



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 03:32 am GMT

PDB ID : 1CKL
Title : N-TERMINAL TWO DOMAINS OF HUMAN CD46 (MEMBRANE COFACT-
TOR PROTEIN, MCP)
Authors : Casasnovas, J.; Larvie, M.; Stehle, T.
Deposited on : 1999-04-22
Resolution : 3.10 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (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

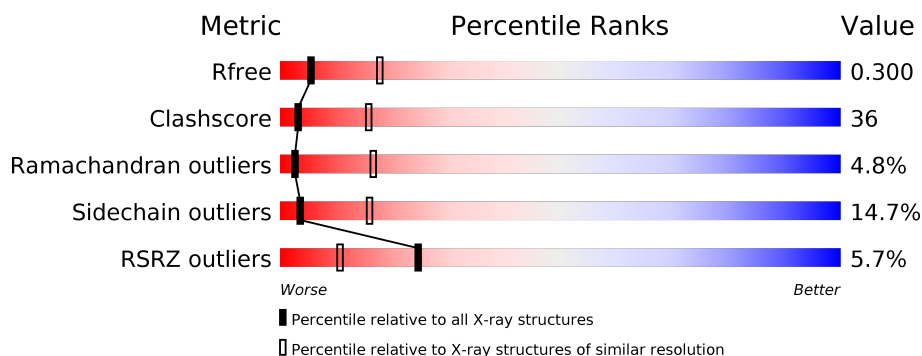
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	126	<div> <div>18%</div> <div>33% 53% 13%</div> </div>
1	B	126	<div> <div>46% 44% 10%</div> </div>
1	C	126	<div> <div>9%</div> <div>37% 52% 10%</div> </div>
1	D	126	<div> <div>5%</div> <div>32% 53% 13%</div> </div>
1	E	126	<div> <div>2%</div> <div>39% 51% 9%</div> </div>
1	F	126	<div> <div>47% 42% 11%</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
2	MAN	E	4180	-	-	X	-
2	MAN	E	5280	-	-	X	-
2	MAN	E	6280	-	-	X	-
5	NAG	C	1049	-	-	-	X
6	NAG	D	1080	-	-	-	X
6	BMA	F	3080	-	-	X	-
6	MAN	F	4080	-	-	X	-
7	MAN	F	4149	-	-	X	-
9	CL	D	4042	-	-	X	X

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 6764 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 PROTEIN (CD46).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	126	Total	C	N	O	S	0	0	0
			1018	659	160	189	10			
1	B	126	Total	C	N	O	S	0	0	0
			1018	659	160	189	10			
1	C	126	Total	C	N	O	S	0	0	0
			1018	659	160	189	10			
1	D	126	Total	C	N	O	S	0	0	0
			1018	659	160	189	10			
1	E	126	Total	C	N	O	S	0	0	0
			1018	659	160	189	10			
1	F	126	Total	C	N	O	S	0	0	0
			1018	659	160	189	10			

- Molecule 2 is a polymer of unknown type called SUGAR (8-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	8	Total	C	N	O	0	0
			94	52	2	40		
2	E	8	Total	C	N	O	0	0
			94	52	2	40		

- Molecule 3 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	3	Total	C	N	O	0	0
			39	22	2	15		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	3	Total	C	N	O	0	0
			39	22	2	15		
4	E	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

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

- Molecule 6 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	D	5	Total	C	N	O	0	0
			61	34	2	25		
6	F	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 7 is a polymer of unknown type called SUGAR (6-MER).

