



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 17, 2026 – 10:20 am BST

PDB ID : 9QE8 / pdb_00009qe8
Title : SMAD4 MH2 domain (residues 314-552) bound by Nanobody A7 (NbA7)
Authors : Pluta, R.; Macias, M.J.; Condeminas, M.
Deposited on : 2025-03-07
Resolution : 3.04 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 Phenix2.2
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 2.2
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

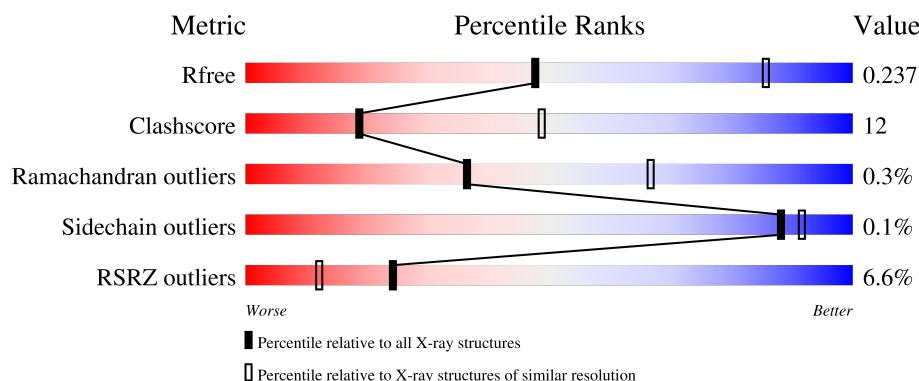
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.04 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	3685 (3.08-3.00)
Clashscore	190562	4007 (3.08-3.00)
Ramachandran outliers	187476	3834 (3.08-3.00)
Sidechain outliers	187428	3836 (3.08-3.00)
RSRZ outliers	180081	3684 (3.08-3.00)

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	240	<div> <div>0.2%</div> <div>66% 12% 21%</div> </div>
1	C	240	<div> <div>3%</div> <div>59% 19% 22%</div> </div>
1	E	240	<div> <div>2%</div> <div>56% 19% 25%</div> </div>
1	G	240	<div> <div>5%</div> <div>63% 16% 21%</div> </div>
1	I	240	<div> <div>2%</div> <div>59% 19% 22%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	K	240	
2	B	126	
2	D	126	
2	F	126	
2	H	126	
2	J	126	
2	L	126	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACT	C	602	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 27470 atoms, of which 13456 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 Mothers against decapentaplegic homolog 4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	189	Total	C	H	N	O	S	0	0	0
			2982	956	1470	271	274	11			
1	C	187	Total	C	H	N	O	S	0	0	0
			2957	948	1459	268	271	11			
1	E	181	Total	C	H	N	O	S	0	0	0
			2862	922	1408	259	262	11			
1	G	190	Total	C	H	N	O	S	0	0	0
			3000	961	1481	272	275	11			
1	I	188	Total	C	H	N	O	S	0	0	0
			2964	951	1461	269	272	11			
1	K	187	Total	C	H	N	O	S	0	0	0
			2921	942	1435	262	271	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	313	GLY	-	expression tag	UNP Q13485
C	313	GLY	-	expression tag	UNP Q13485
E	313	GLY	-	expression tag	UNP Q13485
G	313	GLY	-	expression tag	UNP Q13485
I	313	GLY	-	expression tag	UNP Q13485
K	313	GLY	-	expression tag	UNP Q13485

- Molecule 2 is a protein called Nanobody A7 (NbA7).

