



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 9, 2020 – 03:03 PM GMT

PDB ID : 6TDB
Title : Neuropilin2-b1 domain in a complex with the C-terminal VEGFB167 peptide
Authors : Eldrid, C.; Yu, L.; Yelland, T.; Fotinou, C.; Djordjevic, S.
Deposited on : 2019-11-08
Resolution : 2.45 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.14.6
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) : 2.14.6

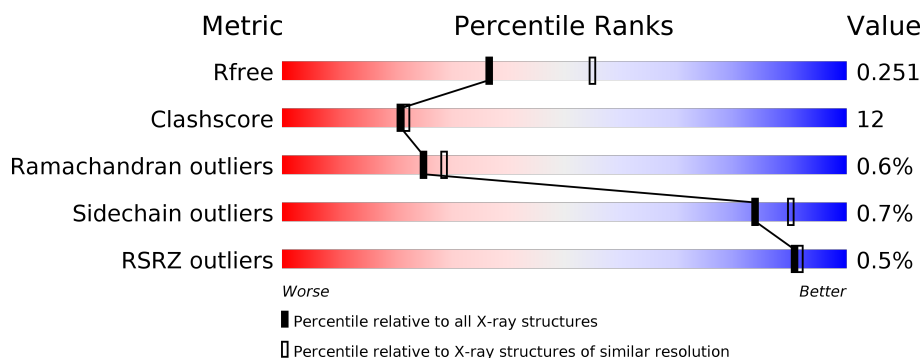
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	162	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 76%, yellow 22%, grey 1%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 76% 22% • </div> </div>
1	B	162	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 79%, yellow 17%, grey 4%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 79% 17% • • </div> </div>
1	C	162	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 72%, yellow 24%, grey 4%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 72% 24% • • </div> </div>
1	D	162	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 73%, yellow 25%, grey 1%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 73% 25% • • </div> </div>
2	F	5	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 40%, yellow 40%, orange 20%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 40% 40% 20% </div> </div>
2	J	5	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 40%, grey 60%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 40% 60% </div> </div>

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Mol	Chain	Length	Quality of chain
2	K	5	<div>20% 40% 40%</div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ACE	F	301	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5469 atoms, of which 18 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 Neuropilin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	158	Total	C	N	O	S	1	2	0
			1287	804	240	237	6			
1	B	157	Total	C	N	O	S	0	1	0
			1264	791	230	237	6			
1	C	157	Total	C	N	O	S	0	1	0
			1260	788	231	235	6			
1	D	159	Total	C	N	O	S	0	0	0
			1254	784	229	235	6			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	272	GLY	-	expression tag	UNP O60462
A	273	HIS	-	expression tag	UNP O60462
A	274	MET	-	expression tag	UNP O60462
A	431	SER	-	expression tag	UNP O60462
A	432	GLY	-	expression tag	UNP O60462
A	433	SER	-	expression tag	UNP O60462
B	272	GLY	-	expression tag	UNP O60462
B	273	HIS	-	expression tag	UNP O60462
B	274	MET	-	expression tag	UNP O60462
B	431	SER	-	expression tag	UNP O60462
B	432	GLY	-	expression tag	UNP O60462
B	433	SER	-	expression tag	UNP O60462
C	272	GLY	-	expression tag	UNP O60462
C	273	HIS	-	expression tag	UNP O60462
C	274	MET	-	expression tag	UNP O60462
C	431	SER	-	expression tag	UNP O60462
C	432	GLY	-	expression tag	UNP O60462
C	433	SER	-	expression tag	UNP O60462
D	272	GLY	-	expression tag	UNP O60462
D	273	HIS	-	expression tag	UNP O60462
D	274	MET	-	expression tag	UNP O60462