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

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	D	1	Total	Ca	0	0
			1	1		
8	E	1	Total	Ca	0	0
			1	1		
8	B	1	Total	Ca	0	0
			1	1		
8	C	1	Total	Ca	0	0
			1	1		
8	A	1	Total	Ca	0	0
			1	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	F	1	Total 1	Ca 1	0	0

- Molecule 9 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total 1	Cl 1	0	0
9	A	1	Total 1	Cl 1	0	0
9	D	1	Total 1	Cl 1	0	0
9	F	1	Total 1	Cl 1	0	0
9	E	1	Total 1	Cl 1	0	0

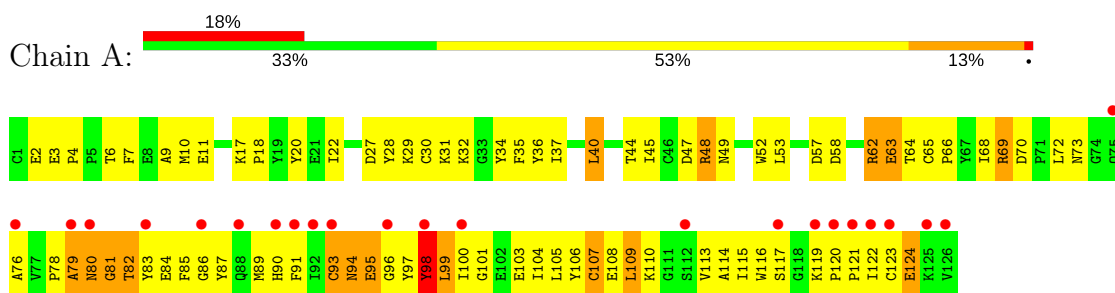
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	2	Total 2	O 2	0	0
10	C	3	Total 3	O 3	0	0
10	D	1	Total 1	O 1	0	0
10	E	2	Total 2	O 2	0	0
10	F	4	Total 4	O 4	0	0

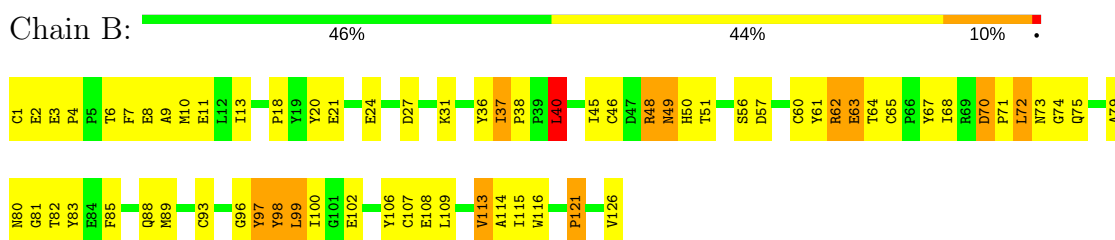
3 Residue-property plots [i](#)

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.

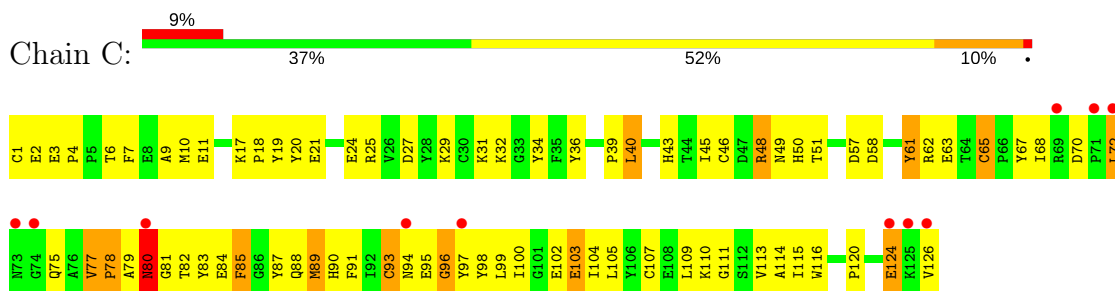
• Molecule 1: PROTEIN (CD46)



