



# wwPDB EM Validation Summary Report ⓘ

Dec 15, 2024 – 11:23 PM EST

PDB ID : 1Q55  
EMDB ID : EMD-1052  
Title : W-shaped trans interactions of cadherins model based on fitting C-cadherin (1L3W) to 3D map of desmosomes obtained by electron tomography  
Authors : He, W.; Cowin, P.; Stokes, D.L.  
Deposited on : 2003-08-06  
Resolution : 30.00 Å(reported)  
Based on initial model : 1L3W

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

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

EMDB validation analysis : 0.0.1.dev113  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

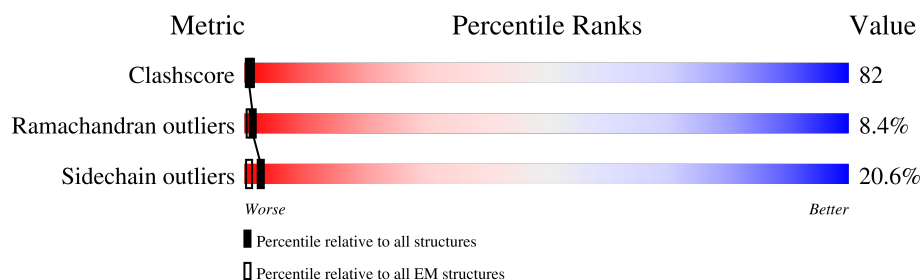
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 30.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	880	16% 30% 11% • 39%
1	B	880	16% 30% 11% • 39%
1	C	880	16% 30% 11% • 39%
1	D	880	17% 30% 11% • 39%

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	NAG	A	801	-	-	X	-
2	NAG	A	805	X	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	806	X	-	X	-
2	NAG	A	807	-	-	X	-
2	NAG	A	809	-	-	X	-
2	NAG	A	810	-	-	X	-
2	NAG	A	902	X	-	X	-
2	NAG	A	903	X	-	-	-
2	NAG	A	904	-	-	X	-
2	NAG	B	801	-	-	X	-
2	NAG	B	805	X	-	X	-
2	NAG	B	806	X	-	X	-
2	NAG	B	807	-	-	X	-
2	NAG	B	809	-	-	X	-
2	NAG	B	810	-	-	X	-
2	NAG	B	902	X	-	X	-
2	NAG	B	903	X	-	-	-
2	NAG	B	904	-	-	X	-
2	NAG	C	801	-	-	X	-
2	NAG	C	805	X	-	X	-
2	NAG	C	806	X	-	X	-
2	NAG	C	807	-	-	X	-
2	NAG	C	809	-	-	X	-
2	NAG	C	810	-	-	X	-
2	NAG	C	902	X	-	X	-
2	NAG	C	903	X	-	-	-
2	NAG	C	904	-	-	X	-
2	NAG	D	801	-	-	X	-
2	NAG	D	805	X	-	X	-
2	NAG	D	806	X	-	X	-
2	NAG	D	807	-	-	X	-
2	NAG	D	809	-	-	X	-
2	NAG	D	810	-	-	X	-
2	NAG	D	902	X	-	X	-
2	NAG	D	903	X	-	-	-
2	NAG	D	904	-	-	X	-
3	NDG	A	811	-	-	X	-
3	NDG	B	811	-	-	X	-
3	NDG	C	811	-	-	X	-

## 2 Entry composition [i](#)

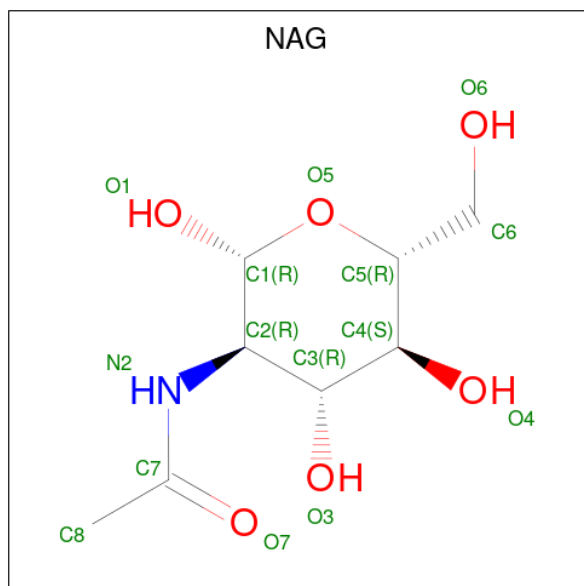
There are 4 unique types of molecules in this entry. The entry contains 17652 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 EP-cadherin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	540	Total	C	N	O	S	0	0
			4191	2635	695	850	11		
1	B	540	Total	C	N	O	S	0	0
			4191	2635	695	850	11		
1	C	540	Total	C	N	O	S	0	0
			4191	2635	695	850	11		
1	D	540	Total	C	N	O	S	0	0
			4191	2635	695	850	11		

