



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:23 PM UTC

PDB ID : 3L89 / pdb_00003l89
Title : Human Adenovirus type 21 knob in complex with domains SCR1 and SCR2
of CD46 (membrane cofactor protein, MCP)
Authors : Cupelli, K.; Stehle, T.
Deposited on : 2009-12-30
Resolution : 3.50 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

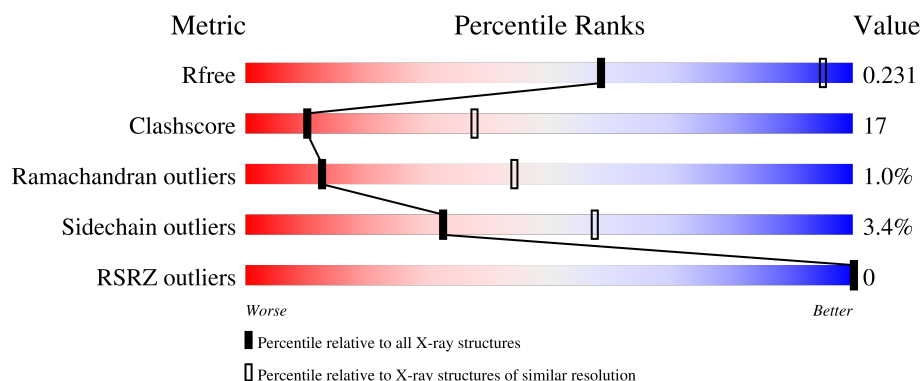
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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	201	66% 24% • 9%
1	B	201	64% 26% • 8%
1	C	201	66% 24% • 8%
1	D	201	58% 31% • 9%
1	E	201	55% 34% • 8%

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Mol	Chain	Length	Quality of chain
1	F	201	 58% 31% 8%
1	G	201	 59% 30% 9%
1	H	201	 60% 30% 9%
1	I	201	 61% 27% 7%
1	J	201	 63% 26% 9%
1	K	201	 65% 25% 8%
1	L	201	 66% 25% 7%
2	M	126	 63% 33% .
2	N	126	 56% 43% .
2	O	126	 64% 33% .
2	P	126	 56% 42% .
2	Q	126	 51% 48% .
2	R	126	 52% 47% .
2	S	126	 61% 37% .
2	T	126	 60% 37% .
2	U	126	 58% 41% .
2	V	126	 67% 29% .
2	W	126	 67% 29% .
2	X	126	 68% 28% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 29017 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 Fiber protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	183	Total	C	N	O	S	0	0	0
			1411	895	231	279	6			
1	B	184	Total	C	N	O	S	0	0	0
			1428	904	234	284	6			
1	C	184	Total	C	N	O	S	0	0	0
			1426	903	234	283	6			
1	D	183	Total	C	N	O	S	0	0	0
			1415	896	232	281	6			
1	E	184	Total	C	N	O	S	0	0	0
			1434	907	234	287	6			
1	F	185	Total	C	N	O	S	0	0	0
			1437	908	236	287	6			
1	G	182	Total	C	N	O	S	0	0	0
			1419	901	232	280	6			
1	H	183	Total	C	N	O	S	0	0	0
			1428	903	234	285	6			
1	I	186	Total	C	N	O	S	0	0	0
			1447	915	237	289	6			
1	J	182	Total	C	N	O	S	0	0	0
			1417	900	231	280	6			
1	K	185	Total	C	N	O	S	0	0	0
			1428	905	235	282	6			
1	L	186	Total	C	N	O	S	0	0	0
			1441	913	236	286	6			

- Molecule 2 is a protein called Membrane cofactor protein.

