (96%)	297 (96%)	12 (4%)	0	100	100
1	D	312/323 (97%)	298 (96%)	13 (4%)	1 (0%)	41	46
1	E	312/323 (97%)	296 (95%)	16 (5%)	0	100	100
1	F	309/323 (96%)	294 (95%)	15 (5%)	0	100	100
1	G	308/323 (95%)	293 (95%)	15 (5%)	0	100	100
1	H	306/323 (95%)	293 (96%)	13 (4%)	0	100	100
All	All	2484/2584 (96%)	2370 (95%)	113 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	322	SER

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	269/275 (98%)	263 (98%)	6 (2%)	52 65
1	B	271/275 (98%)	264 (97%)	7 (3%)	46 58
1	C	267/275 (97%)	259 (97%)	8 (3%)	41 53
1	D	269/275 (98%)	263 (98%)	6 (2%)	52 65
1	E	270/275 (98%)	265 (98%)	5 (2%)	57 71
1	F	267/275 (97%)	259 (97%)	8 (3%)	41 53
1	G	266/275 (97%)	259 (97%)	7 (3%)	46 58
1	H	265/275 (96%)	260 (98%)	5 (2%)	57 71
All	All	2144/2200 (98%)	2092 (98%)	52 (2%)	49 62

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	43	CYS
1	F	144	GLU
1	H	306	LEU
1	E	87	TRP
1	F	43	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 125 ligands modelled in this entry, 94 are monoatomic - leaving 31 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	$\# Z > 2$
3	GOL	A	405	-	5,5,5	0.38	0	5,5,5	0.29	0
3	GOL	H	404	-	5,5,5	0.38	0	5,5,5	0.32	0
2	NAG	H	403	1	14,14,15	0.36	0	17,19,21	0.45	0
2	NAG	D	401	1	14,14,15	0.33	0	17,19,21	0.36	0
3	GOL	D	404	-	5,5,5	0.36	0	5,5,5	0.27	0
2	NAG	B	401	1	14,14,15	0.23	0	17,19,21	0.80	0
3	GOL	B	404	-	5,5,5	0.37	0	5,5,5	0.35	0
2	NAG	G	403	1	14,14,15	0.30	0	17,19,21	0.34	0
2	NAG	F	401	1	14,14,15	0.35	0	17,19,21	0.55	0
2	NAG	F	403	1	14,14,15	0.52	0	17,19,21	1.32	2 (11%)
2	NAG	A	403	1	14,14,15	0.26	0	17,19,21	0.44	0
2	NAG	B	402	1	14,14,15	0.31	0	17,19,21	0.48	0
2	NAG	B	403	1	14,14,15	0.31	0	17,19,21	0.40	0
2	NAG	G	402	1	14,14,15	0.22	0	17,19,21	0.38	0
2	NAG	G	401	1	14,14,15	0.31	0	17,19,21	0.42	0
2	NAG	H	402	1	14,14,15	0.28	0	17,19,21	0.60	0
2	NAG	E	402	1	14,14,15	0.31	0	17,19,21	0.40	0
2	NAG	H	401	1	14,14,15	0.35	0	17,19,21	0.42	0
2	NAG	E	401	1	14,14,15	0.31	0	17,19,21	0.43	0
2	NAG	A	401	1	14,14,15	0.26	0	17,19,21	0.70	1 (5%)
3	GOL	A	406	-	5,5,5	0.36	0	5,5,5	0.22	0
2	NAG	A	402	1	14,14,15	0.24	0	17,19,21	0.45	0
2	NAG	E	403	1	14,14,15	0.31	0	17,19,21	0.38	0
3	GOL	F	404	-	5,5,5	0.38	0	5,5,5	0.29	0
2	NAG	C	402	1	14,14,15	0.20	0	17,19,21	0.50	0
2	NAG	D	403	1	14,14,15	0.25	0	17,19,21	0.43	0
2	NAG	D	402	1	14,14,15	0.20	0	17,19,21	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	403	1	14,14,15	0.21	0	17,19,21	0.41	0
2	NAG	F	402	1	14,14,15	0.17	0	17,19,21	0.53	0
3	GOL	A	404	-	5,5,5	0.38	0	5,5,5	0.14	0