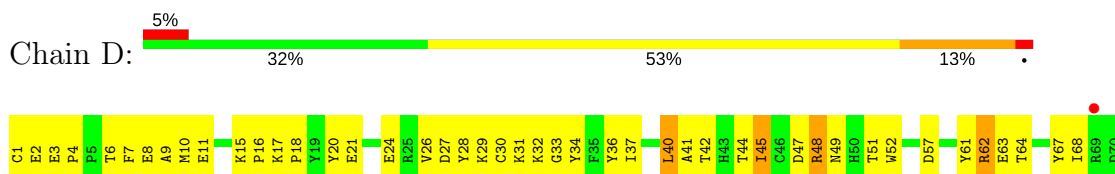
• Molecule 1: PROTEIN (CD46)

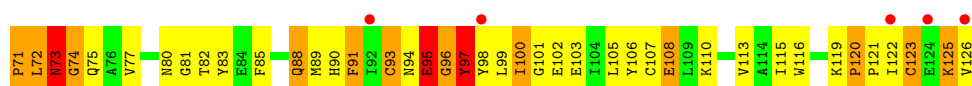


• Molecule 1: PROTEIN (CD46)

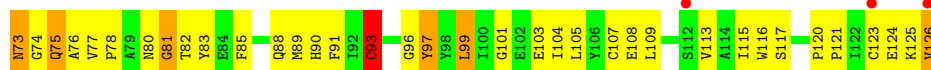


• Molecule 1: PROTEIN (CD46)

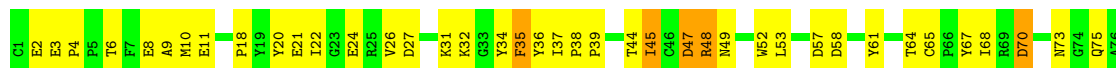




• Molecule 1: PROTEIN (CD46)



• Molecule 1: PROTEIN (CD46)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.82Å 111.20Å 136.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.10 19.84 – 3.10	Depositor EDS
% Data completeness (in resolution range)	92.6 (20.00-3.10) 92.3 (19.84-3.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 3.09Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.244 , 0.298 0.252 , 0.300	Depositor DCC
R_{free} test set	765 reflections (4.05%)	DCC
Wilson B-factor (Å ²)	47.5	Xtriage
Anisotropy	0.601	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	6764	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, CA, BMA, NAG, 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	0.60	0/1052	1.06	5/1432 (0.3%)
1	B	0.59	0/1052	0.97	1/1432 (0.1%)
1	C	0.62	0/1052	1.09	3/1432 (0.2%)
1	D	0.60	0/1052	1.07	6/1432 (0.4%)
1	E	0.57	0/1052	0.99	1/1432 (0.1%)
1	F	0.58	0/1052	1.02	3/1432 (0.2%)
All	All	0.59	0/6312	1.03	19/8592 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	D	0	1
1	F	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	124	GLU	N-CA-C	9.15	135.72	111.00
1	A	99	LEU	N-CA-C	7.77	131.97	111.00
1	E	93	CYS	CA-CB-SG	-7.76	100.04	114.00
1	F	111	GLY	N-CA-C	-7.73	93.77	113.10
1	D	74	GLY	N-CA-C	-6.99	95.64	113.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	98	TYR	Sidechain
1	D	97	TYR	Sidechain
1	F	97	TYR	Sidechain

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	1018	0	962	77	0
1	B	1018	0	962	68	0
1	C	1018	0	962	85	0
1	D	1018	0	962	80	0
1	E	1018	0	962	81	0
1	F	1018	0	962	68	0
2	A	94	0	79	3	0
2	E	94	0	79	17	0
3	A	50	0	43	0	0
4	B	78	0	68	4	0
4	E	39	0	34	3	0
5	C	56	0	50	4	0
5	D	28	0	25	1	0
6	D	61	0	52	1	0
6	F	61	0	52	12	0
7	F	72	0	61	12	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
8	C	1	0	0	0	0
8	D	1	0	0	0	0
8	E	1	0	0	0	0
8	F	1	0	0	0	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
9	D	1	0	0	3	0
9	E	1	0	0	0	0
9	F	1	0	0	0	0
10	B	2	0	0	1	0
10	C	3	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	D	1	0	0	0	0
10	E	2	0	0	1	0
10	F	4	0	0	0	0
All	All	6764	0	6315	477	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 36.