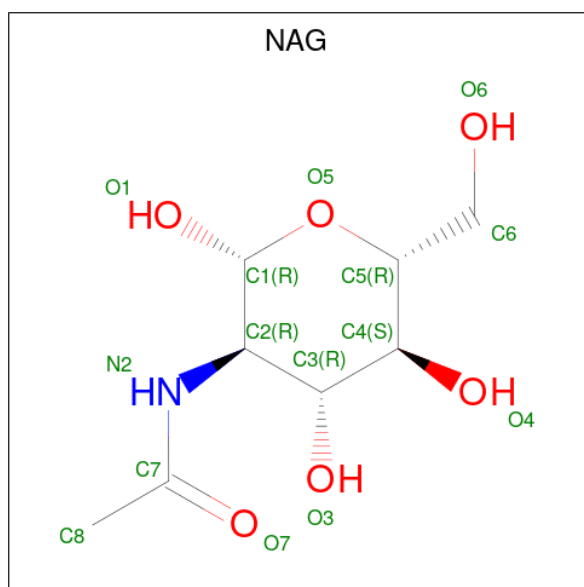
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	126	Total	C	N	O	S	0	0	0
			987	641	153	183	10			
2	N	126	Total	C	N	O	S	0	0	0
			991	641	153	187	10			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	O	126	Total	C	N	O	S	0	0	0
			1011	653	158	190	10			
2	P	126	Total	C	N	O	S	0	0	0
			977	631	151	185	10			
2	Q	125	Total	C	N	O	S	0	0	0
			962	622	149	181	10			
2	R	126	Total	C	N	O	S	0	0	0
			997	645	154	188	10			
2	S	126	Total	C	N	O	S	0	0	0
			976	628	154	184	10			
2	T	124	Total	C	N	O	S	0	0	0
			958	619	148	181	10			
2	U	126	Total	C	N	O	S	0	0	0
			996	645	154	187	10			
2	V	126	Total	C	N	O	S	0	0	0
			991	640	155	186	10			
2	W	125	Total	C	N	O	S	0	0	0
			983	637	154	182	10			
2	X	126	Total	C	N	O	S	0	0	0
			1001	649	156	186	10			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

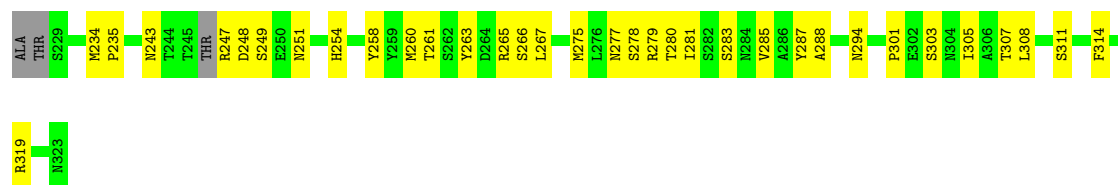


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	M	1	Total	C	N	O	0	0
			14	8	1	5		

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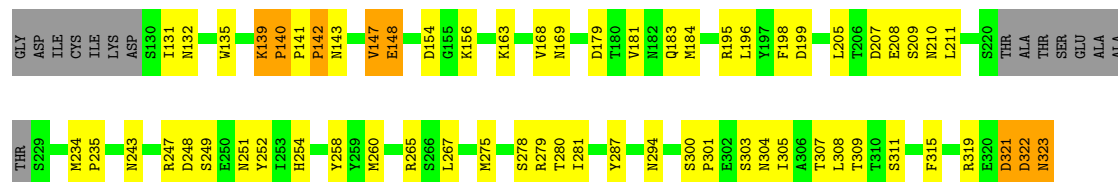
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	P	1	Total	C	N	O	0	0
			14	8	1	5		
3	S	1	Total	C	N	O	0	0
			14	8	1	5		
3	V	1	Total	C	N	O	0	0
			14	8	1	5		