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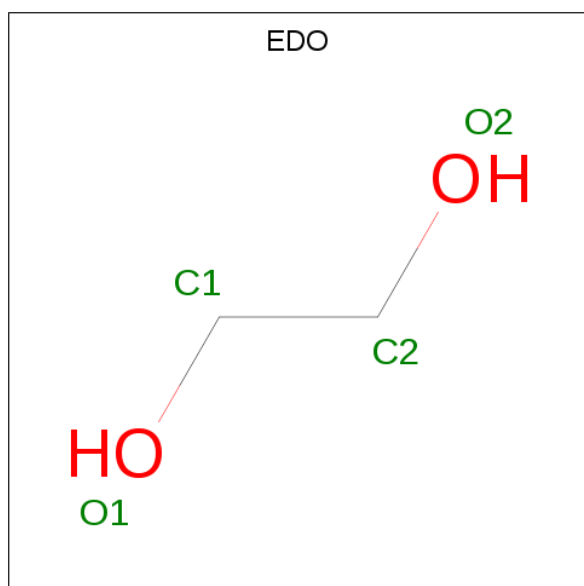
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Chain	Residue	Modelled	Actual	Comment	Reference
D	431	SER	-	expression tag	UNP O60462
D	432	GLY	-	expression tag	UNP O60462
D	433	SER	-	expression tag	UNP O60462

- Molecule 2 is a protein called C-terminal VEGFB167 peptide.

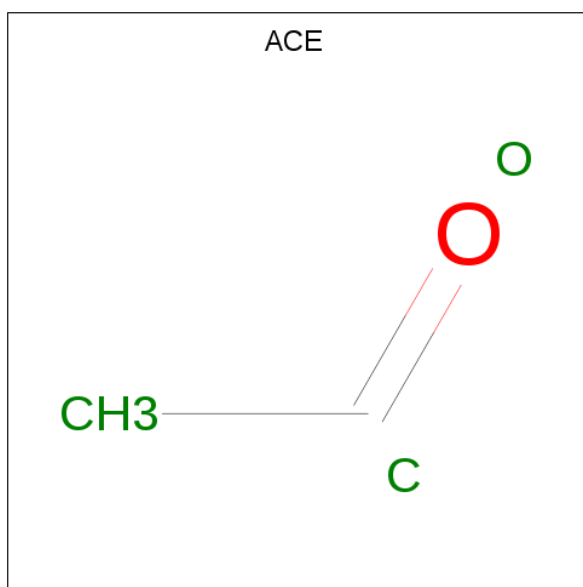
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	F	5	Total	C	N	O	0	0	0
			51	30	15	6			
2	J	2	Total	C	N	O	0	0	0
			17	9	5	3			
2	K	3	Total	C	N	O	0	0	0
			23	13	6	4			

- 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	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		

- Molecule 4 is ACETYL GROUP (three-letter code: ACE) (formula: C_2H_4O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	F	1	Total	C	O	0	0
			3	2	1		

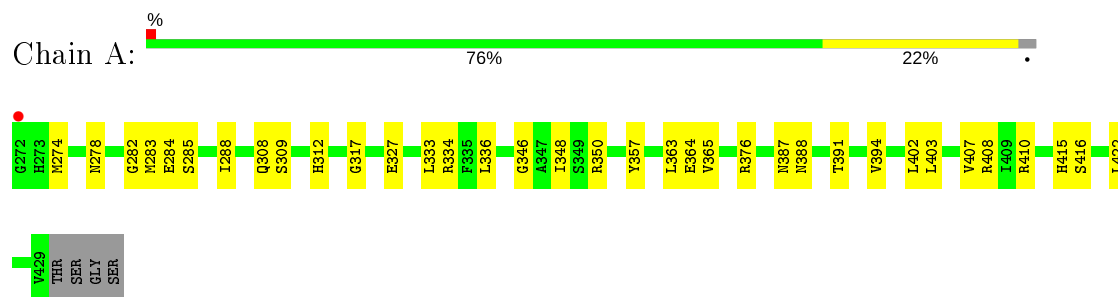
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	87	Total	O	0	1
			88	88		
5	B	84	Total	O	0	1
			85	85		
5	C	47	Total	O	0	1
			48	48		
5	D	55	Total	O	0	0
			55	55		
5	F	2	Total	O	0	0
			2	2		
5	K	2	Total	O	0	0
			2	2		

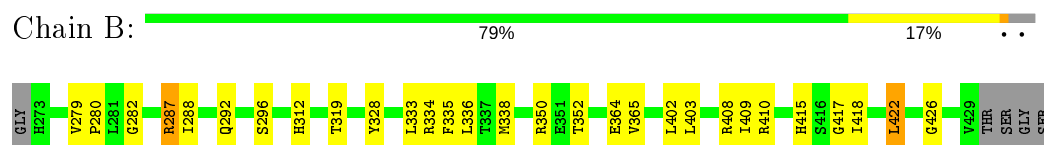
3 Residue-property plots

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.