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

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

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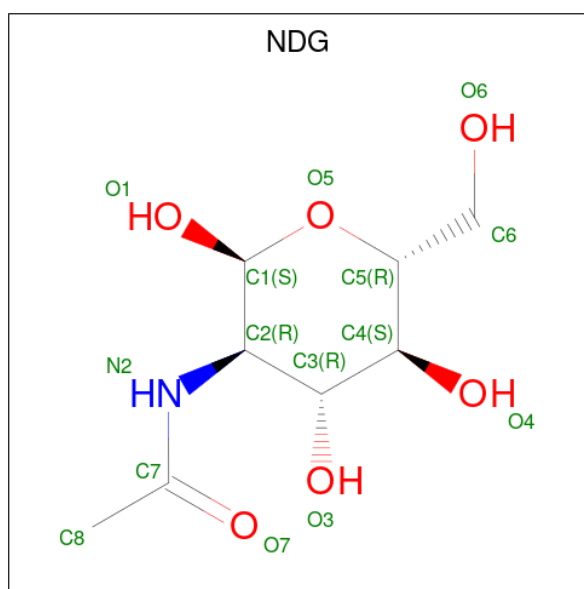
Mol	Chain	Residues	Atoms				AltConf
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	B	1	Total 14	C 8	N 1	O 5	0
2	C	1	Total 14	C 8	N 1	O 5	0
2	C	1	Total 14	C 8	N 1	O 5	0
2	C	1	Total 14	C 8	N 1	O 5	0
2	C	1	Total 14	C 8	N 1	O 5	0
2	C	1	Total 14	C 8	N 1	O 5	0
2	C	1	Total 14	C 8	N 1	O 5	0
2	C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

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

- Molecule 3 is 2-acetamido-2-deoxy- $\alpha$ -D-glucopyranose (three-letter code: NDG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	B	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
3	B	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	C	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	
3	D	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

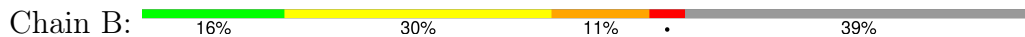
Mol	Chain	Residues	Atoms		AltConf
4	A	12	Total	Ca	0
			12	12	
4	B	12	Total	Ca	0
			12	12	
4	C	12	Total	Ca	0
			12	12	
4	D	12	Total	Ca	0
			12	12	





[illegible]