2	NAG	C	401	1	14,14,15	0.27	0	17,19,21	0.51	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	GOL	A	405	-	-	3/4/4/4	-
3	GOL	H	404	-	-	0/4/4/4	-
2	NAG	H	403	1	-	0/6/23/26	0/1/1/1
2	NAG	D	401	1	-	2/6/23/26	0/1/1/1
3	GOL	D	404	-	-	4/4/4/4	-
2	NAG	B	401	1	-	3/6/23/26	0/1/1/1
3	GOL	B	404	-	-	4/4/4/4	-
2	NAG	G	403	1	-	0/6/23/26	0/1/1/1
2	NAG	F	401	1	-	2/6/23/26	0/1/1/1
2	NAG	F	403	1	-	5/6/23/26	0/1/1/1
2	NAG	A	403	1	-	2/6/23/26	0/1/1/1
2	NAG	B	402	1	-	2/6/23/26	0/1/1/1
2	NAG	B	403	1	-	2/6/23/26	0/1/1/1
2	NAG	G	402	1	-	0/6/23/26	0/1/1/1
2	NAG	G	401	1	-	2/6/23/26	0/1/1/1
2	NAG	H	402	1	-	1/6/23/26	0/1/1/1
2	NAG	E	402	1	-	0/6/23/26	0/1/1/1
2	NAG	H	401	1	-	0/6/23/26	0/1/1/1
2	NAG	E	401	1	-	2/6/23/26	0/1/1/1
2	NAG	A	401	1	-	0/6/23/26	0/1/1/1
3	GOL	A	406	-	-	2/4/4/4	-
2	NAG	A	402	1	-	3/6/23/26	0/1/1/1
2	NAG	E	403	1	-	2/6/23/26	0/1/1/1
3	GOL	F	404	-	-	2/4/4/4	-
2	NAG	C	402	1	-	2/6/23/26	0/1/1/1
2	NAG	D	403	1	-	2/6/23/26	0/1/1/1
2	NAG	D	402	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	403	1	-	2/6/23/26	0/1/1/1
2	NAG	F	402	1	-	0/6/23/26	0/1/1/1
3	GOL	A	404	-	-	2/4/4/4	-
2	NAG	C	401	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	403	NAG	C2-N2-C7	4.39	129.16	122.90
2	A	401	NAG	C1-O5-C5	2.53	115.62	112.19
2	F	403	NAG	C1-C2-N2	2.05	113.98	110.49

There are no chirality outliers.

5 of 53 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	404	GOL	O1-C1-C2-C3
3	A	405	GOL	O1-C1-C2-O2
3	A	405	GOL	O1-C1-C2-C3
3	A	406	GOL	C1-C2-C3-O3
3	B	404	GOL	O1-C1-C2-O2

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	405	GOL	1	0
3	D	404	GOL	1	0
3	B	404	GOL	1	0
2	F	403	NAG	2	0
3	A	406	GOL	2	0
3	F	404	GOL	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	316/323 (97%)	-0.36	7 (2%) 62 59	21, 36, 61, 125	0
1	B	317/323 (98%)	-0.45	6 (1%) 66 65	24, 35, 61, 135	0
1	C	313/323 (96%)	-0.41	2 (0%) 89 88	24, 36, 73, 131	0
1	D	315/323 (97%)	-0.31	9 (2%) 51 49	20, 30, 80, 127	0
1	E	315/323 (97%)	-0.30	7 (2%) 62 59	23, 36, 73, 136	0
1	F	311/323 (96%)	-0.36	6 (1%) 66 65	18, 30, 67, 130	0
1	G	312/323 (96%)	-0.37	7 (2%) 62 59	24, 38, 69, 134	0
1	H	308/323 (95%)	-0.36	1 (0%) 94 93	22, 38, 73, 131	0
All	All	2507/2584 (97%)	-0.36	45 (1%) 68 66	18, 35, 71, 136	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	312	ALA	10.1
1	A	315	PRO	7.3
1	B	317	ARG	7.0
1	E	340	ALA	6.9
1	A	313	SER	6.3

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 monosaccharides 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. 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	B-factors(Å ²)	Q<0.9
3	GOL	A	404	6/6	0.56	0.25	93,96,97,98	0
3	GOL	A	406	6/6	0.60	0.40	63,78,81,83	0