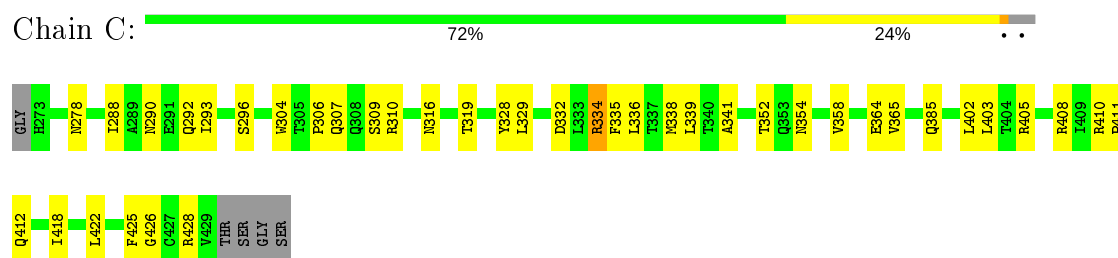
• Molecule 1: Neuropilin-2



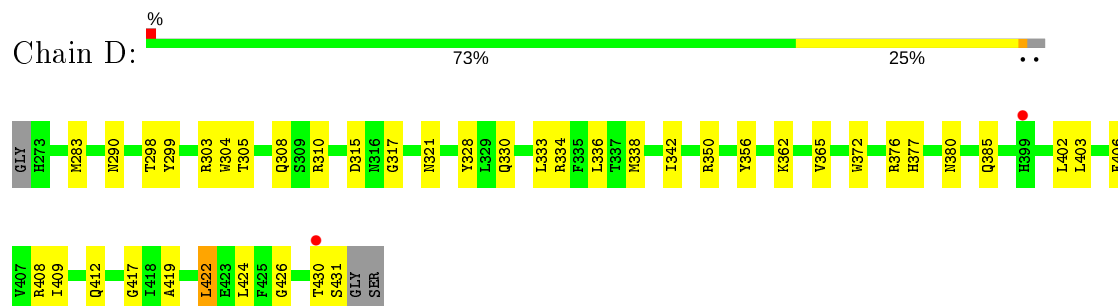
• Molecule 1: Neuropilin-2



• Molecule 1: Neuropilin-2

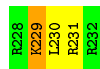


• Molecule 1: Neuropilin-2



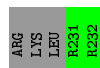
- Molecule 2: C-terminal VEGFB167 peptide

Chain F:  40% 40% 20%

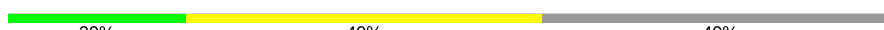


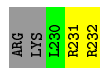
- Molecule 2: C-terminal VEGFB167 peptide

Chain J:  40% 60%



- Molecule 2: C-terminal VEGFB167 peptide

Chain K:  20% 40% 40%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	107.36Å 140.12Å 74.36Å 90.00° 132.97° 90.00°	Depositor
Resolution (Å)	70.06 – 2.45 70.06 – 2.45	Depositor EDS
% Data completeness (in resolution range)	98.8 (70.06-2.45) 98.9 (70.06-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.45Å)	Xtriage
Refinement program	REFMAC 1.14_3260, PHENIX 1.14_3260	Depositor
R, R_{free}	0.183 , 0.250 0.196 , 0.251	Depositor DCC
R_{free} test set	1428 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.157	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 49.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.029 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5469	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.97% 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, ACE

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	0.31	0/1319	0.52	0/1785
1	B	0.30	0/1293	0.52	0/1754
1	C	0.29	0/1292	0.50	0/1753
1	D	0.28	0/1283	0.50	0/1742
2	F	0.29	0/50	0.44	0/61
2	J	0.19	0/16	0.34	0/18
2	K	0.48	0/22	0.69	0/26
All	All	0.29	0/5275	0.51	0/7139

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	1287	0	1253	30	0
1	B	1264	0	1212	28	0
1	C	1260	0	1209	33	0
1	D	1254	0	1188	38	0
2	F	51	0	62	5	0
2	J	17	0	14	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	23	0	18	4	0
3	A	4	6	6	0	0
3	B	4	6	6	0	0
3	C	4	6	6	2	0
4	F	3	0	3	2	0
5	A	88	0	0	6	0
5	B	85	0	0	3	0
5	C	48	0	0	0	0
5	D	55	0	0	1	0
5	F	2	0	0	0	0
5	K	2	0	0	0	0
All	All	5451	18	4977	124	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 12.