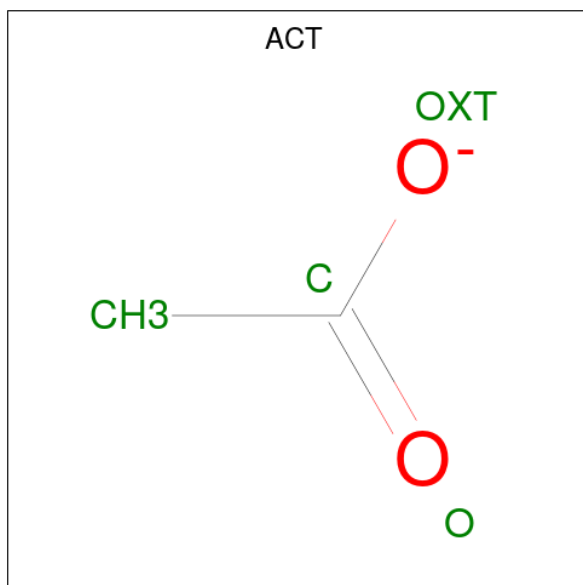
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	113	Total	C	H	N	O	S	0	0	0
			1668	536	811	147	170	4			
2	D	111	Total	C	H	N	O	S	0	0	0
			1651	531	805	147	164	4			
2	F	112	Total	C	H	N	O	S	0	0	0
			1647	530	797	146	170	4			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	113	Total	C	H	N	O	S	0	0	0
			1655	534	801	146	170	4			
2	J	107	Total	C	H	N	O	S	0	0	0
			1586	509	768	143	162	4			
2	L	98	Total	C	H	N	O	S	0	0	0
			1365	454	647	119	141	4			

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



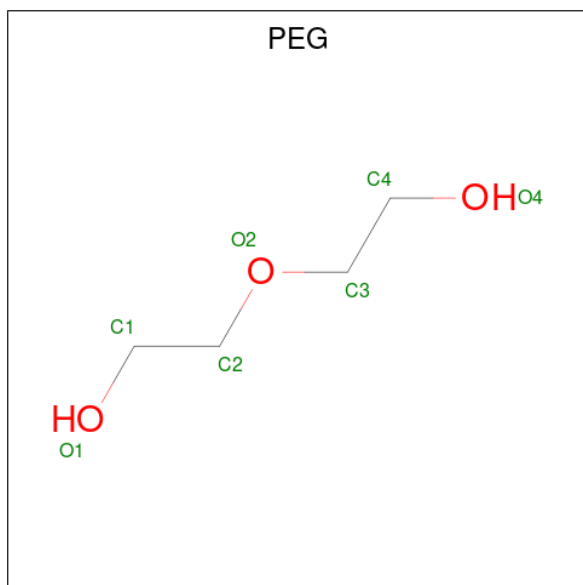
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			7	2	3	2		
3	A	1	Total	C	H	O	0	0
			7	2	3	2		
3	C	1	Total	C	H	O	0	0
			7	2	3	2		
3	C	1	Total	C	H	O	0	0
			7	2	3	2		
3	C	1	Total	C	H	O	0	0
			7	2	3	2		
3	D	1	Total	C	H	O	0	0
			7	2	3	2		
3	E	1	Total	C	H	O	0	0
			7	2	3	2		
3	F	1	Total	C	H	O	0	0
			7	2	3	2		

Continued on next page...

Continued from previous page...

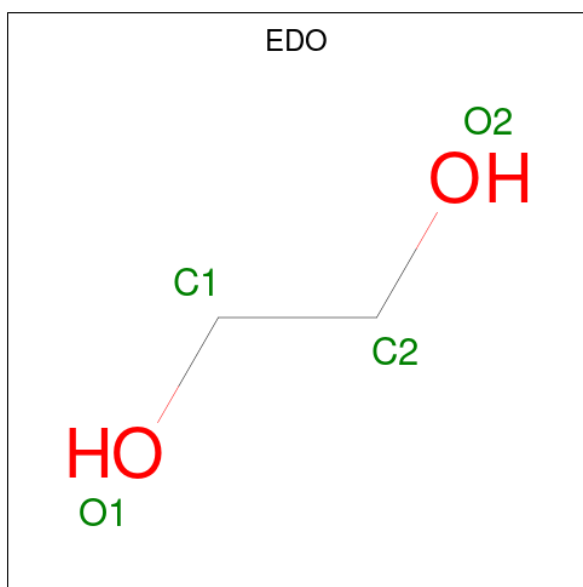
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	F	1	Total	C	H	O	0	0
			7	2	3	2		
3	I	1	Total	C	H	O	0	0
			7	2	3	2		
3	J	1	Total	C	H	O	0	0
			7	2	3	2		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			17	4	10	3		
4	F	1	Total	C	H	O	0	0
			17	4	10	3		
4	G	1	Total	C	H	O	0	0
			17	4	10	3		
4	H	1	Total	C	H	O	0	0
			17	4	10	3		
4	I	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).