2	NAG	C	403	14/15	0.61	0.38	88,102,110,113	0
2	NAG	B	403	14/15	0.66	0.33	71,90,98,100	0
3	GOL	D	404	6/6	0.66	0.25	51,69,73,77	0
3	GOL	H	404	6/6	0.66	0.29	64,72,74,75	0
2	NAG	F	403	14/15	0.68	0.35	88,96,104,104	0
4	CL	A	416	1/1	0.69	0.24	89,89,89,89	0
2	NAG	H	403	14/15	0.72	0.31	71,78,87,91	0
2	NAG	A	403	14/15	0.72	0.26	73,85,89,89	0
3	GOL	F	404	6/6	0.75	0.30	68,75,77,78	0
2	NAG	B	402	14/15	0.76	0.18	58,73,88,91	0
3	GOL	B	404	6/6	0.76	0.29	57,70,75,75	0
2	NAG	E	403	14/15	0.77	0.32	72,79,87,90	0
2	NAG	E	402	14/15	0.77	0.21	65,73,80,82	0
2	NAG	H	402	14/15	0.79	0.21	61,79,86,90	0
3	GOL	A	405	6/6	0.80	0.41	43,62,65,69	0
2	NAG	C	402	14/15	0.82	0.19	55,69,81,81	0
4	CL	H	414	1/1	0.82	0.30	104,104,104,104	0
2	NAG	G	403	14/15	0.83	0.36	70,83,89,91	0
4	CL	G	405	1/1	0.84	0.10	75,75,75,75	0
2	NAG	G	402	14/15	0.85	0.19	44,68,75,76	0
4	CL	C	413	1/1	0.85	0.10	66,66,66,66	0
2	NAG	D	403	14/15	0.86	0.29	68,79,84,86	0
4	CL	C	417	1/1	0.86	0.09	72,72,72,72	0
2	NAG	A	402	14/15	0.87	0.16	52,65,82,84	0
4	CL	G	413	1/1	0.87	0.10	72,72,72,72	0
4	CL	E	412	1/1	0.87	0.18	72,72,72,72	0
2	NAG	F	402	14/15	0.88	0.14	51,63,75,78	0
2	NAG	B	401	14/15	0.88	0.15	39,47,55,60	0
2	NAG	D	402	14/15	0.89	0.16	55,68,83,85	0
4	CL	C	409	1/1	0.89	0.12	65,65,65,65	0
4	CL	F	412	1/1	0.91	0.10	63,63,63,63	0
4	CL	B	416	1/1	0.91	0.08	60,60,60,60	0
4	CL	G	412	1/1	0.91	0.07	60,60,60,60	0
4	CL	B	417	1/1	0.91	0.09	58,58,58,58	0
4	CL	A	411	1/1	0.91	0.11	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	CL	E	414	1/1	0.92	0.21	104,104,104,104	0
2	NAG	G	401	14/15	0.92	0.12	40,46,51,52	0
4	CL	B	409	1/1	0.92	0.07	62,62,62,62	0
4	CL	G	410	1/1	0.93	0.06	62,62,62,62	0
4	CL	G	411	1/1	0.93	0.11	67,67,67,67	0
4	CL	C	411	1/1	0.93	0.14	62,62,62,62	0
4	CL	B	410	1/1	0.93	0.08	62,62,62,62	0
4	CL	E	413	1/1	0.93	0.21	82,82,82,82	0
4	CL	H	407	1/1	0.94	0.20	67,67,67,67	0
4	CL	B	405	1/1	0.94	0.10	47,47,47,47	0
2	NAG	A	401	14/15	0.95	0.14	35,50,58,61	0
4	CL	F	414	1/1	0.95	0.10	50,50,50,50	0
4	CL	F	417	1/1	0.95	0.08	58,58,58,58	0
4	CL	C	412	1/1	0.95	0.07	50,50,50,50	0
2	NAG	C	401	14/15	0.95	0.11	31,45,50,55	0
4	CL	A	415	1/1	0.95	0.11	68,68,68,68	0
2	NAG	F	401	14/15	0.95	0.13	28,40,51,57	0
2	NAG	E	401	14/15	0.95	0.13	40,47,57,58	0
4	CL	C	410	1/1	0.95	0.11	60,60,60,60	0
4	CL	H	413	1/1	0.95	0.10	41,41,41,41	0
4	CL	F	406	1/1	0.95	0.08	47,47,47,47	0
2	NAG	D	401	14/15	0.96	0.09	28,38,43,49	0
4	CL	E	410	1/1	0.96	0.08	47,47,47,47	0
4	CL	H	406	1/1	0.96	0.08	55,55,55,55	0
4	CL	G	406	1/1	0.96	0.06	52,52,52,52	0
4	CL	H	410	1/1	0.96	0.07	50,50,50,50	0
