wwPDB X-ray Structure Validation Summary Report (i)

Nov 6, 2023 – 05:02 AM EST

PDB ID	:	7TA6
Title	:	Trimer-to-Monomer Disruption of Tumor Necrosis Factor-alpha (TNF-alpha) by unnatural alpha/beta-peptide-1
Authors	:	Niu, J.; Bingman, C.A.; Gellman, S.H.
Deposited on	:	2021-12-20
Resolution	:	2.67 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 (i) 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 (i)) were used in the production of this report:

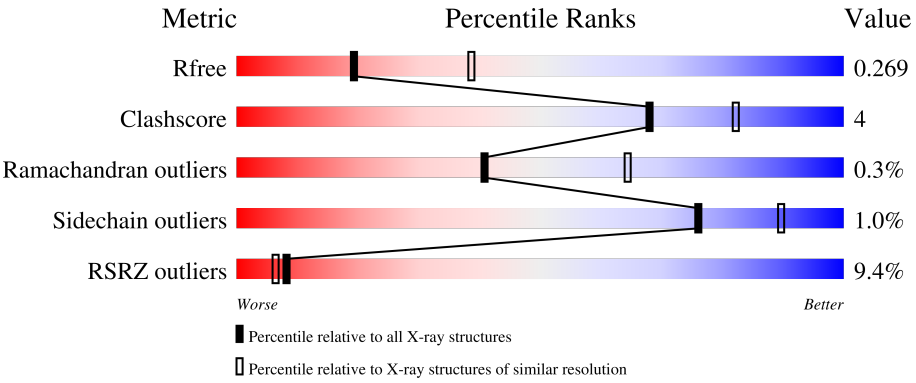
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.67 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3863 (2.70-2.66)
Clashscore	141614	4210 (2.70-2.66)
Ramachandran outliers	138981	4141 (2.70-2.66)
Sidechain outliers	138945	4141 (2.70-2.66)
RSRZ outliers	127900	3780 (2.70-2.66)

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 <=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	158	9% 80% 9% · 11%
1	B	158	7% 74% 8% 18%
1	C	158	11% 84% · 13%
1	D	158	8% 81% 11% 8%
1	E	158	11% 77% 9% 14%

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Mol	Chain	Length	Quality of chain
1	F	158	7% 77% 10% 13%
1	G	158	4% 75% 12% 13%
1	H	158	10% 74% 9% 17%
2	I	29	3% 79% 21%
2	J	29	90% 10%
2	K	29	86% 14%
2	L	29	3% 90% 10%
2	M	29	17% 79% 21%
2	N	29	3% 93% 7%
2	O	29	10% 86% 14%
2	P	29	3% 79% 17%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 20570 atoms, of which 10183 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 Tumor necrosis factor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	141	Total	C	H	N	O	S	0	0	0
			2114	686	1046	179	201	2			
1	B	129	Total	C	H	N	O	S	0	2	0
			1998	649	988	167	192	2			
1	C	138	Total	C	H	N	O	S	0	1	0
			2093	680	1035	177	199	2			
1	D	145	Total	C	H	N	O	S	0	0	0
			2241	717	1120	194	208	2			
1	E	136	Total	C	H	N	O	S	0	0	0
			2082	672	1034	177	197	2			
1	F	138	Total	C	H	N	O	S	0	0	0
			2159	692	1081	185	199	2			
1	G	138	Total	C	H	N	O	S	0	1	0
			2112	686	1045	180	199	2			
1	H	131	Total	C	H	N	O	S	0	0	0
			1997	650	994	167	184	2			

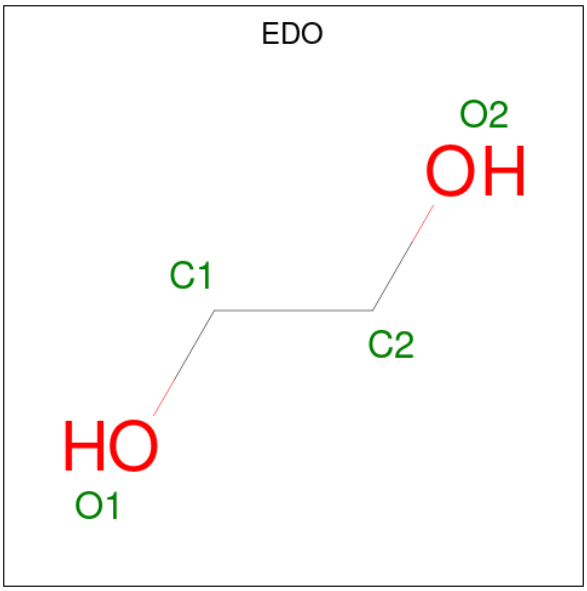
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP P01375
B	0	SER	-	expression tag	UNP P01375
C	0	SER	-	expression tag	UNP P01375
D	0	SER	-	expression tag	UNP P01375
E	0	SER	-	expression tag	UNP P01375
F	0	SER	-	expression tag	UNP P01375
G	0	SER	-	expression tag	UNP P01375
H	0	SER	-	expression tag	UNP P01375