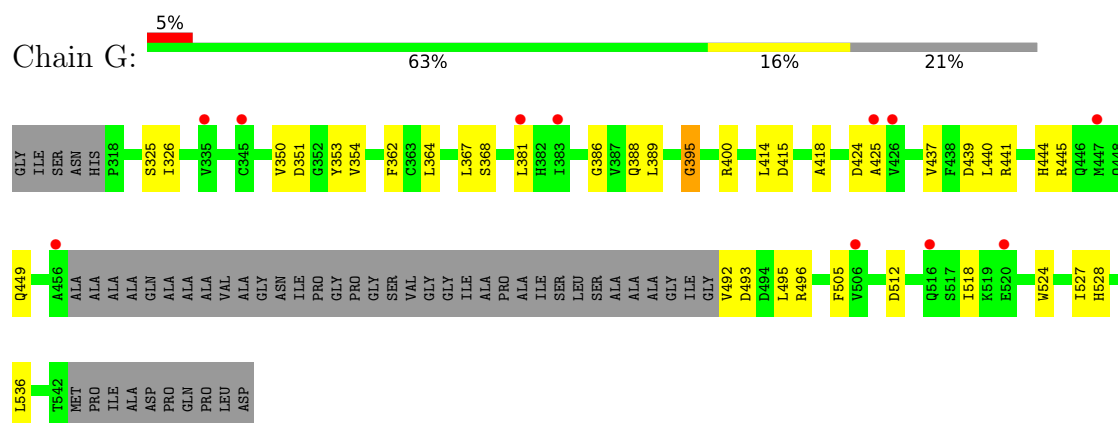


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	C	1	Total	C	H	O	0	0
			10	2	6	2		
5	E	1	Total	C	H	O	0	0
			10	2	6	2		
5	G	1	Total	C	H	O	0	0
			10	2	6	2		
5	K	1	Total	C	H	O	0	0
			10	2	6	2		

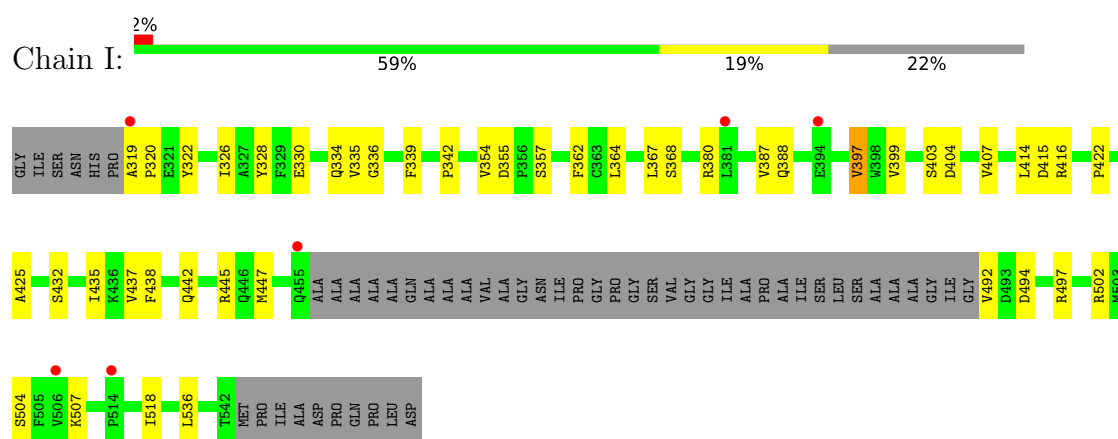
- Molecule 1: Mothers against decapentaplegic homolog 4



