



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 09:43 PM GMT

PDB ID : 3B8R
Title : Crystal structure of the VEGFR2 kinase domain in complex with a naphthamide inhibitor
Authors : Whittington, D.A.; Long, A.M.; Gu, Y.; Zhao, H.
Deposited on : 2007-11-01
Resolution : 2.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

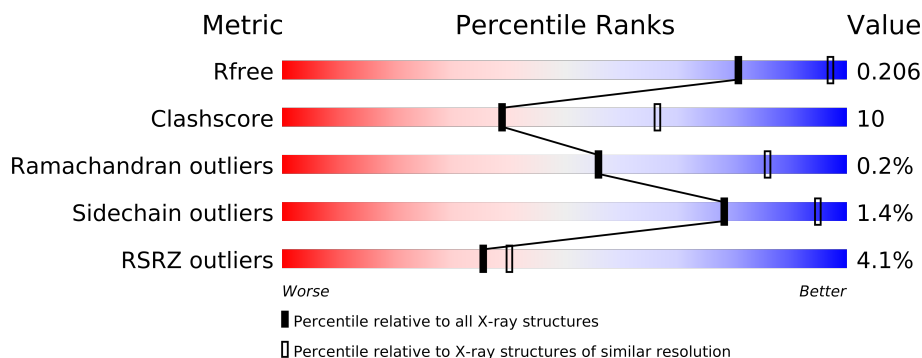
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance



The reported resolution of this entry is 2.70 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}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	314	
1	B	314	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4663 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

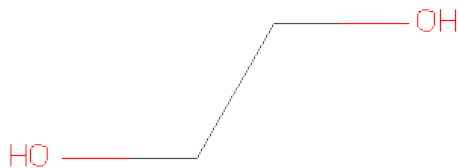
- Molecule 1 is a protein called Vascular endothelial growth factor receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	0	0
			2337	1498	410	413	16			
1	B	267	Total	C	N	O	S	0	0	0
			2148	1385	369	378	16			

There are 20 discrepancies between the modelled and reference sequences:

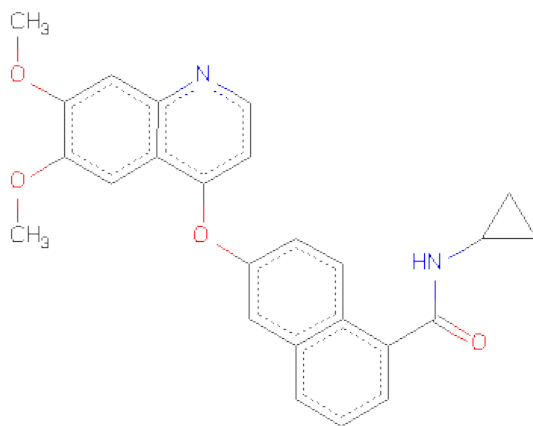
Chain	Residue	Modelled	Actual	Comment	Reference
A	817	ALA	CYS	ENGINEERED	UNP P35968
A	916	THR	VAL	ENGINEERED	UNP P35968
A	990	VAL	GLU	ENGINEERED	UNP P35968
A	1172	ARG	-	EXPRESSION TAG	UNP P35968
A	1173	HIS	-	EXPRESSION TAG	UNP P35968
A	1174	HIS	-	EXPRESSION TAG	UNP P35968
A	1175	HIS	-	EXPRESSION TAG	UNP P35968
A	1176	HIS	-	EXPRESSION TAG	UNP P35968
A	1177	HIS	-	EXPRESSION TAG	UNP P35968
A	1178	HIS	-	EXPRESSION TAG	UNP P35968
B	817	ALA	CYS	ENGINEERED	UNP P35968
B	916	THR	VAL	ENGINEERED	UNP P35968
B	990	VAL	GLU	ENGINEERED	UNP P35968
B	1172	ARG	-	EXPRESSION TAG	UNP P35968
B	1173	HIS	-	EXPRESSION TAG	UNP P35968
B	1174	HIS	-	EXPRESSION TAG	UNP P35968
B	1175	HIS	-	EXPRESSION TAG	UNP P35968
B	1176	HIS	-	EXPRESSION TAG	UNP P35968
B	1177	HIS	-	EXPRESSION TAG	UNP P35968
B	1178	HIS	-	EXPRESSION TAG	UNP P35968

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

- Molecule 3 is N-CYCLOPROPYL-6-[(6,7-DIMETHOXYQUINOLIN-4-YL)OXY]NAPHTH ALENE-1-CARBOXAMIDE (three-letter code: 887) (formula: C₂₅H₂₂N₂O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			31	25	2	4		
3	B	1	Total	C	N	O	0	0
			31	25	2	4		

- Molecule 4 is water.