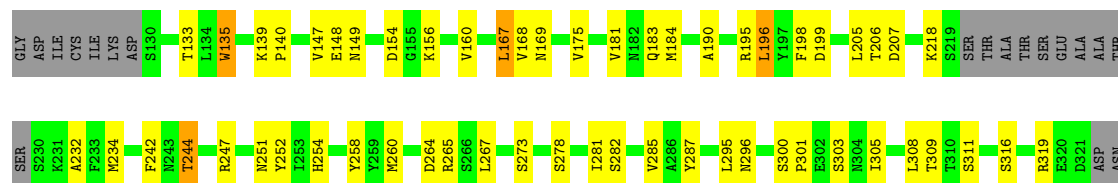
- Molecule 1: Fiber protein

Chain I: 61% 27% 7%



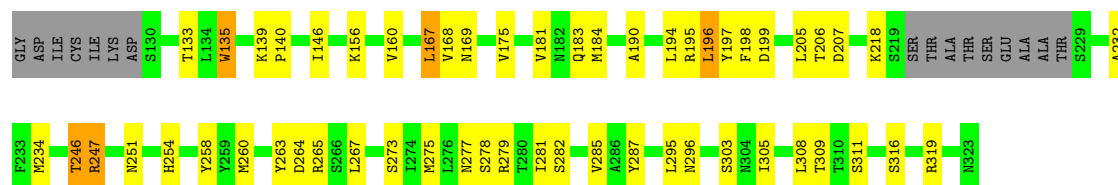
- Molecule 1: Fiber protein

Chain J: 63% 26% 9%



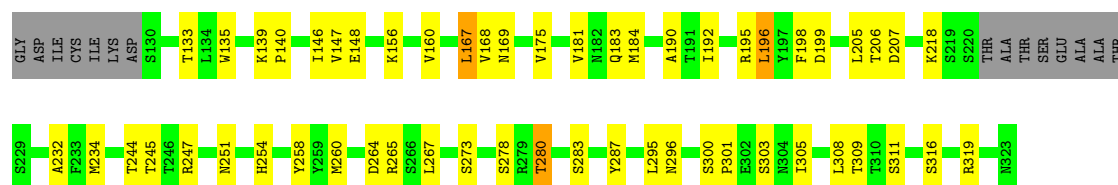
- Molecule 1: Fiber protein

Chain K: 65% 25% 8%



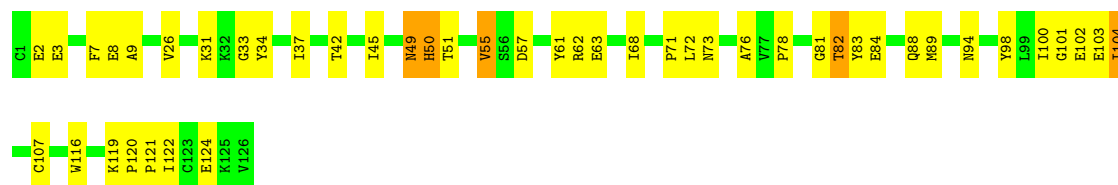
- Molecule 1: Fiber protein

Chain L: 66% 25% 7%



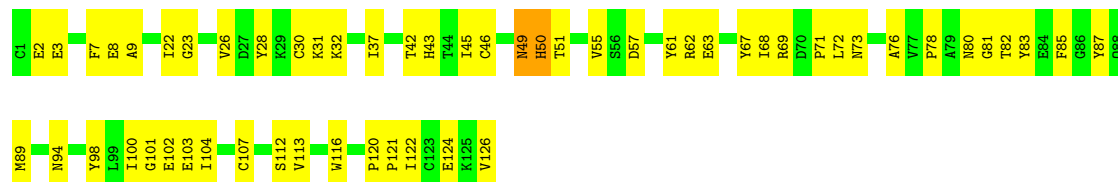
- Molecule 2: Membrane cofactor protein

Chain M: 63% 33% 0%



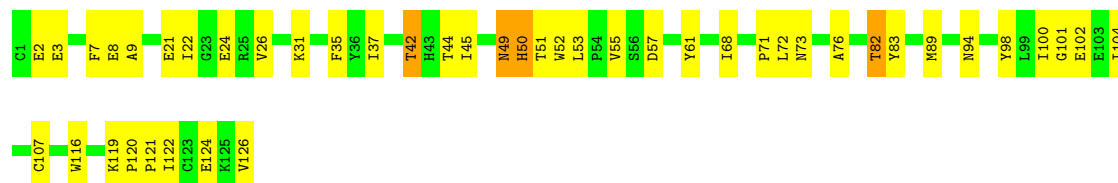
• Molecule 2: Membrane cofactor protein

Chain N: 56% 43%



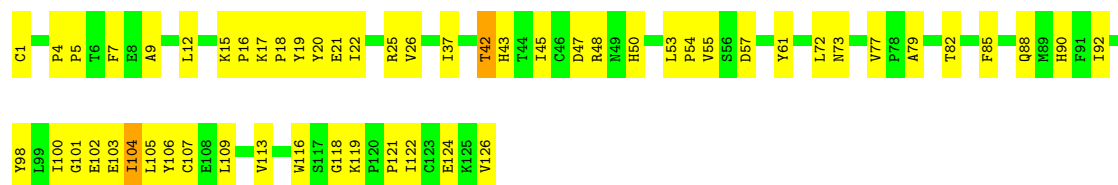
• Molecule 2: Membrane cofactor protein

Chain O: 64% 33%



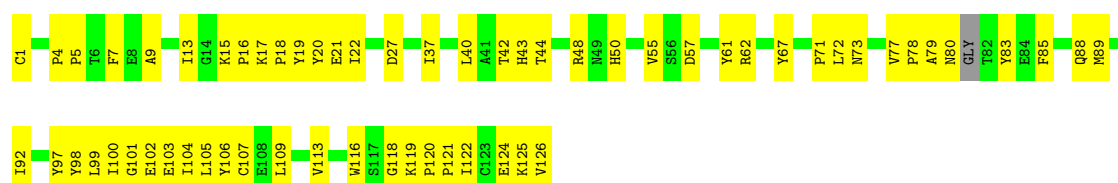
• Molecule 2: Membrane cofactor protein

Chain P: 56% 42%



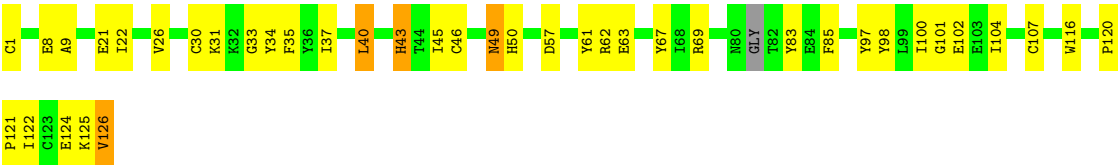
• Molecule 2: Membrane cofactor protein

Chain Q: 51% 48%

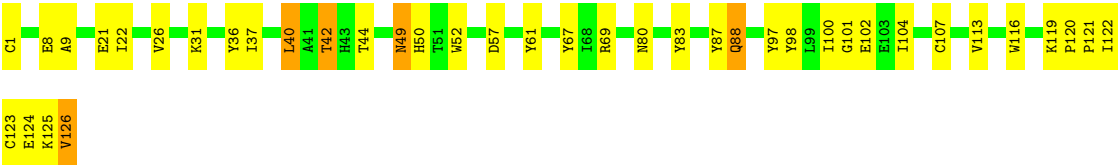


• Molecule 2: Membrane cofactor protein

Chain R: 52% 47%



● Molecule 2: Membrane cofactor protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	94.53Å 107.71Å 154.10Å 90.01° 90.10° 104.70°	Depositor
Resolution (Å)	47.99 – 3.50 47.99 – 3.50	Depositor EDS
% Data completeness (in resolution range)	96.3 (47.99-3.50) 95.9 (47.99-3.50)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.73 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.6 _288	Depositor
R, R_{free}	0.204 , 0.239 0.199 , 0.231	Depositor DCC
R_{free} test set	3574 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	57.6	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 25.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.419 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	29017	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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: NAG