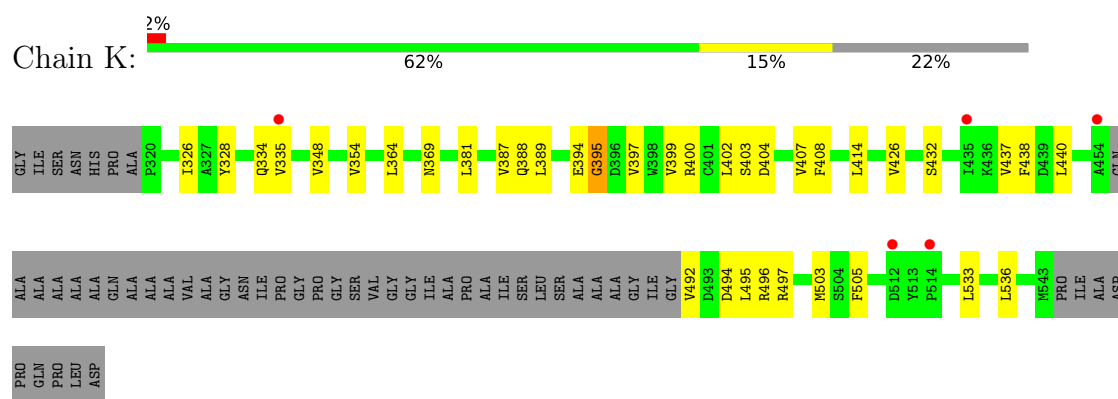
- Molecule 1: Mothers against decapentaplegic homolog 4



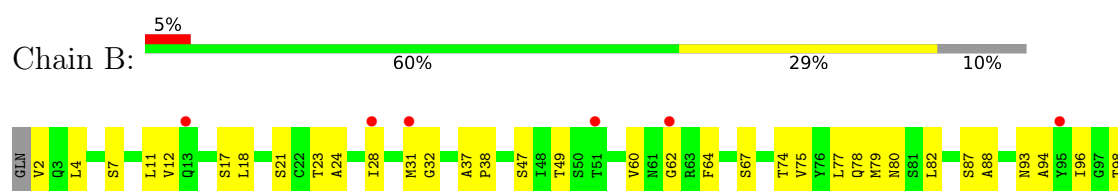
- Molecule 1: Mothers against decapentaplegic homolog 4

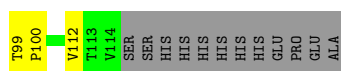


- Molecule 1: Mothers against decapentaplegic homolog 4

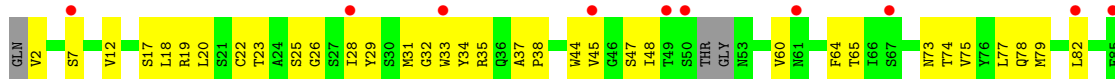
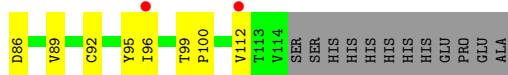


- Molecule 2: Nanobody A7 (NbA7)

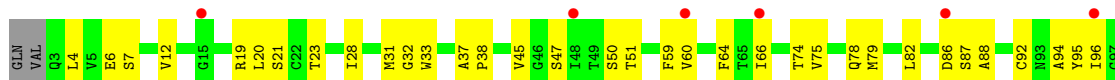
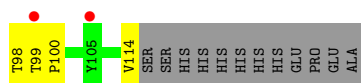




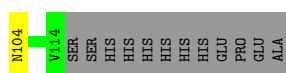
• Molecule 2: Nanobody A7 (NbA7)



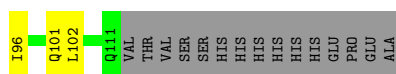
• Molecule 2: Nanobody A7 (NbA7)



• Molecule 2: Nanobody A7 (NbA7)