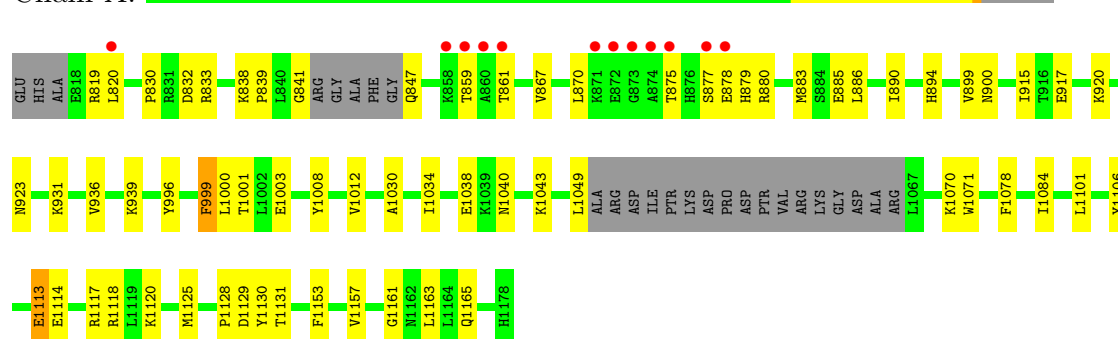
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	84	Total 84	O 84	0	0
4	B	28	Total 28	O 28	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

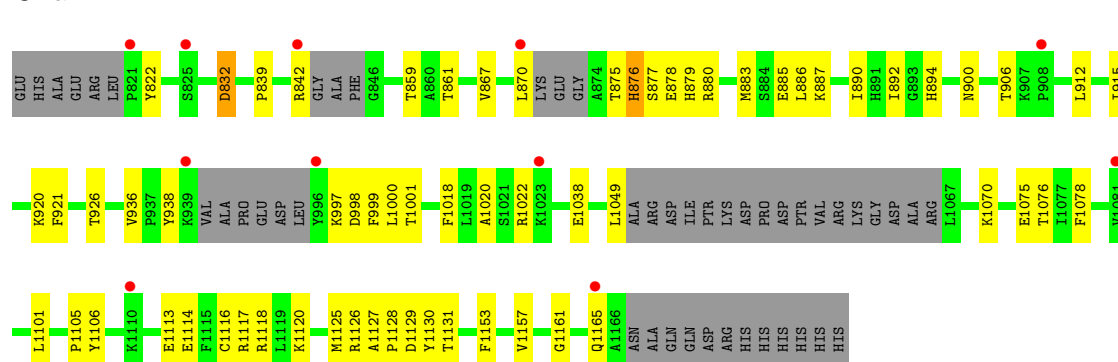
- Molecule 1: Vascular endothelial growth factor receptor 2

Chain A:



- Molecule 1: Vascular endothelial growth factor receptor 2

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.44Å 67.97Å 87.69Å 90.00° 91.36° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 29.22 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.7 (30.00-2.70) 98.3 (29.22-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.68Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.204 , 0.259 0.208 , 0.206	Depositor DCC
R_{free} test set	1401 reflections (8.50%)	DCC
Wilson B-factor (Å ²)	26.1	Xtriage
Anisotropy	0.470	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 19.9	EDS
Estimated twinning fraction	0.026 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 17888 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4663	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.05% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 887, EDO

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	0.37	0/2397	0.62	0/3239
1	B	0.38	0/2199	0.66	1/2966 (0.0%)
All	All	0.37	0/4596	0.64	1/6205 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	997	LYS	N-CA-CB	5.47	120.44	110.60

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2337	0	2326	48	0
1	B	2148	0	2161	42	0
2	A	4	0	6	1	0
3	A	31	0	22	1	0
3	B	31	0	22	0	0
4	A	84	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	28	0	0	1	0
All	All	4663	0	4537	88	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 10.