- Molecule 1: EP-cadherin



ASP	LEU	5066	8441	T380	T316	P250	E186	F108	K33	ALA	ASN
VAL	LEU	P442	V381	V382	A317	G251	T187	T109	SER	PHE	GLY
VAL	LEU	S508	R443	T318	T318	G252	T188	Q110	LYS	THR	THR
PRO	LEU	S509	K383	P263	V319	T252	L189	D111	ARG	ASP	THR
THR	PHE		T446	K384	T320	G254	T190	V112	HIS	CYS	ARG
LEU	LEU	V511	K447	K385	V321	G255	V191		ARG	THR	LEU
LYS	LYS	S512	C448	G386	T322	G256	Q192	S116	SER	THR	ARG
ARG	ARG	L513	D449	I387	V323	G257	A193	V117	GLY	ARG	ASN
LYS	LYS	S514	Q450	V388	E324	G258	T194	R118	GLU	LYS	ALA
PRO	LYS	D515	N451			G259	T195	E119	GLU	HIS	SER
HIS	VAL	A516	P452	K391	N327	K260	L196		ALA	LEU	VAL
VAL	VAL	S517	G392	G392		L261	L197	V127	HIS	GLY	TRP
LYS	LYS	S518	K393	K393	P330	G262	G198	M128	SER	TYR	LEU
ASP	GLU	L457	T458	L457	F331	G263	A199	P47	ARG	ASP	CYS
PRO	PRO	S519	T459	D395	F332	T264	G200	Q48	ARG	VAL	GLY
ARG	ARG	P520	T459	D395	F332	T264	G200	Q48	SER	VAL	LEU
PRO	PRO	Q521	S460	K396	V333	E265	L201	S131	LYS	GLY	LEU
LEU	LEU	S522	D461	E397	F334	G266	S202	A132	LYS	ASP	LEU
LEU	LEU	L522		S398	V334	G266	S202	A132	LEU	ASP	LEU
ASP	ASP	T523	S398	S398	A335	G267	V203	T133	ARG	SER	CYS
SER	PRO	V524	T464	G399	V336	F268		D134	PRO	ARG	LEU
PRO	GLU	V525	P465	V400	S337	G269	T208		VAL	PHE	LEU
ASP	ASP	S526	P466	K338	S337	G270	T209	D137	VAL	ARG	GLN
GLY	GLU	N526	V401	R338	V401	T270	L209	M138	LEU	THR	VAL
SER	ILE		N467	K402	V339	T271	Q210	E56	THR	VAL	VAL
ARG	GLY	V529	T468	N403	D340	T272	T211	I139	PHE	LEU	VAL
ASN	ARG	C530	V469	N404	V341	T273	T212	G58	PRO	PRO	PRO
PHE	ASN	S531	S470	T405	S342	D274	D213	W59	ASP	ASP	SER
ASP	PHE	S531	S470	T405	S342	D274	D213	W59	GLY	THR	GLY
ILE	ASN	C532	V471	V406	E343	G275	A214	L142	THR	GLY	ILE
ASP	ILE	S533	K472	V407	D344	E276	A214	L146	HIS	THR	ASN
LEU	PHE	P534	V473	V408	L345	S277	D216	S147	THR	VAL	ALA
ALA	ASN	G534	S474	I409	S346	G278	N217	T63	GLY	LEU	ASP
MET	TYR		L475	M410	R347	Q279		I150	LEU	VAL	VAL
LEU	TYR	T537	S476	L411	K348	G280	T220	L151	LYS	VAL	LYS
GLY	GLY	C539	H477	V412	E349	T281	F221	K152	ARG	ARG	GLY
ALA	GLU	S539	H477	V412	E349	T281	F221	K152	ARG	ARG	GLY
ALA	GLU	Q540	G478	T413	R350	L282	D222	Q153	LYS	HIS	CYS
ASP	GLY	GLU	S479	D414	K351	T283	P223	D154	LYS	VAL	LYS
ASN	GLY	LYS	D480	D415	I352	T284	K224	P155	LYS	VAL	PRO
ASP	GLY	LEU	L481	C416	S353	A285	T225	E156	LEU	LEU	GLY
ASP	GLY	VAL	T482	V417	L354	K286	V226	E157	D1	HIS	PHE
PRO	GLU		V483	S418		G287	T227	P158	W2	LYS	SER
THR	ASP	GLY	V483	V419	D358	L288	T227	P158	W3	ASP	SER
ALA	GLY	GLY	K484	V419	D358	A228	F159	I159	I4	ASP	SER
GLY	GLN	PHE	A485	G420	P359	G289	L229	P160	P5	THR	ALA
PRO	PRO	ASP	E486	T421	D360	V230	G161	E83	P6	LYS	GLU
ASP	ASP	LEU	L487	C422	K361	E291	P231	L162	P6	LYS	GLU
THR	TYR	LEU	D488	C422	K361	E291	P231	L162	P6	LYS	GLU
ASP	ASP	PRO	D488	T423	Q362	L292	E232	F163	I7	THR	THR
SER	ILE	ILE	S489	G424	Q363	R293	N233	T164	K8	PHE	ILE
LEU	SER	ILE	K490	C424	Q363	R293	N233	T164	K8	ILE	ILE
SER	GLN	LEU	G491	L426	Q365	E234	E234	I165	W2	SER	SER
LEU	GLN	LEU	T492	L427	K366	G296	E234	I165	W3	SER	SER
VAL	VAL	VAL	T492	L427	K366	G296	E234	I165	W3	THR	VAL
HIS	PHE	ILE	S493	L428	L367	L298	G236	R167	P16	TRP	ASN
ARG	ARG	LEU	N494	H429	S368	G299	F237	E168	P17	ASP	ARG
GLY	GLY	LEU	L495	V369	G368	T169	E238	T169	P18	ALA	ARG
THR	THR	GLY	V430	G369	G368	T169	E238	T169	P18	ALA	ARG
GLU	LEU	SER	L496	L431	F370	T301	Q240	V171	K19	ARG	GLU
ASP	ASP	VAL	S497	D432	F370	T301	Q240	V171	K19	GLY	LEU
GLY	GLY	VAL	S497	D432	F370	T301	Q240	V171	K19	GLY	LEU
SER	SER	LEU	P498	V433	G372	P307	R241		Q22	ILE	GLU
LEU	ARG	ALA	T499	N434	K373	F308	L242		Q23	LYS	ARG
ALA	ARG	ALA	T499	N434	K373	F308	L242		Q23	LYS	ARG
PRO	PRO	LEU	Q500	D435	D374	S309	S243	I175	N27	SER	GLY
LEU	LEU	LEU	S501	D436	P375	V310	G176	G176	K28	THR	LYS
LEU	ASP	LEU	O501	N436	P375	V310	G176	G176	K28	THR	LYS
ILE	ILE	ILE	S502	G437	A376	P311	D246	L179	D30	ASN	LEU
ALA	ALA	LEU	R503	V438	R377	L312	L247	D190	R30	ILE	GLY
MET	ARG	PHE	K504	V439	R377	L312	L247	D190	R30	ILE	GLY
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
SER	LEU	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
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LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
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LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
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LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
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LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
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LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
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LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440	L378	G315	N248	R181	F31	ALA	VAL
LEU	ASN	LEU	G505	P440</							