- Molecule 2 is a protein called Alpha/Beta-peptide-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	I	29	Total	C	H	N	O	S	0	0	0
			455	151	224	41	37	2			
2	J	29	Total	C	H	N	O	S	0	0	0
			455	151	224	41	37	2			
2	K	29	Total	C	H	N	O	S	0	0	0
			455	151	224	41	37	2			
2	L	29	Total	C	H	N	O	S	0	0	0
			455	151	224	41	37	2			
2	M	29	Total	C	H	N	O	S	0	0	0
			455	151	224	41	37	2			
2	N	29	Total	C	H	N	O	S	0	0	0
			455	151	224	41	37	2			
2	O	29	Total	C	H	N	O	S	0	0	0
			455	151	224	41	37	2			
2	P	29	Total	C	H	N	O	S	0	0	0
			455	151	224	41	37	2			

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		

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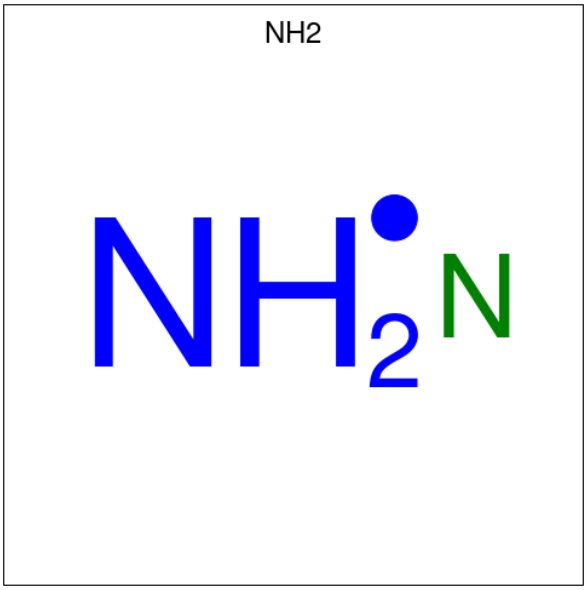
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C H O 10 2 6 2	0	0
3	E	1	Total C H O 10 2 6 2	0	0
3	K	1	Total C H O 10 2 6 2	0	0
3	N	1	Total C H O 10 2 6 2	0	0

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total K 1 1	0	0

- Molecule 5 is AMINO GROUP (three-letter code: NH2) (formula: H_2N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	I	1	Total N 1 1	0	0
5	J	1	Total N 1 1	0	0
5	K	1	Total N 1 1	0	0
5	L	1	Total N 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	M	1	Total N 1 1	0	0
5	N	1	Total N 1 1	0	0
5	O	1	Total N 1 1	0	0
5	P	1	Total N 1 1	0	0

- Molecule 6 is water.

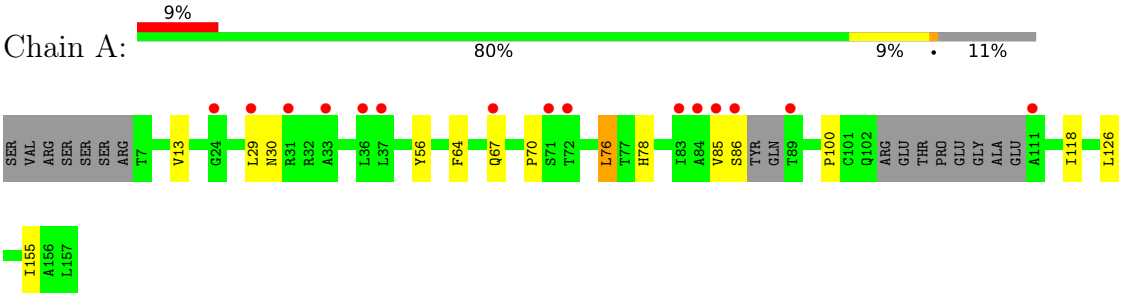
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	4	Total O 4 4	0	0
6	B	6	Total O 6 6	0	0
6	C	6	Total O 6 6	0	0
6	D	3	Total O 3 3	0	0
6	E	1	Total O 1 1	0	0
6	F	3	Total O 3 3	0	0
6	G	4	Total O 4 4	0	0
6	H	2	Total O 2 2	0	0
6	I	2	Total O 2 2	0	0
6	J	1	Total O 1 1	0	0
6	K	3	Total O 3 3	0	0
6	L	7	Total O 7 7	0	0
6	N	1	Total O 1 1	0	0
6	O	2	Total O 2 2	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

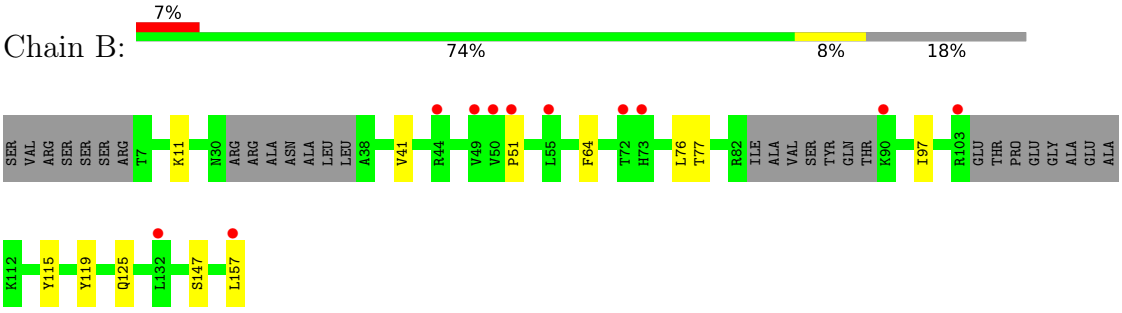
• Molecule 1: Tumor necrosis factor

Chain A:



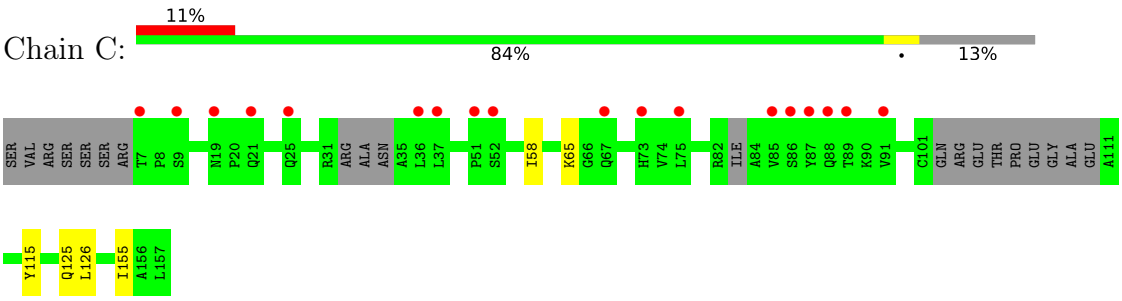
• Molecule 1: Tumor necrosis factor

Chain B:



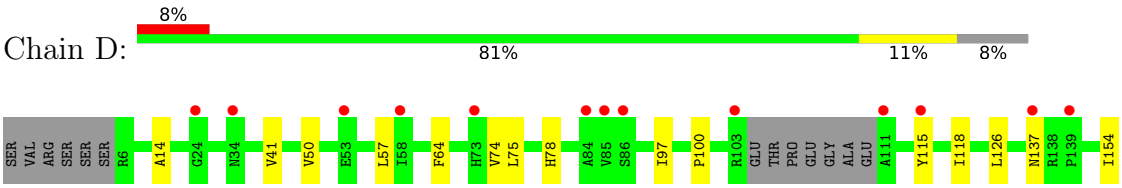
• Molecule 1: Tumor necrosis factor

Chain C:



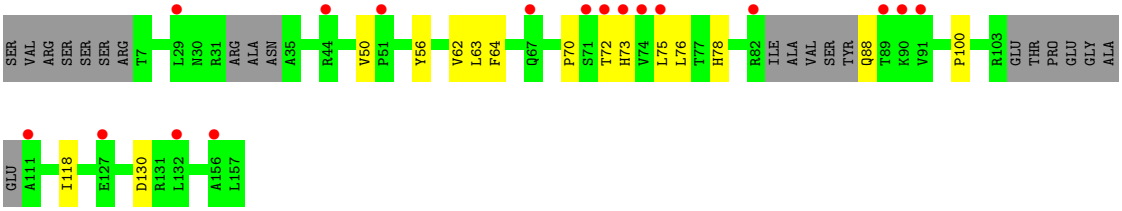
• Molecule 1: Tumor necrosis factor

Chain D:



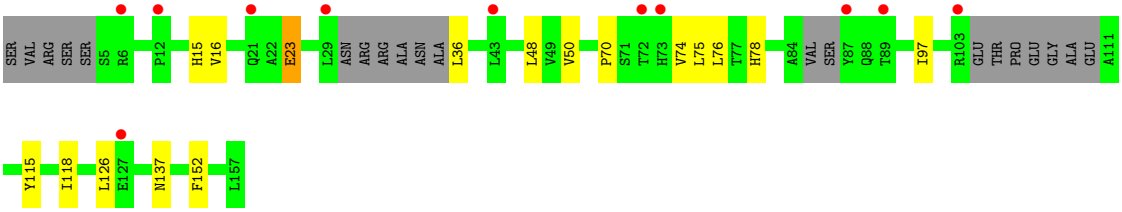
• Molecule 1: Tumor necrosis factor

Chain E:



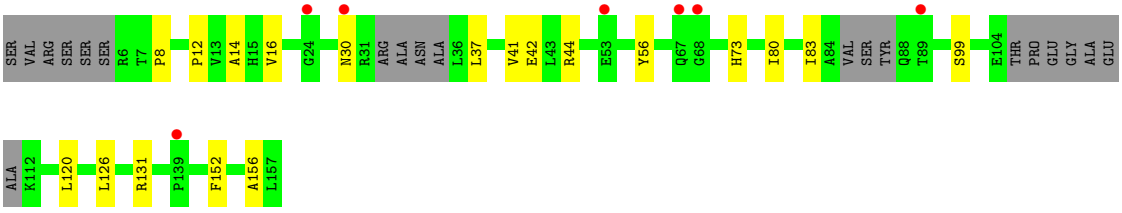
• Molecule 1: Tumor necrosis factor

Chain F:



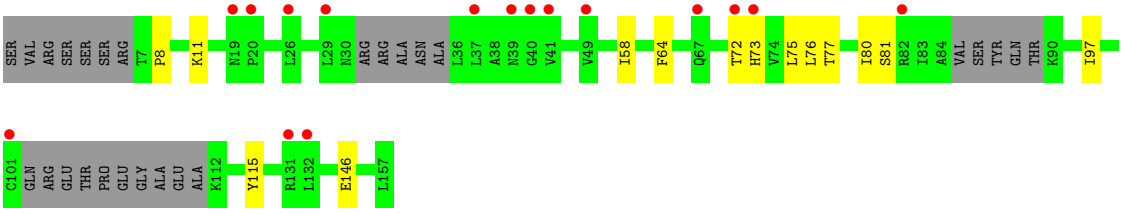
• Molecule 1: Tumor necrosis factor

Chain G:



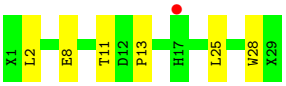
• Molecule 1: Tumor necrosis factor

Chain H:



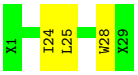
• Molecule 2: Alpha/Beta-peptide-1

Chain I:



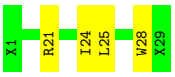
• Molecule 2: Alpha/Beta-peptide-1

Chain J:



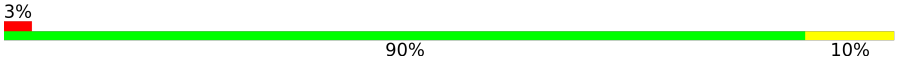
• Molecule 2: Alpha/Beta-peptide-1

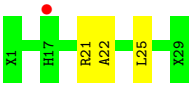
Chain K:



• Molecule 2: Alpha/Beta-peptide-1

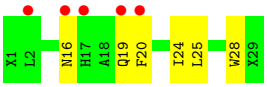
Chain L:





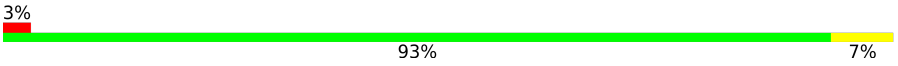
• Molecule 2: Alpha/Beta-peptide-1

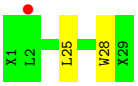
Chain M:



• Molecule 2: Alpha/Beta-peptide-1

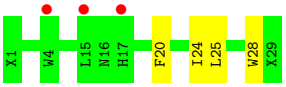
Chain N:





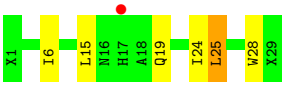
• Molecule 2: Alpha/Beta-peptide-1

Chain O:



• Molecule 2: Alpha/Beta-peptide-1

Chain P:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	143.77Å 143.55Å 76.89Å 90.00° 97.85° 90.00°	Depositor
Resolution (Å)	39.74 – 2.67 39.74 – 2.67	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.74-2.67) 99.9 (39.74-2.67)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.29 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.19.2	Depositor
R, R_{free}	0.245 , 0.273 0.243 , 0.269	Depositor DCC
R_{free} test set	1997 reflections (4.57%)	wwPDB-VP
Wilson B-factor (Å^2)	75.7	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 61.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	20570	wwPDB-VP
Average B, all atoms (Å^2)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.12% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: AIB, EDO, K, XCP, XPC, NH2

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.25	0/1091	0.47	0/1488
1	B	0.25	0/1031	0.47	0/1401
1	C	0.25	0/1080	0.47	0/1470
1	D	0.25	0/1145	0.49	0/1558
1	E	0.24	0/1070	0.47	0/1455
1	F	0.25	0/1100	0.50	0/1492
1	G	0.25	0/1089	0.47	0/1481
1	H	0.25	0/1025	0.47	0/1394
2	I	0.22	0/194	0.46	0/261
2	J	0.23	0/194	0.44	0/261
2	K	0.23	0/194	0.47	0/261
2	L	0.21	0/194	0.48	0/261
2	M	0.21	0/194	0.47	0/261
2	N	0.24	0/194	0.45	0/261
2	O	0.24	0/194	0.46	0/261
2	P	0.22	0/194	0.45	0/261
All	All	0.25	0/10183	0.48	0/13827

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
2	I	0	2
2	J	0	2
2	K	0	2
2	L	0	1
2	M	0	2
2	N	0	2
2	O	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	P	0	2
All	All	0	15

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	I	25	LEU	Peptide
2	I	28	TRP	Peptide
2	J	25	LEU	Peptide
2	J	28	TRP	Peptide
2	K	25	LEU	Peptide