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	0.36	0/1439	0.80	0/1961
1	B	0.37	0/1457	0.82	2/1986 (0.1%)
1	C	0.37	0/1455	0.81	1/1983 (0.1%)
1	D	0.36	0/1443	0.82	3/1966 (0.2%)
1	E	0.36	0/1463	0.82	2/1994 (0.1%)
1	F	0.36	0/1466	0.82	2/1998 (0.1%)
1	G	0.36	0/1447	0.81	2/1969 (0.1%)
1	H	0.35	0/1456	0.82	0/1982
1	I	0.39	0/1476	0.87	5/2011 (0.2%)
1	J	0.34	0/1446	0.81	1/1969 (0.1%)
1	K	0.36	0/1457	0.82	1/1986 (0.1%)
1	L	0.36	0/1470	0.82	1/2004 (0.0%)
2	M	0.34	0/1021	0.73	0/1396
2	N	0.33	0/1024	0.74	0/1397
2	O	0.35	0/1045	0.72	0/1424
2	P	0.36	0/1009	0.75	0/1380
2	Q	0.36	0/993	0.76	0/1355
2	R	0.36	0/1031	0.74	0/1408
2	S	0.36	0/1008	0.69	0/1377
2	T	0.35	0/988	0.70	0/1348
2	U	0.34	0/1030	0.71	0/1406
2	V	0.36	0/1025	0.74	0/1399
2	W	0.33	0/1015	0.71	0/1385
2	X	0.34	0/1035	0.72	0/1411
All	All	0.36	0/29699	0.78	20/40495 (0.0%)

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	140	PRO	CA-C-N	6.94	124.66	119.66
1	I	140	PRO	C-N-CA	6.94	124.66	119.66
1	C	246	THR	N-CA-C	6.11	117.94	111.28
1	I	321	ASP	N-CA-C	5.51	119.18	112.23
1	L	244	THR	N-CA-C	-5.48	106.73	113.41

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1411	0	1357	36	0
1	B	1428	0	1382	40	0
1	C	1426	0	1377	38	0
1	D	1415	0	1364	51	0
1	E	1434	0	1391	58	0
1	F	1437	0	1391	53	0
1	G	1419	0	1383	56	0
1	H	1428	0	1382	59	0
1	I	1447	0	1404	58	0
1	J	1417	0	1378	50	0
1	K	1428	0	1377	51	0
1	L	1441	0	1395	47	0
2	M	987	0	903	36	0
2	N	991	0	908	48	0
2	O	1011	0	942	39	0
2	P	977	0	888	43	0
2	Q	962	0	864	54	0
2	R	997	0	916	57	0
2	S	976	0	888	43	0
2	T	958	0	873	41	0
2	U	996	0	916	49	0
2	V	991	0	904	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	W	983	0	907	28	0
2	X	1001	0	934	35	0
3	M	14	0	13	2	0
3	P	14	0	13	0	0
3	S	14	0	13	0	0
3	V	14	0	13	3	0
All	All	29017	0	27476	969	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 17.

The worst 5 of 969 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:Q:67:TYR:HA	2:Q:83:TYR:HE1	1.33	0.93
2:R:25:ARG:HB2	2:R:45:ILE:HG12	1.49	0.93
1:E:303:SER:HB2	2:P:122:ILE:HD11	1.53	0.88
1:F:303:SER:HB2	2:Q:122:ILE:HD11	1.55	0.86
1:A:251:ASN:HD22	1:A:278:SER:HB2	1.41	0.84