- Molecule 1: EP-cadherin



LEU	VAL	LEU	S508	R443	R382	V319	P253	L189	P106	F31	ALA
ASN	PRO	LEU	I509	T443	K383	T320	A294	T190	K107	N32	SER
SER	THR	PHE	V510	T446	D384	V321	W255	V191	F108	K33	LYS
SER	LEU	PHE	V511	M447	N385	T322	Q256	Q192	T109		ARG
ASN	MET	LYS	C448	C448	N386	V323	A257	A193	Q110	Y36	HIS
SER	PRO	ARG	L512	D449	I387	V324	V258	T194	D111	S37	ARG
ASN	ALA	LYS	S514	Q450	V388	E324	Y259	D195	V112	I38	SER
ASP	PRO	LYS	D515	M451			K260	L196	T39	T39	GLY
GLU	HIS	VAL	A516	P452	N391	N327	L261	E197	S116	Q40	GLU
HIS	TYR	VAL	Q517	P452	G392	E328	R263	G198	V117	Q41	GLU
ASP	ARG	LYS	N518	L457	N393	A329	R262	A199	R118	G42	ALA
TYR	PRO	GLU	N519	T458	N394	F331	N264	G200	E119		SER
ASN	ARG	PRO	N520	T459	D395	F332	E265	L201		N45	HIS
TYR	PRO	LEU	Q521	S460	R396	V333	G266	S202	V127	N45	SER
LEU	SER	LEU	L522	D461	E397	P334	G267	S202	M128	P46	ARG
LEU	ASN	LEU	T523		S398	A335	F268	V203	A129	P47	SER
ASP	PRO	PRO	V524	I464	E399	V336	N270	I208	V130	Q48	LYS
TRP	ASP	GLU	V525	P465	Y400	S337	N270	I209	S131	G49	LEU
GLY	GLU	ASP	N526	P466	V401	R338	I271	Q210	A132	F51	PRO
SER	ILE	ASP		M467	K402	V339	T272	I211	T133	R52	VAL
ARG	GLY	THR	V529	T468	K403	D340	T273	T212	D134	I53	LEU
ARG	ASN	TYR	T537	L475	M410	V341	D274	D213		I61	LEU
PHE	ASN	ARG	K530	P469	L411	G348	I281	F221	L146	M60	THR
ARG	PHE	ASP	S531	P470	V412	E349	L282	D222	L61	V62	GLY
LYS	ILE	ASN	C532	Y471	T413	K360	T283	K224	I150	V62	LEU
LEU	ASP	ILE	E533	K472	D414	I351	T284	K224	L151	T63	LYS
ALA	GLU	PHE	G534	V473	D415	I352	A285	T225	K152	L66	ARG
ASP	ASN	TYR		S474	G416	S353	K286	Y226	Q153	D67	LYS
MET	LEU	TYR	T537	L475	V417	L354	G287	T227	D154	R68	LYS
TYR	ASP	GLY	K538	H477	G478	K360	L288	A228	P155	E69	ARG
GLY	ALA	GLY	C539	S479	T413	K360	L288	A228	P155	D1	LYS
GLY	ALA	GLY	O540	S479	D414	I351	T284	K224	L151	L66	ARG
ASP	ASP	GLY		P490	D415	I352	A285	T225	K152	L66	LYS
ASP	PRO	GLY		L481	G416	S353	K286	Y226	Q153	D67	LYS
GLU	THR	GLU		T482	V417	L354	G287	T227	D154	R68	ARG
GLU	ALA	GLY		W483	S418		L288	A228	P155	E69	ARG
	ALA	ASP		K484	V419	D358	L288	A228	P155	D1	LYS
PRO	PRO	GLN		A485	G420	P359	D289	L229	E156	W2	LYS
PRO	PRO	ASP		E486	T421	D360	E290	V230	E157	V3	ARG
TYR	TYR	TYR		L487	G422	K361	E291	P231	P158	I4	LYS
ASP	ASP	ASP		D488	T423	Q362	L292	E232	I159	P6	ARG
SER	SER	LEU		S489	G424	Q363	R293	N233	P160	P6	LYS
LEU	LEU	SER		K490	G424	Q363	Q363	E234	N161	I7	LYS
LEU	LEU	GLN		C491	T425	I364	Y296	I235	L162	K8	ARG
VAL	VAL	LEU		T492	L426	Q365	V297	G236	F163	E83	LYS
PHE	PHE	LEU		S493	L427	K366	L297	G236	F163		ARG
ASP	ASP	HIS		M494	L428	L367	L298	F237	T164	S86	LYS
TYR	TYR	ARG		L495	H429	S368	Q299	E238	I165	P87	LYS
GLU	GLU	GLY		L496	H429	S368	I300	E238		V88	ARG
GLY	GLU	LEU		S497	V430	Y369	T301	Q240	T169	E89	LYS
ASP	GLY	SER		P498	L431	F370		R241	G170	E90	LYS
SER	SER	ASP		T499	D432	I371	P307	L242	V171	P91	ARG
ALA	GLY	SER		P498	V433	G372	F308	S243	T164	M92	LYS
ARG	GLY	ARG		T499	N434	S309	S309	G243	L174	E93	LYS
PRO	PRO	PRO		Q500	D435	D374	V310	T245	I175	I94	LYS
LEU	GLU	ASP		Q501	N436	P375	P311	D246	G176	T95	LYS
ILE	ALA	ILE		L502	G437	A376	L312	L247	I96	I96	LYS
MET	ALA	ILE		K503	P438	R377		R181			LYS
LEU	ALA	LEU		K504	P438	R377		R181			LYS
ARG	SER	ARG		G505	V439	W378	S315	M249	D100	S26	LYS
ASN	LEU	ASN		D506	P440	L379	T316	P250	Q101	N27	LYS
LEU	SER	ASP		Y507	S441	T380	A317	G251	Y187	K28	LYS
VAL	SER	VAL			P442	V381	T318	T252	T188	R105	LYS