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	1068	1046	1043	8	0
1	B	1010	988	983	10	0
1	C	1058	1035	1028	4	0
1	D	1121	1120	1115	11	0
1	E	1048	1034	1024	8	0
1	F	1078	1081	1078	11	0
1	G	1067	1045	1039	10	0
1	H	1003	994	991	11	0
2	I	231	224	224	4	0
2	J	231	224	224	2	0
2	K	231	224	224	2	0
2	L	231	224	224	1	0
2	M	231	224	224	2	0
2	N	231	224	224	0	0
2	O	231	224	224	2	0
2	P	231	224	224	3	0
3	A	8	12	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	4	6	6	0	0
3	C	8	12	12	0	0
3	E	4	6	6	0	0
3	K	4	6	6	0	0
3	N	4	6	6	0	0
4	H	1	0	0	0	0
5	I	1	0	0	0	0
5	J	1	0	0	0	0
5	K	1	0	0	0	0
5	L	1	0	0	0	0
5	M	1	0	0	0	0
5	N	1	0	0	0	0
5	O	1	0	0	0	0
5	P	1	0	0	0	0
6	A	4	0	0	0	0
6	B	6	0	0	0	0
6	C	6	0	0	0	0
6	D	3	0	0	0	0
6	E	1	0	0	0	0
6	F	3	0	0	0	0
6	G	4	0	0	0	0
6	H	2	0	0	0	0
6	I	2	0	0	0	0
6	J	1	0	0	0	0
6	K	3	0	0	0	0
6	L	7	0	0	0	0
6	N	1	0	0	0	0
6	O	2	0	0	0	0
All	All	10387	10183	10141	77	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 77 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:O:20:PHE:O	2:O:24:ILE:HD12	1.95	0.66
1:A:13:VAL:HG13	1:A:155:ILE:HD13	1.78	0.65
1:B:125:GLN:OE1	1:C:65:LYS:NZ	2.30	0.65
1:G:42:GLU:OE1	1:G:44:ARG:NH2	2.29	0.64
2:M:16:ASN:OD1	2:M:19:GLN:NE2	2.30	0.64

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	135/158 (85%)	125 (93%)	9 (7%)	1 (1%)	22	44
1	B	123/158 (78%)	116 (94%)	7 (6%)	0	100	100
1	C	131/158 (83%)	120 (92%)	11 (8%)	0	100	100
1	D	141/158 (89%)	131 (93%)	10 (7%)	0	100	100
1	E	128/158 (81%)	120 (94%)	7 (6%)	1 (1%)	19	40
1	F	130/158 (82%)	125 (96%)	4 (3%)	1 (1%)	19	40
1	G	131/158 (83%)	122 (93%)	8 (6%)	1 (1%)	19	40
1	H	123/158 (78%)	116 (94%)	7 (6%)	0	100	100
2	I	23/29 (79%)	21 (91%)	2 (9%)	0	100	100
2	J	23/29 (79%)	21 (91%)	2 (9%)	0	100	100
2	K	23/29 (79%)	23 (100%)	0	0	100	100
2	L	23/29 (79%)	22 (96%)	1 (4%)	0	100	100
2	M	23/29 (79%)	19 (83%)	4 (17%)	0	100	100
2	N	23/29 (79%)	21 (91%)	2 (9%)	0	100	100
2	O	23/29 (79%)	21 (91%)	2 (9%)	0	100	100
2	P	23/29 (79%)	23 (100%)	0	0	100	100
All	All	1226/1496 (82%)	1146 (94%)	76 (6%)	4 (0%)	41	64

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	70	PRO
1	G	8	PRO
1	E	70	PRO
1	A	70	PRO

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	113/134 (84%)	112 (99%)	1 (1%)	78 91
1	B	109/134 (81%)	108 (99%)	1 (1%)	78 91
1	C	112/134 (84%)	110 (98%)	2 (2%)	59 81
1	D	120/134 (90%)	119 (99%)	1 (1%)	81 92
1	E	112/134 (84%)	110 (98%)	2 (2%)	59 81
1	F	117/134 (87%)	115 (98%)	2 (2%)	60 82
1	G	113/134 (84%)	113 (100%)	0	100 100
1	H	107/134 (80%)	105 (98%)	2 (2%)	57 80
2	I	20/20 (100%)	20 (100%)	0	100 100
2	J	20/20 (100%)	20 (100%)	0	100 100
2	K	20/20 (100%)	20 (100%)	0	100 100
2	L	20/20 (100%)	20 (100%)	0	100 100
2	M	20/20 (100%)	20 (100%)	0	100 100
2	N	20/20 (100%)	20 (100%)	0	100 100
2	O	20/20 (100%)	20 (100%)	0	100 100
2	P	20/20 (100%)	20 (100%)	0	100 100
All	All	1063/1232 (86%)	1052 (99%)	11 (1%)	76 90

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	23	GLU
1	F	115	TYR
1	H	115	TYR
1	H	81	SER
1	D	115	TYR