All (88) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:875:THR:HG22	1:B:877:SER:H	1.19	1.01
1:A:875:THR:HG22	1:A:877:SER:H	1.29	0.97
1:B:839:PRO:HG2	1:B:842:ARG:HH11	1.33	0.92
1:A:870:LEU:HD11	1:A:879:HIS:HA	1.68	0.75
1:B:1128:PRO:HG2	1:B:1131:THR:HB	1.71	0.72
1:B:1153:PHE:O	1:B:1157:VAL:HG23	1.91	0.69
1:B:1114:GLU:HG3	1:B:1118:ARG:NH2	2.09	0.67
1:A:1128:PRO:HG2	1:A:1131:THR:HB	1.77	0.65
1:A:841:GLY:O	1:A:847:GLN:HB2	1.96	0.65
1:B:875:THR:HG22	1:B:877:SER:N	2.03	0.64
1:B:936:VAL:HG22	1:B:999:PHE:HD2	1.63	0.63
1:B:876:HIS:O	1:B:880:ARG:HG2	1.97	0.63
1:A:886:LEU:O	1:A:890:ILE:HG13	1.98	0.62
1:A:894:HIS:ND1	1:A:900:ASN:OD1	2.35	0.59
1:A:936:VAL:HG22	1:A:999:PHE:HD2	1.68	0.59
1:A:1078:PHE:CE2	1:A:1120:LYS:HG3	2.37	0.59
1:B:1161:GLY:O	1:B:1165:GLN:HG2	2.03	0.59
1:B:926:THR:HB	4:B:1204:HOH:O	2.03	0.58
1:A:1161:GLY:O	1:A:1165:GLN:HG2	2.03	0.58
1:A:875:THR:HG22	1:A:877:SER:N	2.09	0.57
1:B:936:VAL:CG2	1:B:999:PHE:HD2	2.18	0.57
1:A:939:LYS:HE2	1:A:996:TYR:HB2	1.88	0.56
1:B:839:PRO:HG2	1:B:842:ARG:NH1	2.12	0.55
1:B:1078:PHE:CE2	1:B:1120:LYS:HG3	2.41	0.55
1:B:1106:TYR:CE1	1:B:1125:MET:HG3	2.42	0.54
1:A:1114:GLU:HG3	1:A:1118:ARG:NH2	2.23	0.54
1:B:936:VAL:O	1:B:1001:THR:HA	2.09	0.52
1:A:859:THR:O	1:A:861:THR:HG23	2.09	0.52
1:B:1070:LYS:HD3	1:B:1105:PRO:HG2	1.93	0.51
1:B:859:THR:O	1:B:861:THR:HG23	2.09	0.51
1:A:936:VAL:O	1:A:1001:THR:HA	2.11	0.51
1:B:1078:PHE:CZ	1:B:1116:CYS:HB3	2.46	0.51
1:B:886:LEU:O	1:B:890:ILE:HG13	2.11	0.51
1:A:1129:ASP:H	2:A:301:EDO:H21	1.77	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1153:PHE:O	1:A:1157:VAL:HG23	2.13	0.48
1:A:1008:TYR:OH	1:A:1040:ASN:ND2	2.47	0.48
1:A:875:THR:C	1:A:877:SER:H	2.16	0.47
1:A:1114:GLU:OE1	1:A:1117:ARG:NH2	2.47	0.47
1:A:899:VAL:O	1:A:899:VAL:HG13	2.14	0.47
1:A:830:PRO:HA	4:A:1228:HOH:O	2.14	0.47
1:A:1120:LYS:NZ	1:B:1129:ASP:OD2	2.48	0.47
1:A:923:ASN:HA	1:A:1034:ILE:O	2.14	0.47
1:B:1127:ALA:HB1	1:B:1131:THR:HG21	1.95	0.47