The worst 5 of 477 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:E:4180:MAN:C6	2:E:5280:MAN:H3	1.38	1.50
2:E:4180:MAN:H61	2:E:5280:MAN:C3	1.49	1.41
1:D:41:ALA:HA	9:D:4042:CL:CL	1.82	1.17
1:D:48:ARG:HB3	1:F:61:TYR:HE1	1.01	1.12
1:D:97:TYR:HA	1:D:126:VAL:HG23	1.31	1.12

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	124/126 (98%)	94 (76%)	21 (17%)	9 (7%)	1	7
1	B	124/126 (98%)	108 (87%)	11 (9%)	5 (4%)	3	20
1	C	124/126 (98%)	96 (77%)	21 (17%)	7 (6%)	2	12
1	D	124/126 (98%)	99 (80%)	17 (14%)	8 (6%)	1	9
1	E	124/126 (98%)	101 (82%)	18 (14%)	5 (4%)	3	20
1	F	124/126 (98%)	106 (86%)	16 (13%)	2 (2%)	11	43
All	All	744/756 (98%)	604 (81%)	104 (14%)	36 (5%)	2	16

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	40	LEU
1	A	58	ASP
1	A	63	GLU
1	A	66	PRO
1	A	95	GLU

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	110/110 (100%)	94 (86%)	16 (14%)	4	16
1	B	110/110 (100%)	94 (86%)	16 (14%)	4	16
1	C	110/110 (100%)	95 (86%)	15 (14%)	4	19
1	D	110/110 (100%)	92 (84%)	18 (16%)	2	12
1	E	110/110 (100%)	95 (86%)	15 (14%)	4	19
1	F	110/110 (100%)	93 (84%)	17 (16%)	3	14
All	All	660/660 (100%)	563 (85%)	97 (15%)	3	16

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	94	ASN
1	D	75	GLN
1	F	77	VAL
1	C	109	LEU
1	D	40	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	43	HIS
1	E	75	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	73	ASN
1	B	88	GLN
1	C	88	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

