



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 19, 2026 – 06:53 AM UTC

PDB ID : 7PGI / pdb_00007pgi
Title : NaVAb1p (bicelles)
Authors : Lolicato, M.; Arrigoni, C.
Deposited on : 2021-08-14
Resolution : 3.64 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

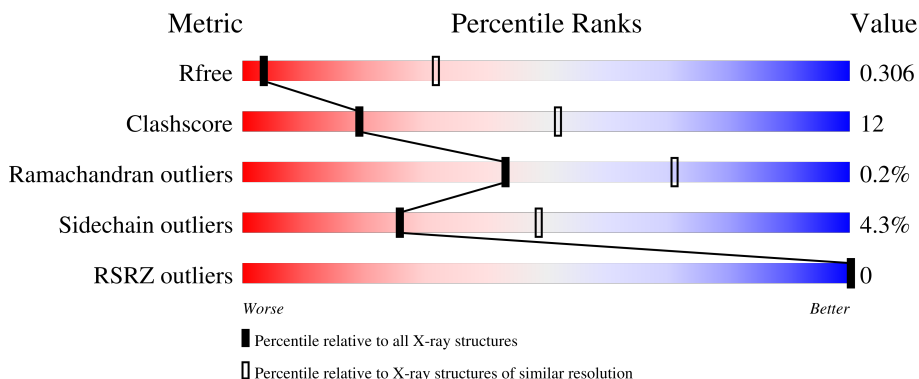
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.64 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	1132 (3.76-3.52)
Clashscore	190562	1014 (3.74-3.54)
Ramachandran outliers	187476	1123 (3.76-3.52)
Sidechain outliers	187428	1121 (3.76-3.52)
RSRZ outliers	180081	1130 (3.76-3.52)

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	150	71% 23% ...
1	B	150	71% 26% ..
1	C	150	71% 25% ..
1	D	150	75% 20% ..
1	E	150	73% 23% ..

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Mol	Chain	Length	Quality of chain
1	F	150	 69% 25% . .
1	G	150	 67% 29% . .
1	H	150	 69% 26% . .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9286 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	146	1158	762	183	202	11	0	0	0
1	B	146	1165	770	184	200	11	0	1	0
1	C	146	1154	760	183	200	11	0	0	0
1	D	147	1159	763	184	201	11	0	0	0
1	E	147	1159	763	184	201	11	0	0	0
1	F	146	1154	760	183	200	11	0	0	0
1	G	146	1154	760	183	200	11	0	0	0
1	H	146	1154	760	183	200	11	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

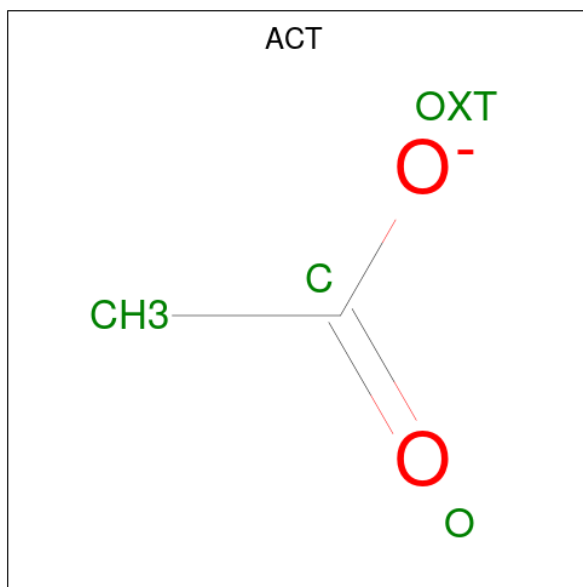
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ALA	deletion	UNP Q0VNY2
A	?	-	ALA	deletion	UNP Q0VNY2
B	?	-	ALA	deletion	UNP Q0VNY2
B	?	-	ALA	deletion	UNP Q0VNY2
C	?	-	ALA	deletion	UNP Q0VNY2
C	?	-	ALA	deletion	UNP Q0VNY2
D	?	-	ALA	deletion	UNP Q0VNY2
D	?	-	ALA	deletion	UNP Q0VNY2
E	?	-	ALA	deletion	UNP Q0VNY2
E	?	-	ALA	deletion	UNP Q0VNY2
F	?	-	ALA	deletion	UNP Q0VNY2
F	?	-	ALA	deletion	UNP Q0VNY2
G	?	-	ALA	deletion	UNP Q0VNY2

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Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	ALA	deletion	UNP Q0VNY2
H	?	-	ALA	deletion	UNP Q0VNY2
H	?	-	ALA	deletion	UNP Q0VNY2

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	E	1	Total C O 4 2 2	0	0
2	G	1	Total C O 4 2 2	0	0
2	H	1	Total C O 4 2 2	0	0

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Na 2 2	0	0
3	F	1	Total Na 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Na	0	0
			1	1		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

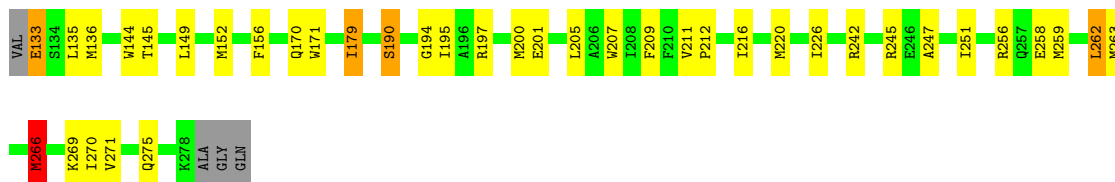
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	1	Total	Mg	0	0
			1	1		

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.