## 4 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of tilted images used	Not provided	
Resolution determination method	Not provided	
CTF correction method	no CTF correction. Imaging at underfocus 0.4 micron with CM200FEG microscope at 50,000 magnification	Depositor
Microscope	FEI/PHILIPS CM200FEG/UT	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1200	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	500	Depositor
Magnification	68276	Depositor
Image detector	GENERIC GATAN	Depositor

## 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: NAG, CA, NDG

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	0.70	8/4276 (0.2%)	1.39	78/5839 (1.3%)
1	B	0.70	8/4276 (0.2%)	1.39	78/5839 (1.3%)
1	C	0.70	8/4276 (0.2%)	1.39	78/5839 (1.3%)
1	D	0.70	8/4276 (0.2%)	1.39	78/5839 (1.3%)
All	All	0.70	32/17104 (0.2%)	1.39	312/23356 (1.3%)

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	4
1	B	0	4
1	C	0	4
1	D	0	4
All	All	0	16

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	335	ALA	CA-CB	-8.36	1.34	1.52
1	C	335	ALA	CA-CB	-8.34	1.34	1.52
1	A	335	ALA	CA-CB	-8.33	1.34	1.52
1	D	335	ALA	CA-CB	-8.33	1.34	1.52
1	D	539	CYS	CB-SG	8.16	1.96	1.82

The worst 5 of 312 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	520	PRO	CA-C-N	-13.29	87.96	117.20
1	A	520	PRO	CA-C-N	-13.29	87.96	117.20
1	D	520	PRO	CA-C-N	-13.27	88.01	117.20
1	C	520	PRO	CA-C-N	-13.27	88.02	117.20
1	C	235	ILE	N-CA-C	12.74	145.40	111.00

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	PHE	Sidechain
1	A	18	PRO	Mainchain
1	A	222	ASP	Mainchain
1	A	520	PRO	Mainchain
1	B	17	PHE	Sidechain

## 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	4191	0	4086	759	0
1	B	4191	0	4089	754	0
1	C	4191	0	4087	719	0
1	D	4191	0	4086	713	0
2	A	182	0	169	93	0
2	B	182	0	169	92	0
2	C	182	0	169	93	0
2	D	182	0	169	93	0
3	A	28	0	24	9	0
3	B	28	0	24	9	0
3	C	28	0	24	9	0
3	D	28	0	24	8	0
4	A	12	0	0	0	0
4	B	12	0	0	0	0
4	C	12	0	0	0	0
4	D	12	0	0	0	0
All	All	17652	0	17120	2844	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 82.

The worst 5 of 2844 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:B:464:ILE:HD12	1:B:465:PRO:CD	1.30	1.61
1:D:464:ILE:HD12	1:D:465:PRO:CD	1.30	1.59
1:A:464:ILE:HD12	1:A:465:PRO:CD	1.30	1.56
1:C:464:ILE:HD12	1:C:465:PRO:CD	1.30	1.56
1:C:24:ILE:HG21	1:D:2:TRP:CA	1.42	1.48

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 PDB entries followed by that with respect to all EM entries.