51 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	1049	1,2	14,14,15	0.59	0	15,19,21	1.64	3 (20%)
3	NAG	A	1080	1,3	14,14,15	1.47	3 (21%)	15,19,21	1.02	1 (6%)
2	NAG	A	2049	2	14,14,15	2.34	6 (42%)	15,19,21	3.69	8 (53%)
3	NAG	A	2080	3	14,14,15	3.52	6 (42%)	15,19,21	3.12	7 (46%)
2	BMA	A	3049	2	11,11,12	3.79	4 (36%)	13,15,17	1.86	3 (23%)
3	BMA	A	3080	3	11,11,12	2.85	6 (54%)	13,15,17	1.52	2 (15%)
2	MAN	A	4049	2	11,11,12	1.33	2 (18%)	13,15,17	1.95	2 (15%)
3	MAN	A	4080	3	11,11,12	0.89	0	13,15,17	1.69	2 (15%)
2	MAN	A	4149	2	11,11,12	0.95	1 (9%)	13,15,17	2.16	5 (38%)
2	MAN	A	5049	2	11,11,12	0.86	1 (9%)	13,15,17	1.22	2 (15%)
2	MAN	A	5149	2	11,11,12	1.22	1 (9%)	13,15,17	1.12	2 (15%)
2	MAN	A	6149	2	11,11,12	0.68	0	13,15,17	1.31	1 (7%)
4	NAG	B	1049	1,4	14,14,15	0.96	0	15,19,21	1.67	5 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	1080	1,4	14,14,15	0.79	0	15,19,21	0.93	0
4	NAG	B	2049	4	14,14,15	1.13	1 (7%)	15,19,21	1.34	2 (13%)
4	NAG	B	2080	4	14,14,15	0.59	0	15,19,21	2.19	8 (53%)
4	BMA	B	3049	4	11,11,12	0.84	0	13,15,17	0.78	1 (7%)
4	BMA	B	3080	4	11,11,12	0.50	0	13,15,17	0.79	0
5	NAG	C	1049	1,5	14,14,15	1.22	2 (14%)	15,19,21	2.16	6 (40%)
5	NAG	C	1080	1,5	14,14,15	1.46	1 (7%)	15,19,21	2.91	6 (40%)
5	NAG	C	2049	5	14,14,15	1.63	2 (14%)	15,19,21	1.06	2 (13%)
5	NAG	C	2080	5	14,14,15	0.44	0	15,19,21	0.67	0
5	NAG	D	1049	1,5	14,14,15	0.56	0	15,19,21	0.98	1 (6%)
6	NAG	D	1080	1,6	14,14,15	0.86	1 (7%)	15,19,21	1.45	2 (13%)
5	NAG	D	2049	5	14,14,15	0.62	0	15,19,21	1.46	2 (13%)
6	NAG	D	2080	6	14,14,15	0.86	1 (7%)	15,19,21	1.05	1 (6%)
6	BMA	D	3080	6	11,11,12	0.87	1 (9%)	13,15,17	1.15	2 (15%)
6	MAN	D	4080	6	11,11,12	0.61	0	13,15,17	0.62	0
6	MAN	D	4180	6	11,11,12	0.65	0	13,15,17	0.61	0
4	NAG	E	1049	1,4	14,14,15	0.78	0	15,19,21	1.29	3 (20%)
2	NAG	E	1080	1,2	14,14,15	0.71	0	15,19,21	1.75	2 (13%)
4	NAG	E	2049	4	14,14,15	1.28	1 (7%)	15,19,21	1.52	3 (20%)
2	NAG	E	2080	2	14,14,15	1.03	0	15,19,21	1.67	4 (26%)
4	BMA	E	3049	4	11,11,12	0.46	0	13,15,17	1.04	1 (7%)
2	BMA	E	3080	2	11,11,12	0.95	1 (9%)	13,15,17	0.98	1 (7%)
2	MAN	E	4080	2	11,11,12	0.55	0	13,15,17	1.69	4 (30%)
2	MAN	E	4180	2	11,11,12	0.78	0	13,15,17	2.29	3 (23%)
2	MAN	E	5180	2	11,11,12	0.61	0	13,15,17	2.13	3 (23%)
2	MAN	E	5280	2	11,11,12	1.25	1 (9%)	13,15,17	3.14	4 (30%)
2	MAN	E	6280	2	11,11,12	0.91	0	13,15,17	1.24	2 (15%)
7	NAG	F	1049	1,7	14,14,15	0.44	0	15,19,21	1.92	1 (6%)
6	NAG	F	1080	1,6	14,14,15	0.37	0	15,19,21	1.12	1 (6%)
7	NAG	F	2049	7	14,14,15	0.87	1 (7%)	15,19,21	2.38	5 (33%)