1:A:885:GLU:HG2	3:A:201:887:H43	1.79	0.46
1:A:1070:LYS:HB2	1:A:1071:TRP:CE3	2.50	0.46
1:A:875:THR:N	1:A:878:GLU:OE2	2.49	0.46
1:A:1003:GLU:OE1	4:A:1248:HOH:O	2.21	0.45
1:B:870:LEU:HD11	1:B:879:HIS:HA	1.98	0.45
1:B:906:THR:HG22	1:B:912:LEU:CD1	2.47	0.45
1:B:875:THR:N	1:B:878:GLU:OE2	2.47	0.45
1:B:1000:LEU:HA	1:B:1000:LEU:HD23	1.87	0.44
1:A:819:ARG:HG3	1:A:820:LEU:N	2.33	0.44
1:B:906:THR:HG22	1:B:912:LEU:HD11	1.99	0.44
1:A:1113:GLU:HB3	1:B:1126:ARG:CZ	2.48	0.44
1:B:920:LYS:HE3	1:B:921:PHE:CZ	2.53	0.44
1:A:880:ARG:HA	1:A:883:MET:HB2	2.00	0.43
1:A:875:THR:C	1:A:877:SER:N	2.72	0.43
1:A:885:GLU:HG3	1:A:1049:LEU:HD21	2.00	0.43
1:A:1106:TYR:CE1	1:A:1125:MET:HG3	2.53	0.43
1:A:1163:LEU:HA	1:A:1163:LEU:HD23	1.79	0.43
1:A:939:LYS:HE2	1:A:996:TYR:CB	2.49	0.43
1:B:880:ARG:HA	1:B:883:MET:HB2	2.00	0.43
1:B:1075:GLU:HG2	1:B:1076:THR:N	2.34	0.43
1:A:1101:LEU:HD12	1:A:1130:TYR:CZ	2.54	0.43
1:B:832:ASP:N	1:B:832:ASP:OD1	2.50	0.43
1:A:867:VAL:HG22	1:A:915:ILE:HG23	2.01	0.42
1:A:838:LYS:HA	1:A:839:PRO:HD3	1.83	0.42
1:B:1117:ARG:O	1:B:1120:LYS:HB2	2.19	0.42
1:B:883:MET:O	1:B:886:LEU:HB3	2.20	0.42
1:A:1120:LYS:HE2	1:A:1120:LYS:HB3	1.83	0.42
1:B:938:TYR:C	1:B:938:TYR:CD1	2.93	0.42
1:A:996:TYR:O	1:A:999:PHE:HB2	2.20	0.42
1:B:892:ILE:CG2	1:B:1018:PHE:HE2	2.33	0.41
1:B:920:LYS:HE2	1:B:1038:GLU:CD	2.41	0.41
1:A:1008:TYR:O	1:A:1012:VAL:HG23	2.20	0.41
1:B:885:GLU:HG3	1:B:1049:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:883:MET:HE3	1:B:887:LYS:HE3	2.03	0.41
1:A:830:PRO:O	1:A:833:ARG:HB2	2.21	0.41
1:B:867:VAL:HG22	1:B:915:ILE:HG23	2.03	0.41
1:A:1084:ILE:HG13	4:A:1220:HOH:O	2.19	0.41
1:B:894:HIS:ND1	1:B:900:ASN:OD1	2.54	0.41
1:A:830:PRO:HB2	1:A:833:ARG:HG2	2.03	0.41
1:A:931:LYS:HB2	1:A:1000:LEU:HD12	2.03	0.41
1:A:920:LYS:HE2	1:A:1038:GLU:CD	2.41	0.41
1:B:1020:ALA:C	1:B:1022:ARG:H	2.22	0.41
1:A:917:GLU:OE1	1:A:1043:LYS:HE3	2.21	0.40
1:A:1030:ALA:HB2	1:A:1071:TRP:CD1	2.56	0.40
1:B:1101:LEU:HD12	1:B:1130:TYR:CZ	2.56	0.40