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	538/880 (61%)	401 (74%)	92 (17%)	45 (8%)	0	9
1	B	538/880 (61%)	401 (74%)	92 (17%)	45 (8%)	0	9
1	C	538/880 (61%)	401 (74%)	92 (17%)	45 (8%)	0	9
1	D	538/880 (61%)	401 (74%)	92 (17%)	45 (8%)	0	9
All	All	2152/3520 (61%)	1604 (74%)	368 (17%)	180 (8%)	1	9

5 of 180 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	91	PRO
1	A	155	PRO
1	A	235	ILE
1	A	347	ARG
1	A	363	GLN



### 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 PDB entries followed by that with respect to all EM entries.

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	480/779 (62%)	381 (79%)	99 (21%)	1	6
1	B	480/779 (62%)	381 (79%)	99 (21%)	1	6
1	C	480/779 (62%)	381 (79%)	99 (21%)	1	6
1	D	480/779 (62%)	381 (79%)	99 (21%)	1	6
All	All	1920/3116 (62%)	1524 (79%)	396 (21%)	3	6

5 of 396 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	261	ILE
1	C	492	THR
1	C	284	THR
1	C	382	ASN
1	D	27	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	278	ASN
1	D	45	ASN
1	C	373	ASN
1	C	467	ASN
1	D	138	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 108 ligands modelled in this entry, 48 are monoatomic - leaving 60 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	$\# Z  > 2$
2	NAG	D	808	1	14,14,15	0.66	0	17,19,21	0.69	0
2	NAG	D	904	1	14,14,15	0.77	1 (7%)	17,19,21	0.70	1 (5%)
2	NAG	A	807	1	14,14,15	0.65	0	17,19,21	1.19	2 (11%)
2	NAG	C	903	1	14,14,15	0.55	0	17,19,21	0.79	0
2	NAG	A	810	1	14,14,15	0.67	0	17,19,21	1.34	4 (23%)
2	NAG	C	802	1	14,14,15	0.77	1 (7%)	17,19,21	0.85	0
2	NAG	C	902	1	14,14,15	1.14	1 (7%)	17,19,21	1.09	2 (11%)
2	NAG	B	801	1	14,14,15	0.69	0	17,19,21	0.98	1 (5%)
3	NDG	A	811	1	14,14,15	0.87	0	17,19,21	1.96	1 (5%)
3	NDG	B	811	1	14,14,15	0.87	0	17,19,21	1.97	1 (5%)
2	NAG	B	808	1	14,14,15	0.67	0	17,19,21	0.69	0
2	NAG	B	810	1	14,14,15	0.66	0	17,19,21	1.33	4 (23%)
2	NAG	D	806	1	14,14,15	0.56	0	17,19,21	1.39	3 (17%)
2	NAG	B	803	1	14,14,15	1.00	1 (7%)	17,19,21	1.17	2 (11%)
2	NAG	D	807	1	14,14,15	0.64	0	17,19,21	1.19	2 (11%)
2	NAG	B	812	1	14,14,15	0.83	1 (7%)	17,19,21	0.76	1 (5%)
2	NAG	D	805	1	14,14,15	0.71	0	17,19,21	1.05	1 (5%)
3	NDG	D	811	1	14,14,15	0.87	0	17,19,21	1.97	1 (5%)
2	NAG	D	902	1	14,14,15	1.14	1 (7%)	17,19,21	1.09	2 (11%)
2	NAG	C	812	1	14,14,15	0.83	1 (7%)	17,19,21	0.76	1 (5%)
2	NAG	D	801	1	14,14,15	0.72	0	17,19,21	0.98	1 (5%)
3	NDG	C	804	1	14,14,15	0.64	0	17,19,21	0.78	0
2	NAG	A	808	1	14,14,15	0.66	0	17,19,21	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	D	903	1	14,14,15	0.55	0	17,19,21	0.78	0
2	NAG	B	807	1	14,14,15	0.64	0	17,19,21	1.19	2 (11%)
2	NAG	D	802	1	14,14,15	0.77	1 (7%)	17,19,21	0.85	0
2	NAG	A	903	1	14,14,15	0.55	0	17,19,21	0.79	0
2	NAG	B	809	1	14,14,15	0.78	1 (7%)	17,19,21	0.94	0
2	NAG	C	801	1	14,14,15	0.71	0	17,19,21	0.98	1 (5%)
3	NDG	D	804	1	14,14,15	0.66	0	17,19,21	0.78	0
2	NAG	C	809	1	14,14,15	0.77	1 (7%)	17,19,21	0.94	0
2	NAG	A	902	1	14,14,15	1.14	1 (7%)	17,19,21	1.09	1 (5%)
2	NAG	D	809	1	14,14,15	0.77	1 (7%)	17,19,21	0.94	0
2	NAG	D	803	1	14,14,15	1.00	1 (7%)	17,19,21	1.17	2 (11%)
2	NAG	C	810	1	14,14,15	0.65	0	17,19,21	1.33	4 (23%)
2	NAG	A	806	1	14,14,15	0.56	0	17,19,21	1.38	3 (17%)
2	NAG	D	812	1	14,14,15	0.84	1 (7%)	17,19,21	0.76	1 (5%)
2	NAG	A	812	1	14,14,15	0.84	1 (7%)	17,19,21	0.75	1 (5%)
2	NAG	C	803	1	14,14,15	1.00	1 (7%)	17,19,21	1.16	2 (11%)
2	NAG	B	806	1	14,14,15	0.57	0	17,19,21	1.39	3 (17%)
2	NAG	D	810	1	14,14,15	0.66	0	17,19,21	1.33	4 (23%)
2	NAG	A	805	1	14,14,15	0.72	0	17,19,21	1.05	1 (5%)
2	NAG	B	805	1	14,14,15	0.72	0	17,19,21	1.05	1 (5%)
2	NAG	C	807	1	14,14,15	0.64	0	17,19,21	1.20	2 (11%)
2	NAG	B	902	1	14,14,15	1.13	1 (7%)	17,19,21	1.09	1 (5%)
2	NAG	C	806	1	14,14,15	0.57	0	17,19,21	1.39	3 (17%)
2	NAG	A	802	1	14,14,15	0.78	1 (7%)	17,19,21	0.85	0
2	NAG	C	904	1	14,14,15	0.79	1 (7%)	17,19,21	0.70	1 (5%)
2	NAG	C	808	1	14,14,15	0.66	0	17,19,21	0.69	0
2	NAG	A	809	1	14,14,15	0.77	1 (7%)	17,19,21	0.93	0
2	NAG	A	904	1	14,14,15	0.77	1 (7%)	17,19,21	0.70	1 (5%)
2	NAG	A	801	1	14,14,15	0.70	0	17,19,21	0.98	1 (5%)
2	NAG	B	802	1	14,14,15	0.78	1 (7%)	17,19,21	0.85	0
2	NAG	C	805	1	14,14,15	0.71	0	17,19,21	1.05	1 (5%)
3	NDG	A	804	1	14,14,15	0.65	0	17,19,21	0.78	0
3	NDG	C	811	1	14,14,15	0.87	0	17,19,21	1.95	1 (5%)
2	NAG	B	904	1	14,14,15	0.77	1 (7%)	17,19,21	0.69	1 (5%)
3	NDG	B	804	1	14,14,15	0.65	0	17,19,21	0.77	0
2	NAG	B	903	1	14,14,15	0.55	0	17,19,21	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	A	803	1	14,14,15	0.99	1 (7%)	17,19,21	1.17	2 (11%)