6	NAG	F	2080	6	14,14,15	0.79	0	15,19,21	1.63	3 (20%)
7	BMA	F	3049	7	11,11,12	0.86	0	13,15,17	1.58	3 (23%)
6	BMA	F	3080	6	11,11,12	0.82	0	13,15,17	1.76	3 (23%)
6	MAN	F	4080	6	11,11,12	0.68	0	13,15,17	0.92	1 (7%)
7	MAN	F	4149	7	11,11,12	1.30	2 (18%)	13,15,17	1.25	1 (7%)
6	MAN	F	4180	6	11,11,12	0.54	0	13,15,17	1.82	3 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	MAN	F	5149	7	11,11,12	1.01	1 (9%)	13,15,17	0.94	1 (7%)
7	MAN	F	5249	7	11,11,12	0.67	0	13,15,17	1.13	1 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1049	1,2	-	0/6/23/26	0/1/1/1
3	NAG	A	1080	1,3	-	0/6/23/26	0/1/1/1
2	NAG	A	2049	2	-	0/6/23/26	0/1/1/1
3	NAG	A	2080	3	-	0/6/23/26	0/1/1/1
2	BMA	A	3049	2	-	0/2/19/22	0/1/1/1
3	BMA	A	3080	3	-	0/2/19/22	0/1/1/1
2	MAN	A	4049	2	-	0/2/19/22	0/1/1/1
3	MAN	A	4080	3	-	0/2/19/22	0/1/1/1
2	MAN	A	4149	2	-	0/2/19/22	0/1/1/1
2	MAN	A	5049	2	-	0/2/19/22	0/1/1/1
2	MAN	A	5149	2	-	0/2/19/22	0/1/1/1
2	MAN	A	6149	2	-	0/2/19/22	0/1/1/1
4	NAG	B	1049	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	1080	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	2049	4	-	0/6/23/26	0/1/1/1
4	NAG	B	2080	4	-	0/6/23/26	0/1/1/1
4	BMA	B	3049	4	-	0/2/19/22	0/1/1/1
4	BMA	B	3080	4	-	0/2/19/22	0/1/1/1
5	NAG	C	1049	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	1080	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	2049	5	-	0/6/23/26	0/1/1/1
5	NAG	C	2080	5	-	0/6/23/26	0/1/1/1
5	NAG	D	1049	1,5	-	0/6/23/26	0/1/1/1
6	NAG	D	1080	1,6	-	0/6/23/26	0/1/1/1
5	NAG	D	2049	5	-	0/6/23/26	0/1/1/1
6	NAG	D	2080	6	-	0/6/23/26	0/1/1/1
6	BMA	D	3080	6	-	0/2/19/22	0/1/1/1
6	MAN	D	4080	6	-	0/2/19/22	0/1/1/1
6	MAN	D	4180	6	-	0/2/19/22	0/1/1/1
4	NAG	E	1049	1,4	-	0/6/23/26	0/1/1/1
2	NAG	E	1080	1,2	-	0/6/23/26	0/1/1/1
4	NAG	E	2049	4	-	0/6/23/26	0/1/1/1
2	NAG	E	2080	2	-	0/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BMA	E	3049	4	-	0/2/19/22	0/1/1/1
2	BMA	E	3080	2	-	0/2/19/22	0/1/1/1
2	MAN	E	4080	2	-	0/2/19/22	0/1/1/1
2	MAN	E	4180	2	-	0/2/19/22	0/1/1/1
2	MAN	E	5180	2	-	0/2/19/22	0/1/1/1
2	MAN	E	5280	2	-	0/2/19/22	0/1/1/1
2	MAN	E	6280	2	-	0/2/19/22	0/1/1/1
7	NAG	F	1049	1,7	-	0/6/23/26	0/1/1/1
6	NAG	F	1080	1,6	-	0/6/23/26	0/1/1/1
7	NAG	F	2049	7	-	0/6/23/26	0/1/1/1
6	NAG	F	2080	6	-	0/6/23/26	0/1/1/1
7	BMA	F	3049	7	-	0/2/19/22	0/1/1/1
6	BMA	F	3080	6	-	0/2/19/22	0/1/1/1
6	MAN	F	4080	6	-	0/2/19/22	0/1/1/1
7	MAN	F	4149	7	-	0/2/19/22	0/1/1/1
6	MAN	F	4180	6	-	0/2/19/22	0/1/1/1
7	MAN	F	5149	7	-	0/2/19/22	0/1/1/1
7	MAN	F	5249	7	-	0/2/19/22	0/1/1/1