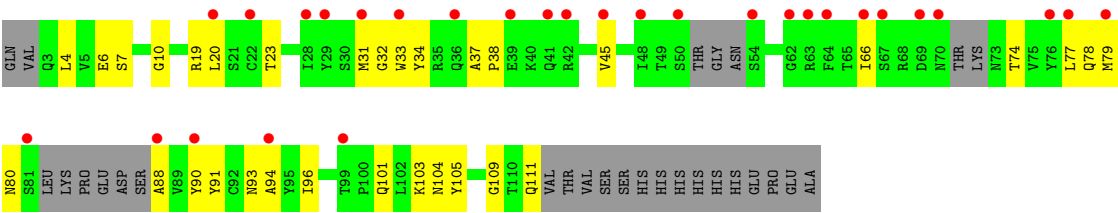


• Molecule 2: Nanobody A7 (NbA7)



• Molecule 2: Nanobody A7 (NbA7)





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	42.13Å 147.90Å 148.86Å 119.93° 94.33° 89.31°	Depositor
Resolution (Å)	74.22 – 3.04 74.22 – 3.04	Depositor EDS
% Data completeness (in resolution range)	47.0 (74.22-3.04) 47.0 (74.22-3.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 3.07Å)	Xtriage
Refinement program	PHENIX 1.21rc1_5107	Depositor
R, R_{free}	0.227 , 0.274 0.230 , 0.237	Depositor DCC
R_{free} test set	1332 reflections (2.23%)	wwPDB-VP
Wilson B-factor (Å ²)	36.9	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 48.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.048 for -h,k,-k-l	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	27470	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.08% 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: EDO, ACT, PEG

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	0.16	0/1549	0.41	0/2098
1	C	0.17	0/1535	0.45	0/2080
1	E	0.15	0/1491	0.37	0/2020
1	G	0.17	0/1557	0.43	0/2110
1	I	0.16	0/1540	0.41	0/2087
1	K	0.16	0/1523	0.44	0/2065
2	B	0.20	0/875	0.45	0/1190
2	D	0.20	0/863	0.44	0/1171
2	F	0.20	0/868	0.49	0/1181
2	H	0.20	0/872	0.48	0/1187
2	J	0.20	0/834	0.45	0/1131
2	L	0.17	0/732	0.46	0/994
All	All	0.17	0/14239	0.44	0/19314

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	1512	1470	1470	20	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1498	1459	1459	38	0
1	E	1454	1408	1408	36	0
1	G	1519	1481	1480	26	0
1	I	1503	1461	1461	34	1
1	K	1486	1435	1435	27	1
2	B	857	811	811	33	1
2	D	846	805	805	33	1
2	F	850	797	797	26	0
2	H	854	801	802	27	1
2	J	818	768	767	23	0
2	L	718	647	643	24	0
3	A	8	6	6	0	0
3	C	12	9	9	5	0
3	D	4	3	3	0	0
3	E	4	3	3	0	0
3	F	8	6	6	0	0
3	I	4	3	3	0	0
3	J	4	3	3	0	0
4	A	7	10	10	0	0
4	F	7	10	10	0	0
4	G	7	10	10	0	0
4	H	7	10	10	0	1
4	I	7	10	10	2	0
5	A	4	6	6	0	0
5	C	4	6	6	0	0
5	E	4	6	6	0	0
5	G	4	6	6	1	0
5	K	4	6	6	0	0
All	All	14014	13456	13451	328	3

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 12.

The worst 5 of 328 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:C:416:ARG:NH1	1:C:442:GLN:OE1	2.04	0.89
1:I:494:ASP:OD1	1:I:497:ARG:NH1	2.06	0.88
2:H:31:MET:HE2	2:H:75:VAL:HG11	1.56	0.86
1:C:504:SER:OG	1:C:507:LYS:O	1.98	0.82
1:C:492:VAL:HA	1:C:495:LEU:HD23	1.60	0.81

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:78:GLN:HE22	1:K:432:SER:O[1_556]	1.49	0.11
2:H:13:GLN:OE1	4:H:201:PEG:O1[1_455]	2.17	0.03
2:B:78:GLN:HE22	1:I:432:SER:O[1_566]	1.59	0.01