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	D	808	1	-	3/6/23/26	0/1/1/1
2	NAG	D	904	1	-	3/6/23/26	0/1/1/1
2	NAG	A	807	1	-	5/6/23/26	0/1/1/1
2	NAG	C	903	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	C	902	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	A	810	1	-	3/6/23/26	0/1/1/1
2	NAG	C	802	1	-	2/6/23/26	0/1/1/1
2	NAG	B	801	1	-	4/6/23/26	0/1/1/1
3	NDG	A	811	1	-	2/6/23/26	0/1/1/1
3	NDG	B	811	1	-	2/6/23/26	0/1/1/1
2	NAG	B	808	1	-	3/6/23/26	0/1/1/1
2	NAG	B	810	1	-	3/6/23/26	0/1/1/1
2	NAG	D	806	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	B	803	1	-	2/6/23/26	0/1/1/1
2	NAG	D	807	1	-	5/6/23/26	0/1/1/1
2	NAG	D	805	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	B	812	1	-	4/6/23/26	0/1/1/1
3	NDG	D	811	1	-	2/6/23/26	0/1/1/1
2	NAG	D	902	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	C	812	1	-	4/6/23/26	0/1/1/1
2	NAG	D	801	1	-	4/6/23/26	0/1/1/1
3	NDG	C	804	1	-	0/6/23/26	0/1/1/1
2	NAG	A	808	1	-	3/6/23/26	0/1/1/1
2	NAG	D	903	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	B	807	1	-	5/6/23/26	0/1/1/1
2	NAG	D	802	1	-	2/6/23/26	0/1/1/1
2	NAG	A	903	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	B	809	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	801	1	-	4/6/23/26	0/1/1/1
3	NDG	D	804	1	-	0/6/23/26	0/1/1/1
2	NAG	C	809	1	-	2/6/23/26	0/1/1/1
2	NAG	A	902	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	D	809	1	-	2/6/23/26	0/1/1/1
2	NAG	D	803	1	-	2/6/23/26	0/1/1/1
2	NAG	C	810	1	-	3/6/23/26	0/1/1/1
2	NAG	A	806	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	D	812	1	-	4/6/23/26	0/1/1/1
2	NAG	A	812	1	-	4/6/23/26	0/1/1/1
2	NAG	C	803	1	-	2/6/23/26	0/1/1/1
2	NAG	B	806	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	D	810	1	-	3/6/23/26	0/1/1/1
2	NAG	A	805	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	B	805	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	C	807	1	-	5/6/23/26	0/1/1/1
2	NAG	B	902	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	C	806	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	A	802	1	-	2/6/23/26	0/1/1/1
2	NAG	C	904	1	-	3/6/23/26	0/1/1/1
2	NAG	C	808	1	-	3/6/23/26	0/1/1/1
2	NAG	A	809	1	-	2/6/23/26	0/1/1/1
2	NAG	A	904	1	-	3/6/23/26	0/1/1/1
2	NAG	C	805	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	A	801	1	-	4/6/23/26	0/1/1/1
2	NAG	B	802	1	-	2/6/23/26	0/1/1/1
3	NDG	A	804	1	-	0/6/23/26	0/1/1/1
3	NDG	C	811	1	-	2/6/23/26	0/1/1/1
2	NAG	B	904	1	-	3/6/23/26	0/1/1/1
3	NDG	B	804	1	-	0/6/23/26	0/1/1/1
2	NAG	B	903	1	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	A	803	1	-	2/6/23/26	0/1/1/1