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2049	NAG	C4-C5	-3.36	1.45	1.53
3	A	2080	NAG	O5-C1	-3.36	1.38	1.43
2	A	4149	MAN	O5-C1	-2.36	1.39	1.43
7	F	4149	MAN	C2-C3	-2.34	1.49	1.52
2	A	3049	BMA	O5-C1	-2.22	1.40	1.43

The worst 5 of 129 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	5280	MAN	C1-C2-C3	-9.79	97.24	109.65
7	F	1049	NAG	C4-C3-C2	-6.32	101.75	111.02
5	C	1049	NAG	C3-C4-C5	-5.57	100.41	110.22
5	C	1080	NAG	O5-C1-C2	-5.31	104.08	111.47
6	F	2080	NAG	C4-C3-C2	-4.96	103.75	111.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

28 monomers are involved in 57 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2049	NAG	2	0
2	A	3049	BMA	2	0
2	A	4149	MAN	1	0
2	A	5149	MAN	1	0
4	B	1080	NAG	2	0
4	B	2080	NAG	3	0
4	B	3080	BMA	2	0
5	C	1049	NAG	1	0
5	C	1080	NAG	2	0
5	C	2049	NAG	1	0
5	C	2080	NAG	3	0
5	D	1049	NAG	1	0
6	D	3080	BMA	1	0
6	D	4080	MAN	1	0
4	E	2049	NAG	3	0
2	E	2080	NAG	2	0
4	E	3049	BMA	3	0
2	E	4180	MAN	7	0
2	E	5180	MAN	3	0
2	E	5280	MAN	12	0
2	E	6280	MAN	8	0
7	F	1049	NAG	2	0
6	F	2080	NAG	4	0
6	F	3080	BMA	10	0
6	F	4080	MAN	8	0
7	F	4149	MAN	10	0
7	F	5149	MAN	5	0
7	F	5249	MAN	5	0

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 11 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	126/126 (100%)	0.96	23 (18%) 1 1	47, 108, 157, 173	0
1	B	126/126 (100%)	-0.04	0 100 100	35, 70, 105, 123	0
1	C	126/126 (100%)	0.54	11 (8%) 11 4	46, 88, 144, 159	0
1	D	126/126 (100%)	0.16	6 (4%) 31 14	44, 71, 131, 145	0
1	E	126/126 (100%)	-0.02	3 (2%) 59 37	34, 69, 120, 133	0
1	F	126/126 (100%)	-0.22	0 100 100	37, 64, 98, 111	0
All	All	756/756 (100%)	0.23	43 (5%) 24 11	34, 73, 141, 173	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	92	ILE	10.4
1	C	126	VAL	8.7
1	A	126	VAL	8.3
1	A	122	ILE	6.3
1	C	72	LEU	5.5