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	185/240 (77%)	172 (93%)	13 (7%)	0	100	100
1	C	183/240 (76%)	170 (93%)	12 (7%)	1 (0%)	24	57
1	E	177/240 (74%)	165 (93%)	10 (6%)	2 (1%)	11	39
1	G	186/240 (78%)	173 (93%)	12 (6%)	1 (0%)	24	57
1	I	184/240 (77%)	171 (93%)	12 (6%)	1 (0%)	24	57
1	K	183/240 (76%)	168 (92%)	14 (8%)	1 (0%)	24	57
2	B	111/126 (88%)	103 (93%)	8 (7%)	0	100	100
2	D	107/126 (85%)	96 (90%)	11 (10%)	0	100	100
2	F	110/126 (87%)	104 (94%)	6 (6%)	0	100	100
2	H	111/126 (88%)	102 (92%)	9 (8%)	0	100	100
2	J	103/126 (82%)	96 (93%)	7 (7%)	0	100	100
2	L	90/126 (71%)	87 (97%)	3 (3%)	0	100	100
All	All	1730/2196 (79%)	1607 (93%)	117 (7%)	6 (0%)	36	67

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	395	GLY
1	E	511	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	395	GLY
1	I	422	PRO
1	C	395	GLY

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	162/191 (85%)	162 (100%)	0	100	100
1	C	161/191 (84%)	161 (100%)	0	100	100
1	E	157/191 (82%)	157 (100%)	0	100	100
1	G	163/191 (85%)	163 (100%)	0	100	100
1	I	161/191 (84%)	160 (99%)	1 (1%)	78	85
1	K	159/191 (83%)	159 (100%)	0	100	100
2	B	91/106 (86%)	91 (100%)	0	100	100
2	D	89/106 (84%)	89 (100%)	0	100	100
2	F	90/106 (85%)	90 (100%)	0	100	100
2	H	90/106 (85%)	90 (100%)	0	100	100
2	J	86/106 (81%)	86 (100%)	0	100	100
2	L	70/106 (66%)	70 (100%)	0	100	100
All	All	1479/1782 (83%)	1478 (100%)	1 (0%)	88	91

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	397	VAL

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

Mol	Chain	Res	Type
1	K	444	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	K	427	HIS
1	I	448	GLN
2	H	36	GLN
1	K	388	GLN

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](#)

21 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	$\# Z > 2$
4	PEG	I	601	-	6,6,6	0.27	0	5,5,5	0.46	0
5	EDO	E	602	-	3,3,3	0.28	0	2,2,2	0.22	0
3	ACT	E	601	-	3,3,3	1.30	0	3,3,3	1.28	0
5	EDO	A	604	-	3,3,3	0.28	0	2,2,2	0.24	0
4	PEG	G	601	-	6,6,6	0.23	0	5,5,5	0.28	0
3	ACT	J	201	-	3,3,3	1.24	0	3,3,3	1.19	0
4	PEG	A	602	-	6,6,6	0.22	0	5,5,5	0.49	0
3	ACT	C	603	-	3,3,3	1.22	0	3,3,3	1.30	0
3	ACT	C	601	-	3,3,3	1.23	0	3,3,3	1.22	0
3	ACT	C	602	-	3,3,3	1.22	0	3,3,3	1.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ACT	D	201	-	3,3,3	1.24	0	3,3,3	1.27	0
3	ACT	F	202	-	3,3,3	1.22	0	3,3,3	1.18	0
4	PEG	F	201	-	6,6,6	0.25	0	5,5,5	0.32	0
3	ACT	F	203	-	3,3,3	1.24	0	3,3,3	1.10	0
3	ACT	A	601	-	3,3,3	1.24	0	3,3,3	1.19	0
5	EDO	K	601	-	3,3,3	0.28	0	2,2,2	0.17	0
5	EDO	C	604	-	3,3,3	0.28	0	2,2,2	0.24	0
3	ACT	I	602	-	3,3,3	1.23	0	3,3,3	1.22	0
4	PEG	H	201	-	6,6,6	0.24	0	5,5,5	0.24	0
3	ACT	A	603	-	3,3,3	1.23	0	3,3,3	1.25	0
5	EDO	G	602	-	3,3,3	0.28	0	2,2,2	0.21	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PEG	A	602	-	-	1/4/4/4	-
4	PEG	I	601	-	-	1/4/4/4	-
5	EDO	E	602	-	-	0/1/1/1	-
4	PEG	H	201	-	-	1/4/4/4	-
5	EDO	K	601	-	-	1/1/1/1	-
5	EDO	C	604	-	-	1/1/1/1	-
5	EDO	A	604	-	-	1/1/1/1	-
4	PEG	G	601	-	-	2/4/4/4	-
5	EDO	G	602	-	-	0/1/1/1	-
4	PEG	F	201	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	601	PEG	O1-C1-C2-O2
4	I	601	PEG	O1-C1-C2-O2
5	A	604	EDO	O1-C1-C2-O2
4	A	602	PEG	O1-C1-C2-O2
4	G	601	PEG	C1-C2-O2-C3