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

48 non-standard protein/DNA/RNA residues 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	AIB	J	18	2	1,5,6	1.18	0	2,7,9	0.93	0
2	AIB	N	22	2	1,5,6	1.25	0	2,7,9	0.88	0
2	XCP	N	1	2	8,8,9	0.62	0	4,10,12	0.94	0
2	AIB	K	9	2	1,5,6	1.22	0	2,7,9	1.05	0
2	AIB	K	18	2	1,5,6	1.26	0	2,7,9	0.80	0
2	AIB	I	22	2	1,5,6	1.18	0	2,7,9	0.75	0
2	AIB	O	22	2	1,5,6	1.20	0	2,7,9	0.77	0
2	XPC	L	26	2	6,8,9	0.52	0	4,10,12	1.19	0
2	XCP	P	29	5,2	8,8,9	0.62	0	4,10,12	0.96	0
2	XCP	J	29	5,2	8,8,9	0.63	0	4,10,12	1.00	0
2	XCP	M	1	2	8,8,9	0.72	0	4,10,12	1.00	0
2	XPC	K	26	2	6,8,9	0.60	0	4,10,12	1.16	0
2	XCP	O	29	5,2	8,8,9	0.74	0	4,10,12	1.18	0
2	AIB	P	9	2	1,5,6	1.17	0	2,7,9	0.86	0
2	AIB	M	18	2	1,5,6	1.26	0	2,7,9	0.80	0
2	AIB	N	9	2	1,5,6	1.20	0	2,7,9	0.93	0
2	AIB	M	9	2	1,5,6	1.18	0	2,7,9	0.85	0
2	XPC	P	26	2	6,8,9	0.52	0	4,10,12	1.14	0
2	AIB	N	18	2	1,5,6	1.15	0	2,7,9	0.93	0
2	AIB	K	22	2	1,5,6	1.17	0	2,7,9	0.83	0
2	AIB	J	22	2	1,5,6	1.21	0	2,7,9	0.83	0
2	XPC	J	26	2	6,8,9	0.65	0	4,10,12	0.94	0
2	XCP	L	29	5,2	8,8,9	0.64	0	4,10,12	0.87	0
2	XCP	P	1	2	8,8,9	0.65	0	4,10,12	1.02	0
2	AIB	L	18	2	1,5,6	1.23	0	2,7,9	0.85	0
2	AIB	M	22	2	1,5,6	1.20	0	2,7,9	1.05	0
2	AIB	P	18	2	1,5,6	1.24	0	2,7,9	0.75	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	XCP	K	29	5,2	8,8,9	0.76	0	4,10,12	1.10	0
2	AIB	O	18	2	1,5,6	1.20	0	2,7,9	1.07	0
2	XCP	I	1	2	8,8,9	0.47	0	4,10,12	0.79	0
2	XPC	I	26	2	6,8,9	0.47	0	4,10,12	1.27	0
2	AIB	J	9	2	1,5,6	1.24	0	2,7,9	0.82	0
2	AIB	L	9	2	1,5,6	1.22	0	2,7,9	0.78	0
2	XCP	O	1	2	8,8,9	0.64	0	4,10,12	0.98	0
2	AIB	I	18	2	1,5,6	1.25	0	2,7,9	0.73	0
2	XCP	M	29	5,2	8,8,9	0.55	0	4,10,12	0.99	0
2	AIB	O	9	2	1,5,6	1.23	0	2,7,9	0.88	0
2	XPC	O	26	2	6,8,9	0.61	0	4,10,12	1.27	0
2	XPC	M	26	2	6,8,9	0.65	0	4,10,12	1.35	0
2	XCP	I	29	5,2	8,8,9	0.60	0	4,10,12	1.05	0
2	XPC	N	26	2	6,8,9	0.58	0	4,10,12	1.16	0
2	AIB	I	9	2	1,5,6	1.30	0	2,7,9	0.82	0
2	XCP	J	1	2	8,8,9	0.68	0	4,10,12	1.08	0
2	AIB	P	22	2	1,5,6	1.22	0	2,7,9	0.93	0
2	AIB	L	22	2	1,5,6	1.20	0	2,7,9	0.85	0
2	XCP	N	29	5,2	8,8,9	0.69	0	4,10,12	1.22	0
2	XCP	L	1	2	8,8,9	0.60	0	4,10,12	1.19	0
2	XCP	K	1	2	8,8,9	0.67	0	4,10,12	0.78	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
2	AIB	J	18	2	-	2/2/3/6	-
2	AIB	N	22	2	-	0/2/3/6	-
2	XCP	N	1	2	-	1/1/12/14	0/1/1/1
2	AIB	K	9	2	-	0/2/3/6	-
2	AIB	K	18	2	-	0/2/3/6	-
2	AIB	I	22	2	-	0/2/3/6	-
2	AIB	O	22	2	-	0/2/3/6	-
2	XPC	L	26	2	-	1/1/12/14	0/1/1/1
2	XCP	P	29	5,2	-	1/1/12/14	0/1/1/1
2	XCP	J	29	5,2	-	0/1/12/14	0/1/1/1
2	XCP	M	1	2	-	1/1/12/14	0/1/1/1
2	XPC	K	26	2	-	1/1/12/14	0/1/1/1
2	XCP	O	29	5,2	-	1/1/12/14	0/1/1/1
2	AIB	P	9	2	-	0/2/3/6	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AIB	M	18	2	-	2/2/3/6	-
2	AIB	N	9	2	-	0/2/3/6	-
2	AIB	M	9	2	-	1/2/3/6	-
2	XPC	P	26	2	-	1/1/12/14	0/1/1/1
2	AIB	N	18	2	-	0/2/3/6	-
2	AIB	K	22	2	-	0/2/3/6	-
2	AIB	J	22	2	-	0/2/3/6	-
2	XPC	J	26	2	-	1/1/12/14	0/1/1/1
2	XCP	L	29	5,2	-	1/1/12/14	0/1/1/1
2	XCP	P	1	2	-	1/1/12/14	0/1/1/1
2	AIB	L	18	2	-	0/2/3/6	-
2	AIB	M	22	2	-	0/2/3/6	-
2	AIB	P	18	2	-	2/2/3/6	-
2	XCP	K	29	5,2	-	0/1/12/14	0/1/1/1
2	AIB	O	18	2	-	0/2/3/6	-
2	XCP	I	1	2	-	1/1/12/14	0/1/1/1
2	XPC	I	26	2	-	1/1/12/14	0/1/1/1
2	AIB	J	9	2	-	0/2/3/6	-
2	AIB	L	9	2	-	0/2/3/6	-
2	XCP	O	1	2	-	1/1/12/14	0/1/1/1
2	AIB	I	18	2	-	0/2/3/6	-
2	XCP	M	29	5,2	-	1/1/12/14	0/1/1/1
2	AIB	O	9	2	-	0/2/3/6	-
2	XPC	O	26	2	-	1/1/12/14	0/1/1/1
2	XPC	M	26	2	-	1/1/12/14	0/1/1/1
2	XCP	I	29	5,2	-	1/1/12/14	0/1/1/1
2	XPC	N	26	2	-	1/1/12/14	0/1/1/1
2	AIB	I	9	2	-	0/2/3/6	-
2	XCP	J	1	2	-	0/1/12/14	0/1/1/1
2	AIB	P	22	2	-	0/2/3/6	-
2	AIB	L	22	2	-	0/2/3/6	-
2	XCP	N	29	5,2	-	1/1/12/14	0/1/1/1
2	XCP	L	1	2	-	1/1/12/14	0/1/1/1
2	XCP	K	1	2	-	1/1/12/14	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L	26	XPC	O-C-CA-CB
2	M	26	XPC	O-C-CA-CB
2	L	1	XCP	O-C-CA-CB
2	M	1	XCP	O-C-CA-CB
2	I	26	XPC	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	22	AIB	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 17 ligands modelled in this entry, 1 is monoatomic and 8 are modelled with single atom - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	EDO	E	201	-	3,3,3	0.44	0	2,2,2	0.48	0
3	EDO	K	102	-	3,3,3	0.49	0	2,2,2	0.32	0
3	EDO	C	201	-	3,3,3	0.46	0	2,2,2	0.53	0
3	EDO	B	201	-	3,3,3	0.44	0	2,2,2	0.58	0
3	EDO	N	102	-	3,3,3	0.47	0	2,2,2	0.42	0
3	EDO	C	202	-	3,3,3	0.44	0	2,2,2	0.59	0
3	EDO	A	202	-	3,3,3	0.46	0	2,2,2	0.52	0
3	EDO	A	201	-	3,3,3	0.48	0	2,2,2	0.26	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	E	201	-	-	0/1/1/1	-
3	EDO	K	102	-	-	0/1/1/1	-
3	EDO	C	201	-	-	0/1/1/1	-
3	EDO	B	201	-	-	0/1/1/1	-
3	EDO	N	102	-	-	1/1/1/1	-
3	EDO	C	202	-	-	1/1/1/1	-
3	EDO	A	202	-	-	0/1/1/1	-
3	EDO	A	201	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	N	102	EDO	O1-C1-C2-O2
3	C	202	EDO	O1-C1-C2-O2