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

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

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	NAG	C	1049	14/15	0.78	0.29	5.53	85,97,113,119	0
6	NAG	D	1080	14/15	0.75	0.33	2.29	93,104,108,115	0
5	NAG	D	1049	14/15	0.91	0.22	1.87	49,65,87,87	0
7	NAG	F	1049	14/15	0.85	0.20	0.36	72,81,94,104	0
4	NAG	B	1080	14/15	0.82	0.26	0.05	73,86,97,102	0
5	NAG	C	1080	14/15	0.65	0.36	0.03	134,140,143,146	0
2	NAG	E	1080	14/15	0.75	0.29	-0.23	83,93,104,113	0
6	NAG	F	1080	14/15	0.95	0.16	-1.46	46,64,79,80	0
2	MAN	E	4180	11/12	0.47	0.45	-	143,147,152,153	0
4	NAG	E	1049	14/15	0.71	0.35	-	120,124,127,139	0
6	NAG	D	2080	14/15	0.73	0.34	-	99,112,129,142	0
7	MAN	F	5249	11/12	0.48	0.77	-	159,163,168,169	0
2	NAG	A	1049	14/15	0.61	0.36	-	115,123,131,138	0
2	MAN	E	5180	11/12	0.70	0.59	-	136,153,156,158	0
4	NAG	B	2080	14/15	0.77	0.31	-	106,122,131,143	0
5	NAG	D	2049	14/15	0.68	0.42	-	101,110,116,118	0
4	NAG	B	2049	14/15	0.45	0.54	-	132,136,144,147	0
5	NAG	C	2049	14/15	0.53	0.67	-	132,140,147,155	0
2	MAN	E	5280	11/12	0.75	0.56	-	130,150,156,159	0
4	NAG	B	1049	14/15	0.78	0.29	-	100,112,123,126	0
2	NAG	E	2080	14/15	0.68	0.31	-	84,113,121,128	0
2	MAN	E	4080	11/12	0.70	0.40	-	112,118,132,137	0
6	BMA	F	3080	11/12	0.65	0.49	-	137,148,155,158	0
7	NAG	F	2049	14/15	0.83	0.38	-	107,111,120,127	0
6	MAN	F	4080	11/12	0.59	0.50	-	137,158,167,171	0
6	NAG	F	2080	14/15	0.81	0.26	-	92,105,122,126	0
3	NAG	A	2080	14/15	0.45	0.54	-	149,154,158,162	0
2	MAN	A	5149	11/12	0.52	0.60	-	140,151,156,158	0
2	MAN	A	4049	11/12	0.62	0.81	-	137,148,151,151	0
7	MAN	F	4149	11/12	0.66	0.47	-	123,136,143,149	0
3	MAN	A	4080	11/12	0.72	0.56	-	162,167,170,174	0
6	MAN	F	4180	11/12	0.52	0.70	-	149,159,163,163	0
4	BMA	B	3080	11/12	0.49	0.47	-	144,152,155,159	0
4	BMA	E	3049	11/12	0.24	0.60	-	125,147,150,152	0
6	MAN	D	4180	11/12	0.70	0.46	-	131,144,153,155	0
7	BMA	F	3049	11/12	0.68	0.45	-	136,137,141,143	0
4	BMA	B	3049	11/12	0.47	0.77	-	134,146,150,151	0
2	NAG	A	2049	14/15	0.43	0.66	-	144,148,152,154	0
7	MAN	F	5149	11/12	0.37	0.62	-	112,121,130,133	0
6	BMA	D	3080	11/12	0.87	0.22	-	127,133,140,141	0
3	NAG	A	1080	14/15	0.52	0.46	-	113,142,150,153	0
2	MAN	A	5049	11/12	0.39	0.67	-	144,150,154,157	0
4	NAG	E	2049	14/15	0.65	0.60	-	143,147,149,151	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	MAN	A	4149	11/12	0.37	0.68	-	145,152,156,156	0
5	NAG	C	2080	14/15	0.69	0.55	-	138,141,147,151	0
2	MAN	A	6149	11/12	0.57	0.84	-	145,154,156,162	0
3	BMA	A	3080	11/12	0.68	0.59	-	150,158,165,165	0
2	MAN	E	6280	11/12	0.67	0.69	-	142,152,158,159	0
2	BMA	E	3080	11/12	0.69	0.22	-	113,122,131,140	0
2	BMA	A	3049	11/12	0.11	0.70	-	147,150,153,154	0
6	MAN	D	4080	11/12	0.61	0.35	-	123,137,140,143	0

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
9	CL	D	4042	1/1	0.64	0.47	5.50	104,104,104,104	0
9	CL	B	2042	1/1	0.94	0.10	-1.99	47,47,47,47	0
9	CL	E	5042	1/1	0.96	0.10	-2.79	57,57,57,57	0
8	CA	E	5057	1/1	0.94	0.06	-	89,89,89,89	0
9	CL	A	1042	1/1	0.81	0.16	-	65,65,65,65	0
8	CA	C	3057	1/1	0.82	0.18	-	109,109,109,109	0
8	CA	A	1057	1/1	0.91	0.07	-	87,87,87,87	0
8	CA	B	2057	1/1	0.97	0.06	-	67,67,67,67	0
8	CA	D	4057	1/1	0.92	0.12	-	89,89,89,89	0
9	CL	F	6042	1/1	0.98	0.06	-	31,31,31,31	0
8	CA	F	6057	1/1	0.94	0.11	-	62,62,62,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.