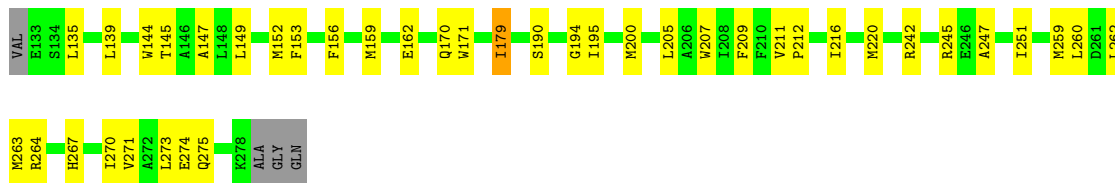
- Molecule 1: Ion transport protein

Chain A: 



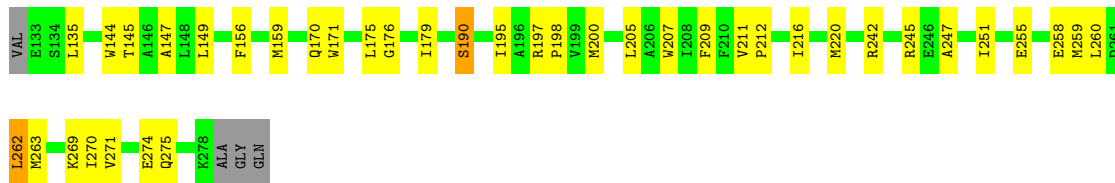
- Molecule 1: Ion transport protein

Chain B: 



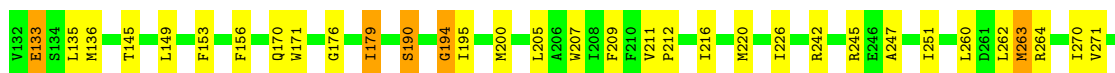
- Molecule 1: Ion transport protein

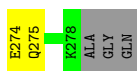
Chain C: 



- Molecule 1: Ion transport protein

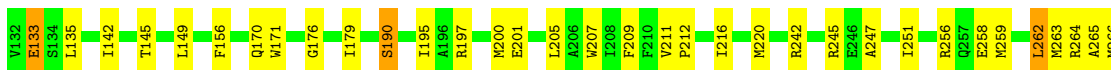
Chain D: 





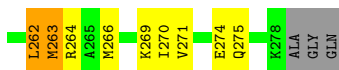
- Molecule 1: Ion transport protein

Chain E: 73% 23% ..



- Molecule 1: Ion transport protein

Chain F: 69% 25% ..



- Molecule 1: Ion transport protein

Chain G: 67% 29% ..



- Molecule 1: Ion transport protein

Chain H: 69% 26% ..



4 Data and refinement statistics i

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	178.18Å 191.80Å 192.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.99 – 3.64 14.99 – 3.64	Depositor EDS
% Data completeness (in resolution range)	99.0 (14.99-3.64) 98.3 (14.99-3.64)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 3.66Å)	Xtrriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.287 , 0.303 0.291 , 0.306	Depositor DCC
R_{free} test set	1798 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	129.2	Xtrriage
Anisotropy	0.028	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 86.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtrriage
Estimated twinning fraction	0.250 for -h,-l,-k	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9286	wwPDB-VP
Average B, all atoms (Å ²)	130.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% 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: NA, MG, ACT

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	0.35	0/1187	0.65	2/1609 (0.1%)
1	B	0.28	0/1199	0.57	0/1627
1	C	0.23	0/1183	0.49	0/1604
1	D	0.22	0/1188	0.52	0/1611
1	E	0.22	0/1188	0.56	2/1611 (0.1%)
1	F	0.20	0/1183	0.51	0/1604
1	G	0.26	0/1183	0.52	0/1604
1	H	0.21	0/1183	0.56	0/1604
All	All	0.25	0/9494	0.55	4/12874 (0.0%)

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
1	D	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	266	MET	CB-CG-SD	-7.54	90.10	112.70
1	A	256	ARG	NE-CZ-NH2	5.64	124.28	119.20
1	E	133	GLU	CA-C-N	5.01	131.29	122.42
1	E	133	GLU	C-N-CA	5.01	131.29	122.42