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

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	141/158 (89%)	0.88	15 (10%) 6 4	64, 91, 133, 162	0
1	B	129/158 (81%)	0.67	11 (8%) 10 8	63, 89, 129, 176	0
1	C	138/158 (87%)	0.82	18 (13%) 3 2	68, 89, 131, 143	0
1	D	145/158 (91%)	0.83	13 (8%) 9 7	64, 89, 149, 188	0
1	E	136/158 (86%)	0.80	17 (12%) 3 3	68, 95, 133, 155	0
1	F	138/158 (87%)	0.62	11 (7%) 12 10	64, 90, 125, 148	0
1	G	138/158 (87%)	0.77	7 (5%) 28 26	67, 96, 138, 158	0
1	H	131/158 (82%)	0.88	16 (12%) 4 3	69, 94, 130, 172	0
2	I	23/29 (79%)	0.53	1 (4%) 35 33	63, 76, 119, 125	0
2	J	23/29 (79%)	0.48	0 100 100	65, 71, 85, 89	0
2	K	23/29 (79%)	0.38	0 100 100	64, 73, 102, 116	0
2	L	23/29 (79%)	0.36	1 (4%) 35 33	61, 71, 92, 99	0
2	M	23/29 (79%)	1.06	5 (21%) 0 0	69, 81, 123, 148	0
2	N	23/29 (79%)	0.33	1 (4%) 35 33	60, 66, 76, 83	0
2	O	23/29 (79%)	0.63	3 (13%) 3 2	67, 72, 99, 115	0
2	P	23/29 (79%)	0.47	1 (4%) 35 33	71, 90, 116, 133	0
All	All	1280/1496 (85%)	0.75	120 (9%) 8 6	60, 90, 132, 188	0

The worst 5 of 120 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	72	THR	7.7
1	A	86	SER	5.3
1	E	73	HIS	5.3
1	D	34	ASN	5.0
1	H	29	LEU	4.8