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	177/201 (88%)	164 (93%)	11 (6%)	2 (1%)	11 43
1	B	180/201 (90%)	168 (93%)	12 (7%)	0	100 100
1	C	180/201 (90%)	167 (93%)	12 (7%)	1 (1%)	21 54
1	D	177/201 (88%)	168 (95%)	6 (3%)	3 (2%)	7 35
1	E	180/201 (90%)	169 (94%)	9 (5%)	2 (1%)	11 43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	181/201 (90%)	169 (93%)	8 (4%)	4 (2%)	5	30
1	G	176/201 (88%)	165 (94%)	10 (6%)	1 (1%)	21	54
1	H	177/201 (88%)	165 (93%)	11 (6%)	1 (1%)	21	54
1	I	182/201 (90%)	166 (91%)	13 (7%)	3 (2%)	7	36
1	J	178/201 (89%)	169 (95%)	8 (4%)	1 (1%)	21	54
1	K	181/201 (90%)	169 (93%)	9 (5%)	3 (2%)	7	35
1	L	182/201 (90%)	172 (94%)	8 (4%)	2 (1%)	11	43
2	M	124/126 (98%)	114 (92%)	7 (6%)	3 (2%)	4	29
2	N	124/126 (98%)	113 (91%)	9 (7%)	2 (2%)	7	36
2	O	124/126 (98%)	114 (92%)	7 (6%)	3 (2%)	4	29
2	P	124/126 (98%)	112 (90%)	12 (10%)	0	100	100
2	Q	121/126 (96%)	107 (88%)	13 (11%)	1 (1%)	16	49
2	R	124/126 (98%)	111 (90%)	13 (10%)	0	100	100
2	S	124/126 (98%)	112 (90%)	12 (10%)	0	100	100
2	T	120/126 (95%)	107 (89%)	13 (11%)	0	100	100
2	U	124/126 (98%)	112 (90%)	12 (10%)	0	100	100
2	V	124/126 (98%)	114 (92%)	9 (7%)	1 (1%)	16	49
2	W	121/126 (96%)	111 (92%)	8 (7%)	2 (2%)	7	35
2	X	124/126 (98%)	116 (94%)	7 (6%)	1 (1%)	16	49
All	All	3629/3924 (92%)	3354 (92%)	239 (7%)	36 (1%)	12	44

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	131	ILE
1	E	148	GLU
1	I	148	GLU
1	L	245	THR
2	W	21	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	159/182 (87%)	155 (98%)	4 (2%)	42	63
1	B	163/182 (90%)	158 (97%)	5 (3%)	35	59
1	C	162/182 (89%)	157 (97%)	5 (3%)	35	59
1	D	161/182 (88%)	158 (98%)	3 (2%)	50	68
1	E	165/182 (91%)	161 (98%)	4 (2%)	43	64
1	F	165/182 (91%)	157 (95%)	8 (5%)	23	49
1	G	162/182 (89%)	158 (98%)	4 (2%)	42	63
1	H	164/182 (90%)	160 (98%)	4 (2%)	43	64
1	I	166/182 (91%)	160 (96%)	6 (4%)	31	57
1	J	162/182 (89%)	159 (98%)	3 (2%)	50	68
1	K	161/182 (88%)	159 (99%)	2 (1%)	63	73
1	L	164/182 (90%)	161 (98%)	3 (2%)	51	69
2	M	102/110 (93%)	95 (93%)	7 (7%)	14	39
2	N	103/110 (94%)	99 (96%)	4 (4%)	28	54
2	O	108/110 (98%)	103 (95%)	5 (5%)	24	50
2	P	101/110 (92%)	97 (96%)	4 (4%)	28	54
2	Q	97/110 (88%)	95 (98%)	2 (2%)	47	66
2	R	105/110 (96%)	101 (96%)	4 (4%)	29	55
2	S	101/110 (92%)	97 (96%)	4 (4%)	28	54
2	T	99/110 (90%)	95 (96%)	4 (4%)	28	54
2	U	105/110 (96%)	103 (98%)	2 (2%)	50	68
2	V	103/110 (94%)	96 (93%)	7 (7%)	14	40
2	W	103/110 (94%)	96 (93%)	7 (7%)	14	40
2	X	106/110 (96%)	98 (92%)	8 (8%)	12	37
All	All	3187/3504 (91%)	3078 (97%)	109 (3%)	32	57

5 of 109 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	M	104	ILE
2	Q	92	ILE
2	W	104	ILE

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Mol	Chain	Res	Type
2	N	50	HIS
2	O	51	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 126 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	296	ASN
2	U	90	HIS
1	K	290	GLN
2	U	80	ASN
2	W	80	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](#)