There are no symmetry-related clashes.

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	283/314 (90%)	272 (96%)	11 (4%)	0	100	100
1	B	257/314 (82%)	245 (95%)	11 (4%)	1 (0%)	43	76
All	All	540/628 (86%)	517 (96%)	22 (4%)	1 (0%)	56	86

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	822	TYR

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	254/270 (94%)	251 (99%)	3 (1%)	82	96
1	B	234/270 (87%)	230 (98%)	4 (2%)	73	94
All	All	488/540 (90%)	481 (99%)	7 (1%)	78	95

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	832	ASP
1	A	999	PHE
1	A	1113	GLU
1	B	832	ASP
1	B	876	HIS
1	B	998	ASP
1	B	1113	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	847	GLN
1	A	891	HIS
1	A	933	ASN
1	A	1040	ASN
1	A	1165	GLN
1	B	847	GLN
1	B	933	ASN
1	B	1040	ASN
1	B	1165	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

3 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	887	A	201	-	35,35,35	2.08	14 (40%)	50,50,50	2.83	9 (18%)
2	EDO	A	301	-	3,3,3	0.79	0	2,2,2	0.63	0
3	887	B	202	-	35,35,35	1.98	11 (31%)	50,50,50	2.96	8 (16%)

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	887	A	201	-	-	0/16/18/18	0/0/5/5
2	EDO	A	301	-	-	0/1/1/1	0/0/0/0
3	887	B	202	-	-	0/16/18/18	0/0/5/5

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	202	887	C29-C28	4.51	1.44	1.36
3	A	201	887	O32-C27	4.18	1.43	1.37
3	A	201	887	C29-C28	4.15	1.44	1.36
3	A	201	887	C26-C27	4.09	1.44	1.36
3	A	201	887	C2-C1	3.93	1.44	1.37
3	B	202	887	C26-C27	3.85	1.43	1.36
3	B	202	887	O32-C27	3.59	1.42	1.37
3	B	202	887	C12-C13	3.56	1.44	1.37
3	B	202	887	C2-C1	3.45	1.43	1.37
3	A	201	887	O33-C28	3.20	1.42	1.37
3	B	202	887	O33-C28	2.79	1.41	1.37
3	A	201	887	C12-C13	2.68	1.42	1.37
3	B	202	887	C23-C18	2.56	1.44	1.38
3	A	201	887	C13-C4	2.57	1.47	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	201	887	C23-C18	2.56	1.44	1.38
3	A	201	887	C11-C10	2.50	1.42	1.36
3	A	201	887	C5-C6	2.49	1.41	1.36
3	A	201	887	C22-N21	2.47	1.37	1.32
3	B	202	887	C5-C6	2.35	1.41	1.36
3	A	201	887	C6-C1	2.24	1.43	1.38
3	A	201	887	C4-C3	2.11	1.46	1.42
3	B	202	887	C27-C28	2.10	1.45	1.40
3	A	201	887	C42-N43	2.09	1.38	1.34
3	B	202	887	C11-C10	2.08	1.41	1.36
3	B	202	887	C6-C1	2.02	1.42	1.38

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	202	887	C46-C44-N43	-15.04	101.06	118.23
3	A	201	887	C46-C44-N43	-13.98	102.27	118.23
3	B	202	887	O32-C27-C26	-7.43	115.89	125.25
3	A	201	887	O32-C27-C26	-6.92	116.53	125.25
3	B	202	887	O32-C27-C28	6.33	124.60	115.42
3	A	201	887	O32-C27-C28	6.00	124.13	115.42
3	B	202	887	C29-C20-N21	4.61	122.06	117.86
3	A	201	887	C29-C20-N21	4.61	122.05	117.86
3	A	201	887	C47-C44-N43	4.31	123.15	118.23
3	B	202	887	C47-C44-N43	4.22	123.05	118.23
3	A	201	887	C19-C20-N21	-4.09	118.64	122.91
3	B	202	887	C19-C20-N21	-4.04	118.69	122.91
3	B	202	887	C22-N21-C20	3.52	121.90	116.94
3	A	201	887	C22-N21-C20	3.48	121.85	116.94
3	A	201	887	C28-C29-C20	2.32	122.06	120.19
3	B	202	887	O33-C28-C27	2.02	118.35	115.42
3	A	201	887	C4-C13-C42	2.01	123.52	120.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	289/314 (92%)	-0.33	12 (4%) 35 39	5, 17, 53, 70	0
1	B	267/314 (85%)	0.09	11 (4%) 35 40	12, 31, 64, 79	0
All	All	556/628 (88%)	-0.13	23 (4%) 35 40	5, 24, 62, 79	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	996	TYR	5.8
1	A	859	THR	5.5
1	A	858	LYS	5.4
1	B	1165	GLN	3.6
1	A	860	ALA	3.5
1	B	1023	LYS	3.4
1	A	871	LYS	3.3
1	B	842	ARG	3.2
1	A	873	GLY	3.2
1	A	874	ALA	3.1
1	A	875	THR	3.1
1	B	825	SER	2.8
1	A	877	SER	2.7
1	B	1110	LYS	2.6
1	B	939	LYS	2.6
1	B	1081	VAL	2.6
1	A	872	GLU	2.4
1	A	820	LEU	2.2
1	B	821	PRO	2.1
1	A	861	THR	2.1
1	A	878	GLU	2.1
1	B	908	PRO	2.1
1	B	870	LEU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	EDO	A	301	4/4	0.12	0.87	13,19,20,21	0
3	887	A	201	31/31	0.15	0.46	6,14,20,21	0
3	887	B	202	31/31	0.13	-0.27	13,18,30,31	0

6.5 Other polymers ⓘ

There are no such residues in this entry.