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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
2	XCP	K	29	8/9	0.77	0.23	94,101,121,121	0
2	XPC	M	26	8/9	0.86	0.21	76,78,91,92	0
2	XCP	O	29	8/9	0.86	0.27	75,90,99,101	0
2	XCP	M	29	8/9	0.87	0.27	78,90,108,108	0
2	XCP	I	29	8/9	0.88	0.29	67,79,91,92	0
2	XCP	L	29	8/9	0.88	0.21	94,101,117,117	0
2	XCP	J	1	8/9	0.89	0.25	73,95,114,114	0
2	XPC	K	26	8/9	0.89	0.14	67,77,88,96	0
2	XCP	P	29	8/9	0.90	0.20	72,84,90,90	0
2	AIB	K	18	6/7	0.91	0.21	80,91,109,109	0
2	XCP	L	1	8/9	0.92	0.23	62,77,86,86	0
2	XCP	K	1	8/9	0.92	0.26	63,80,87,87	0
2	XCP	N	29	8/9	0.92	0.20	61,68,80,82	0
2	AIB	M	18	6/7	0.92	0.32	131,144,163,173	0
2	AIB	P	18	6/7	0.92	0.20	117,124,149,149	0
2	XCP	O	1	8/9	0.93	0.26	67,86,95,95	0
2	XCP	P	1	8/9	0.93	0.27	67,91,105,105	0
2	AIB	O	22	6/7	0.93	0.23	66,74,86,90	0
2	XCP	M	1	8/9	0.93	0.17	66,79,88,88	0
2	AIB	P	22	6/7	0.94	0.21	92,106,127,127	0
2	XPC	J	26	8/9	0.94	0.21	60,65,79,79	0
2	AIB	O	18	6/7	0.94	0.27	74,86,103,103	0
2	XCP	I	1	8/9	0.94	0.20	54,81,88,90	0
2	XPC	N	26	8/9	0.94	0.15	62,69,81,87	0
2	AIB	I	18	6/7	0.94	0.17	108,121,145,145	0
2	XCP	N	1	8/9	0.95	0.35	70,88,121,121	0
2	XPC	I	26	8/9	0.95	0.13	72,77,91,93	0
2	AIB	O	9	6/7	0.95	0.24	69,73,88,88	0
2	AIB	I	22	6/7	0.95	0.28	79,97,114,116	0
2	AIB	N	22	6/7	0.95	0.23	57,72,79,86	0
2	AIB	P	9	6/7	0.95	0.16	92,99,115,115	0
2	XPC	O	26	8/9	0.95	0.17	68,73,87,88	0
2	AIB	I	9	6/7	0.96	0.12	73,82,93,93	0
2	XCP	J	29	8/9	0.96	0.18	65,79,84,84	0
2	AIB	L	18	6/7	0.96	0.18	83,90,108,108	0
2	XPC	L	26	8/9	0.96	0.13	68,76,90,92	0
2	AIB	K	9	6/7	0.96	0.22	66,76,92,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	AIB	L	9	6/7	0.96	0.18	64,71,85,85	0
2	AIB	J	18	6/7	0.96	0.22	71,81,98,98	0
2	XPC	P	26	8/9	0.96	0.12	78,83,100,101	0
2	AIB	M	9	6/7	0.97	0.20	78,91,108,108	0
2	AIB	N	9	6/7	0.97	0.24	56,67,82,82	0
2	AIB	J	9	6/7	0.97	0.20	65,71,86,86	0
2	AIB	K	22	6/7	0.97	0.19	65,72,81,87	0
2	AIB	M	22	6/7	0.97	0.24	82,92,110,111	0
2	AIB	N	18	6/7	0.97	0.19	66,78,94,94	0
2	AIB	J	22	6/7	0.98	0.22	64,71,84,84	0
2	AIB	L	22	6/7	0.98	0.23	69,79,90,95	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	EDO	C	202	4/4	0.75	0.36	88,107,117,129	0
3	EDO	E	201	4/4	0.76	0.20	92,111,123,140	0
3	EDO	K	102	4/4	0.81	0.18	74,89,94,106	0
3	EDO	A	202	4/4	0.83	0.21	105,126,145,155	0
3	EDO	C	201	4/4	0.85	0.32	73,88,107,107	0
3	EDO	A	201	4/4	0.85	0.34	77,95,114,114	0
5	NH2	M	101	1/1	0.85	0.60	84,84,84,84	0
5	NH2	O	101	1/1	0.85	0.17	97,97,97,97	0
5	NH2	L	101	1/1	0.86	1.52	113,113,113,113	0
3	EDO	B	201	4/4	0.87	0.24	69,84,91,91	0
4	K	H	201	1/1	0.89	0.15	108,108,108,108	0
3	EDO	N	102	4/4	0.89	0.19	81,97,113,113	0
5	NH2	K	101	1/1	0.92	0.55	93,93,93,93	0
5	NH2	J	101	1/1	0.94	0.14	67,67,67,67	0
5	NH2	P	101	1/1	0.94	0.25	74,74,74,74	0
5	NH2	I	101	1/1	0.98	0.34	73,73,73,73	0
5	NH2	N	101	1/1	0.98	0.04	66,66,66,66	0

6.5 Other polymers (i)

There are no such residues in this entry.