The worst 5 of 124 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:A:282:GLY:HA3	1:A:288:ILE:HG13	1.53	0.88
2:F:229:LYS:H	4:F:301:ACE:H2	1.44	0.81
1:C:365:VAL:HG21	1:C:402:LEU:HD21	1.65	0.77
1:C:336:LEU:HD22	1:C:403:LEU:HG	1.66	0.76
1:B:292:GLN:HG2	1:B:334:ARG:HE	1.55	0.71

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	158/162 (98%)	146 (92%)	10 (6%)	2 (1%)	12 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	156/162 (96%)	146 (94%)	10 (6%)	0	100	100
1	C	156/162 (96%)	146 (94%)	10 (6%)	0	100	100
1	D	157/162 (97%)	145 (92%)	12 (8%)	0	100	100
2	F	3/5 (60%)	2 (67%)	0	1 (33%)	0	0
2	K	1/5 (20%)	0	0	1 (100%)	0	0
All	All	631/658 (96%)	585 (93%)	42 (7%)	4 (1%)	25	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	285	SER
2	F	229	LYS
2	K	231	ARG
1	A	278	ASN

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	139/140 (99%)	139 (100%)	0	100	100
1	B	136/140 (97%)	134 (98%)	2 (2%)	65	76
1	C	135/140 (96%)	134 (99%)	1 (1%)	84	90
1	D	132/140 (94%)	131 (99%)	1 (1%)	81	88
2	F	5/5 (100%)	5 (100%)	0	100	100
2	J	1/5 (20%)	1 (100%)	0	100	100
2	K	1/5 (20%)	1 (100%)	0	100	100
All	All	549/575 (96%)	545 (99%)	4 (1%)	84	90

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	287	ARG
1	B	422	LEU
1	C	334	ARG
1	D	422	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	353	GLN
1	D	399	HIS
1	D	354	ASN
1	C	377	HIS
1	D	377	HIS

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 monosaccharides 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	$\# Z > 2$
4	ACE	F	301	2	1,2,2	0.81	0	1,1,1	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	C	501	-	3,3,3	0.56	0	2,2,2	0.15	0
3	EDO	A	501	-	3,3,3	0.46	0	2,2,2	0.30	0
3	EDO	B	501	-	3,3,3	0.53	0	2,2,2	0.19	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	C	501	-	-	1/1/1/1	-
3	EDO	A	501	-	-	0/1/1/1	-
3	EDO	B	501	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	501	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	301	ACE	2	0
3	C	501	EDO	2	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	158/162 (97%)	0.00	1 (0%) 89 89	33, 42, 57, 85	1 (0%)
1	B	157/162 (96%)	-0.13	0 100 100	31, 43, 59, 87	0
1	C	157/162 (96%)	-0.01	0 100 100	36, 47, 64, 85	0
1	D	159/162 (98%)	0.04	2 (1%) 77 76	40, 52, 71, 93	0
2	F	5/5 (100%)	0.42	0 100 100	57, 58, 69, 70	0
2	J	2/5 (40%)	1.98	0 100 100	67, 67, 67, 77	1 (50%)
2	K	3/5 (60%)	1.23	0 100 100	74, 74, 86, 87	0
All	All	641/663 (96%)	-0.01	3 (0%) 91 92	31, 46, 69, 93	2 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	272	GLY	3.7
1	D	430	THR	2.6
1	D	399	HIS	2.2

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 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
4	ACE	F	301	3/3	0.69	0.23	47,47,51,61	0
3	EDO	C	501	4/4	0.71	0.21	48,61,78,78	0
3	EDO	B	501	4/4	0.82	0.21	43,52,56,61	0
3	EDO	A	501	4/4	0.96	0.19	47,56,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.