2	NAG	H	401	14/15	0.96	0.11	34,46,50,52	0
4	CL	A	413	1/1	0.96	0.06	52,52,52,52	0
4	CL	C	414	1/1	0.97	0.06	40,40,40,40	0
4	CL	C	416	1/1	0.97	0.13	90,90,90,90	0
4	CL	A	409	1/1	0.97	0.08	50,50,50,50	0
4	CL	D	413	1/1	0.97	0.08	58,58,58,58	0
4	CL	E	405	1/1	0.97	0.08	55,55,55,55	0
4	CL	E	406	1/1	0.97	0.08	43,43,43,43	0
4	CL	G	404	1/1	0.97	0.11	50,50,50,50	0
4	CL	H	412	1/1	0.97	0.11	56,56,56,56	0
4	CL	B	413	1/1	0.97	0.09	48,48,48,48	0
4	CL	A	414	1/1	0.97	0.12	57,57,57,57	0
4	CL	F	407	1/1	0.98	0.12	44,44,44,44	0
4	CL	F	411	1/1	0.98	0.17	59,59,59,59	0
4	CL	C	407	1/1	0.98	0.14	51,51,51,51	0
4	CL	F	413	1/1	0.98	0.08	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	CL	D	409	1/1	0.98	0.07	38,38,38,38	0
4	CL	F	415	1/1	0.98	0.10	36,36,36,36	0
4	CL	D	410	1/1	0.98	0.11	44,44,44,44	0
4	CL	D	411	1/1	0.98	0.09	51,51,51,51	0
4	CL	D	412	1/1	0.98	0.10	41,41,41,41	0
4	CL	C	408	1/1	0.98	0.06	66,66,66,66	0
4	CL	G	407	1/1	0.98	0.07	46,46,46,46	0
4	CL	G	409	1/1	0.98	0.10	51,51,51,51	0
4	CL	E	404	1/1	0.98	0.10	44,44,44,44	0
4	CL	B	412	1/1	0.98	0.08	46,46,46,46	0
4	CL	B	408	1/1	0.98	0.08	45,45,45,45	0
4	CL	E	407	1/1	0.98	0.10	54,54,54,54	0
4	CL	G	414	1/1	0.98	0.07	51,51,51,51	0
4	CL	H	405	1/1	0.98	0.08	48,48,48,48	0
4	CL	B	414	1/1	0.98	0.06	40,40,40,40	0
4	CL	A	408	1/1	0.98	0.07	45,45,45,45	0
4	CL	H	408	1/1	0.98	0.09	50,50,50,50	0
4	CL	H	409	1/1	0.98	0.16	44,44,44,44	0
4	CL	A	407	1/1	0.98	0.09	52,52,52,52	0
4	CL	H	411	1/1	0.98	0.10	42,42,42,42	0
4	CL	C	404	1/1	0.98	0.11	43,43,43,43	0
4	CL	F	405	1/1	0.98	0.12	47,47,47,47	0
4	CL	C	405	1/1	0.98	0.09	56,56,56,56	0
4	CL	D	407	1/1	0.99	0.11	31,31,31,31	0
4	CL	D	408	1/1	0.99	0.10	34,34,34,34	0
4	CL	G	408	1/1	0.99	0.11	42,42,42,42	0
4	CL	B	411	1/1	0.99	0.06	49,49,49,49	0
4	CL	B	406	1/1	0.99	0.07	56,56,56,56	0
4	CL	A	412	1/1	0.99	0.09	50,50,50,50	0
4	CL	C	406	1/1	0.99	0.09	46,46,46,46	0
4	CL	F	408	1/1	0.99	0.10	36,36,36,36	0
4	CL	F	409	1/1	0.99	0.10	39,39,39,39	0
4	CL	G	415	1/1	0.99	0.09	37,37,37,37	0
4	CL	F	410	1/1	0.99	0.08	44,44,44,44	0
4	CL	A	417	1/1	0.99	0.08	37,37,37,37	0
4	CL	C	415	1/1	0.99	0.06	42,42,42,42	0
4	CL	B	415	1/1	0.99	0.10	41,41,41,41	0
4	CL	A	410	1/1	0.99	0.07	48,48,48,48	0
4	CL	D	405	1/1	0.99	0.14	43,43,43,43	0
4	CL	F	416	1/1	0.99	0.08	65,65,65,65	0
4	CL	E	409	1/1	0.99	0.07	38,38,38,38	0
4	CL	D	406	1/1	0.99	0.07	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	CL	E	411	1/1	0.99	0.10	40,40,40,40	0
4	CL	E	408	1/1	1.00	0.10	50,50,50,50	0
4	CL	B	407	1/1	1.00	0.07	46,46,46,46	0
4	CL	A	418	1/1	1.00	0.08	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.