4 ligands 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	$\# Z > 2$
3	NAG	M	1080	2	14,14,15	0.45	0	17,19,21	0.97	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	P	1080	2	14,14,15	0.45	0	17,19,21	0.94	1 (5%)
3	NAG	V	1080	2	14,14,15	0.48	0	17,19,21	1.03	1 (5%)
3	NAG	S	1080	2	14,14,15	0.49	0	17,19,21	1.03	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
3	NAG	M	1080	2	-	2/6/23/26	0/1/1/1
3	NAG	P	1080	2	-	2/6/23/26	0/1/1/1
3	NAG	V	1080	2	-	2/6/23/26	0/1/1/1
3	NAG	S	1080	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	S	1080	NAG	C1-O5-C5	-2.23	109.19	112.19
3	M	1080	NAG	C1-C2-N2	2.20	113.90	110.43
3	S	1080	NAG	C1-C2-N2	2.18	113.87	110.43
3	P	1080	NAG	C1-C2-N2	2.03	113.63	110.43
3	V	1080	NAG	C2-N2-C7	-2.03	120.18	122.90

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	S	1080	NAG	O5-C5-C6-O6
3	M	1080	NAG	O5-C5-C6-O6
3	S	1080	NAG	C4-C5-C6-O6
3	V	1080	NAG	O5-C5-C6-O6
3	V	1080	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	M	1080	NAG	2	0
3	V	1080	NAG	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	183/201 (91%)	-1.45	0 100 100	34, 49, 74, 90	0
1	B	184/201 (91%)	-1.43	0 100 100	34, 48, 75, 92	0
1	C	184/201 (91%)	-1.44	0 100 100	34, 49, 68, 85	0
1	D	183/201 (91%)	-1.43	0 100 100	36, 50, 72, 90	0
1	E	184/201 (91%)	-1.43	0 100 100	35, 50, 77, 92	0
1	F	185/201 (92%)	-1.44	0 100 100	35, 49, 74, 87	0
1	G	182/201 (90%)	-1.38	0 100 100	35, 50, 72, 83	0
1	H	183/201 (91%)	-1.41	0 100 100	35, 51, 72, 94	0
1	I	186/201 (92%)	-1.42	0 100 100	35, 50, 71, 88	0
1	J	182/201 (90%)	-1.45	0 100 100	34, 49, 74, 90	0
1	K	185/201 (92%)	-1.43	0 100 100	33, 49, 77, 91	0
1	L	186/201 (92%)	-1.42	0 100 100	34, 49, 73, 86	0
2	M	126/126 (100%)	-1.39	0 100 100	45, 64, 93, 99	0
2	N	126/126 (100%)	-1.44	0 100 100	46, 65, 85, 98	0
2	O	126/126 (100%)	-1.38	0 100 100	46, 64, 92, 98	0
2	P	126/126 (100%)	-1.39	0 100 100	43, 67, 106, 117	0
2	Q	125/126 (99%)	-1.31	0 100 100	43, 70, 114, 121	0
2	R	126/126 (100%)	-1.39	0 100 100	43, 67, 100, 117	0
2	S	126/126 (100%)	-1.36	0 100 100	44, 66, 107, 119	0
2	T	124/126 (98%)	-1.26	0 100 100	45, 69, 117, 120	0
2	U	126/126 (100%)	-1.30	0 100 100	44, 67, 102, 118	0
2	V	126/126 (100%)	-1.41	0 100 100	44, 63, 89, 96	0
2	W	125/126 (99%)	-1.43	0 100 100	44, 64, 82, 96	0
2	X	126/126 (100%)	-1.42	0 100 100	44, 64, 84, 95	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3715/3924 (94%)	-1.41	0 100 100	33, 56, 90, 121	0

There are no RSRZ outliers to report.

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 oligosaccharides 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	NAG	M	1080	14/15	0.99	0.03	61,64,70,75	0
3	NAG	S	1080	14/15	0.99	0.04	54,60,64,64	0
3	NAG	V	1080	14/15	0.99	0.05	62,65,72,73	0
3	NAG	P	1080	14/15	1.00	0.03	52,59,62,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.