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	902	NAG	C1-C2	3.42	1.57	1.52
2	C	902	NAG	C1-C2	3.41	1.57	1.52
2	D	902	NAG	C1-C2	3.40	1.57	1.52
2	B	902	NAG	C1-C2	3.35	1.56	1.52
2	C	803	NAG	O5-C5	2.69	1.48	1.43

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	811	NDG	C2-N2-C7	-7.46	112.91	122.90
3	D	811	NDG	C2-N2-C7	-7.43	112.94	122.90
3	A	811	NDG	C2-N2-C7	-7.42	112.96	122.90
3	C	811	NDG	C2-N2-C7	-7.40	112.98	122.90
2	C	806	NAG	C2-N2-C7	-3.63	118.03	122.90

5 of 16 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	805	NAG	C1
2	A	806	NAG	C1
2	A	902	NAG	C1
2	A	903	NAG	C1
2	B	805	NAG	C1

5 of 152 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	807	NAG	C3-C2-N2-C7
2	A	808	NAG	C1-C2-N2-C7
2	A	810	NAG	C1-C2-N2-C7
2	A	812	NAG	C1-C2-N2-C7
2	A	902	NAG	C3-C2-N2-C7

There are no ring outliers.

52 monomers are involved in 406 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	808	NAG	2	0
2	D	904	NAG	8	0
2	A	807	NAG	17	0
2	A	810	NAG	13	0
2	C	902	NAG	8	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	NAG	21	0
3	A	811	NDG	7	0
3	B	811	NDG	7	0
2	B	808	NAG	2	0
2	B	810	NAG	13	0
2	D	806	NAG	12	0
2	B	803	NAG	4	0
2	D	807	NAG	16	0
2	B	812	NAG	3	0
2	D	805	NAG	7	0
3	D	811	NDG	6	0
2	D	902	NAG	8	0
2	C	812	NAG	3	0
2	D	801	NAG	22	0
3	C	804	NDG	2	0
2	A	808	NAG	2	0
2	B	807	NAG	17	0
2	B	809	NAG	8	0
2	C	801	NAG	22	0
3	D	804	NDG	2	0
2	C	809	NAG	8	0
2	A	902	NAG	8	0
2	D	809	NAG	8	0
2	D	803	NAG	4	0
2	C	810	NAG	13	0
2	A	806	NAG	11	0
2	D	812	NAG	3	0
2	A	812	NAG	3	0
2	C	803	NAG	4	0
2	B	806	NAG	11	0
2	D	810	NAG	13	0
2	A	805	NAG	7	0
2	B	805	NAG	7	0
2	C	807	NAG	16	0
2	B	902	NAG	8	0
2	C	806	NAG	12	0
2	C	904	NAG	8	0
2	C	808	NAG	2	0
2	A	809	NAG	8	0
2	A	904	NAG	8	0
2	A	801	NAG	22	0
2	C	805	NAG	7	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	804	NDG	2	0
3	C	811	NDG	7	0
2	B	904	NAG	8	0
3	B	804	NDG	2	0
2	A	803	NAG	4	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 Tomogram visualisation

This section contains visualisations of the EMDB entry EMD-1052. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

### 6.1 Orthogonal projections

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

### 6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

### 6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

## 7 Tomogram analysis

This section contains the results of statistical analysis of the tomogram.

### 7.1 Map-value distribution

This section was not generated.

## 8 Map-model fit

This section was not generated.