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	601	PEG	2	0
3	C	602	ACT	5	0
4	H	201	PEG	0	1
5	G	602	EDO	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	189/240 (78%)	0.23	3 (1%) 70 47	21, 46, 76, 108	0
1	C	187/240 (77%)	0.55	8 (4%) 40 21	25, 48, 76, 103	0
1	E	181/240 (75%)	0.35	5 (2%) 55 31	21, 42, 74, 93	0
1	G	190/240 (79%)	0.55	11 (5%) 29 14	19, 49, 80, 104	0
1	I	188/240 (78%)	0.37	6 (3%) 50 28	24, 47, 83, 110	0
1	K	187/240 (77%)	0.45	5 (2%) 56 32	28, 53, 82, 113	0
2	B	113/126 (89%)	0.62	6 (5%) 32 16	36, 57, 80, 96	0
2	D	111/126 (88%)	0.99	12 (10%) 11 6	52, 70, 91, 103	0
2	F	112/126 (88%)	0.85	8 (7%) 22 11	39, 80, 106, 124	0
2	H	113/126 (89%)	0.72	13 (11%) 9 5	28, 52, 78, 102	0
2	J	107/126 (84%)	1.02	12 (11%) 10 5	51, 77, 102, 123	0
2	L	98/126 (77%)	1.56	29 (29%) 1 1	60, 85, 105, 116	0
All	All	1776/2196 (80%)	0.61	118 (6%) 24 12	19, 55, 95, 124	0

The worst 5 of 118 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	33	TRP	7.3
2	L	28	ILE	5.9
2	J	27	SER	5.6
2	L	90	TYR	5.6
2	L	62	GLY	4.8

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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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	ACT	D	201	4/4	0.54	0.27	38,47,57,66	0
3	ACT	I	602	4/4	0.68	0.21	40,49,49,54	0
3	ACT	F	203	4/4	0.70	0.25	44,50,61,61	0
5	EDO	K	601	4/4	0.71	0.24	60,73,77,77	0
4	PEG	F	201	7/7	0.73	0.16	48,61,89,89	0
4	PEG	G	601	7/7	0.76	0.12	15,32,39,39	0
3	ACT	F	202	4/4	0.76	0.26	45,57,70,70	0
3	ACT	A	601	4/4	0.78	0.21	42,51,59,69	0
3	ACT	J	201	4/4	0.79	0.30	45,60,73,73	0
5	EDO	C	604	4/4	0.81	0.14	37,59,76,92	0
3	ACT	E	601	4/4	0.82	0.19	40,44,48,50	0
4	PEG	I	601	7/7	0.82	0.21	48,65,76,89	0
5	EDO	E	602	4/4	0.84	0.18	20,26,36,44	0
3	ACT	C	601	4/4	0.85	0.21	30,37,38,45	0
5	EDO	G	602	4/4	0.87	0.17	41,62,75,75	0
4	PEG	H	201	7/7	0.87	0.15	37,61,80,80	0
3	ACT	A	603	4/4	0.88	0.12	22,40,58,58	0
5	EDO	A	604	4/4	0.89	0.10	32,41,55,55	0
4	PEG	A	602	7/7	0.91	0.12	25,37,70,70	0
3	ACT	C	603	4/4	0.97	0.07	5,18,54,54	0
3	ACT	C	602	4/4	0.98	0.07	16,49,59,59	0

6.5 Other polymers ⓘ

There are no such residues in this entry.