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	133	GLU	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	1158	0	1146	42	0
1	B	1165	0	1152	48	0
1	C	1154	0	1142	37	0
1	D	1159	0	1144	28	0
1	E	1159	0	1144	25	0
1	F	1154	0	1142	32	0
1	G	1154	0	1141	40	0
1	H	1154	0	1142	35	0
2	A	4	0	3	0	0
2	C	4	0	3	0	0
2	D	4	0	3	0	0
2	E	4	0	3	0	0
2	G	4	0	3	0	0
2	H	4	0	3	0	0
3	A	2	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
4	E	1	0	0	0	0
All	All	9286	0	9171	215	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 215 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:266:MET:HE2	1:B:267:HIS:HD2	1.05	1.17
1:A:266:MET:HE2	1:B:267:HIS:CD2	1.83	1.12
1:A:266:MET:HE3	1:B:270:ILE:HB	1.36	1.03
1:A:263:MET:HG2	1:B:263:MET:HE1	1.42	1.01
1:C:263:MET:HG2	1:D:263:MET:HE1	1.41	1.00

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	144/150 (96%)	139 (96%)	5 (4%)	0	100	100
1	B	145/150 (97%)	143 (99%)	2 (1%)	0	100	100
1	C	144/150 (96%)	141 (98%)	3 (2%)	0	100	100
1	D	145/150 (97%)	141 (97%)	3 (2%)	1 (1%)	18	48
1	E	145/150 (97%)	141 (97%)	3 (2%)	1 (1%)	18	48
1	F	144/150 (96%)	140 (97%)	4 (3%)	0	100	100
1	G	144/150 (96%)	142 (99%)	2 (1%)	0	100	100
1	H	144/150 (96%)	141 (98%)	3 (2%)	0	100	100
All	All	1155/1200 (96%)	1128 (98%)	25 (2%)	2 (0%)	43	71

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	133	GLU
1	D	194	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	119/124 (96%)	113 (95%)	6 (5%)	22	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	119/124 (96%)	116 (98%)	3 (2%)	42	59
1	C	118/124 (95%)	114 (97%)	4 (3%)	32	53
1	D	118/124 (95%)	113 (96%)	5 (4%)	26	49
1	E	118/124 (95%)	113 (96%)	5 (4%)	26	49
1	F	118/124 (95%)	112 (95%)	6 (5%)	21	45
1	G	118/124 (95%)	113 (96%)	5 (4%)	26	49
1	H	118/124 (95%)	111 (94%)	7 (6%)	18	42
All	All	946/992 (95%)	905 (96%)	41 (4%)	26	49

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	270	ILE
1	H	159	MET
1	G	135	LEU
1	G	190	SER
1	H	190	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	267	HIS
1	H	184	GLN
1	D	267	HIS
1	E	184	GLN
1	E	267	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 5 are monoatomic - leaving 6 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
2	ACT	H	401	-	3,3,3	1.40	1 (33%)	3,3,3	1.38	0
2	ACT	D	401	3	3,3,3	1.41	1 (33%)	3,3,3	1.51	0
2	ACT	G	302	-	3,3,3	1.35	0	3,3,3	1.38	0
2	ACT	E	302	3	3,3,3	1.39	0	3,3,3	1.51	0
2	ACT	C	301	3	3,3,3	1.43	1 (33%)	3,3,3	1.53	0
2	ACT	A	501	3	3,3,3	1.41	1 (33%)	3,3,3	1.36	0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	ACT	CH3-C	2.09	1.57	1.49
2	D	401	ACT	CH3-C	2.05	1.57	1.49
2	A	501	ACT	CH3-C	2.03	1.57	1.49
2	H	401	ACT	CH3-C	2.01	1.57	1.49

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 [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	146/150 (97%)	-1.57	0 100 100	89, 124, 186, 255	0
1	B	146/150 (97%)	-1.59	0 100 100	87, 125, 188, 246	1 (0%)
1	C	146/150 (97%)	-1.57	0 100 100	87, 125, 182, 251	0
1	D	147/150 (98%)	-1.61	0 100 100	88, 126, 191, 255	0
1	E	147/150 (98%)	-1.59	0 100 100	88, 127, 183, 261	0
1	F	146/150 (97%)	-1.57	0 100 100	88, 126, 187, 262	0
1	G	146/150 (97%)	-1.58	0 100 100	87, 126, 189, 263	0
1	H	146/150 (97%)	-1.59	0 100 100	88, 126, 187, 252	0
All	All	1170/1200 (97%)	-1.58	0 100 100	87, 126, 191, 263	1 (0%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ACT	A	501	4/4	0.99	0.03	85,95,109,119	0
2	ACT	C	301	4/4	0.99	0.06	95,101,123,125	0
2	ACT	D	401	4/4	0.99	0.08	89,92,114,122	0
2	ACT	H	401	4/4	0.99	0.05	89,117,139,155	0
3	NA	A	502	1/1	0.99	0.05	113,113,113,113	0
3	NA	F	301	1/1	0.99	0.02	106,106,106,106	0
3	NA	G	301	1/1	0.99	0.03	68,68,68,68	0
3	NA	A	503	1/1	1.00	0.02	68,68,68,68	0
2	ACT	E	302	4/4	1.00	0.03	68,98,108,127	0
2	ACT	G	302	4/4	1.00	0.06	83,94,100,103	0
4	MG	E	301	1/1	1.00	0.03	113,113,113,113	0

6.5 Other polymers [i](#)

There are no such residues in this entry.