wwPDB X-ray Structure Validation Summary Report (i)

Aug 10, 2020 – 09:57 AM BST

PDB ID	:	2GOO
Title	:	Ternary Complex of BMP-2 bound to BMPR-Ia-ECD and ActRII-ECD
Authors	:	Allendorph, G.P.; Choe, S.
Deposited on	:	2006-04-13
Resolution	:	2.20 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 following versions of software and data (see references (1)) were used in the production of this report:

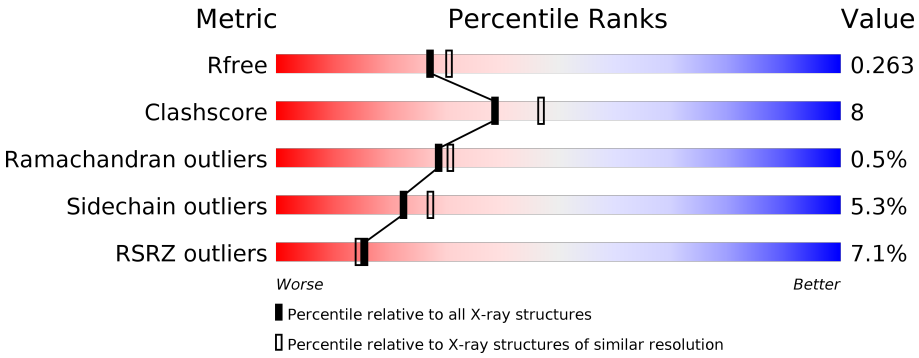
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=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	114	% 84% 6% 10%
1	D	114	% 82% 6% • 9%
2	B	131	7% 52% 11% • 35%
2	E	131	3% 56% 8% • • 33%
3	C	102	15% 68% 20% • 10%
3	F	102	10% 68% 21% • 9%

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	NDG	C	402	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4862 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 Bone morphogenetic protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	103	Total	C	N	O	S	0	0	0
			805	510	135	151	9			
1	D	104	Total	C	N	O	S	0	0	0
			814	516	137	152	9			

- Molecule 2 is a protein called Bone morphogenetic protein receptor type IA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	85	Total	C	N	O	S	0	0	0
			654	400	112	131	11			
2	E	88	Total	C	N	O	S	0	0	0
			677	417	115	134	11			

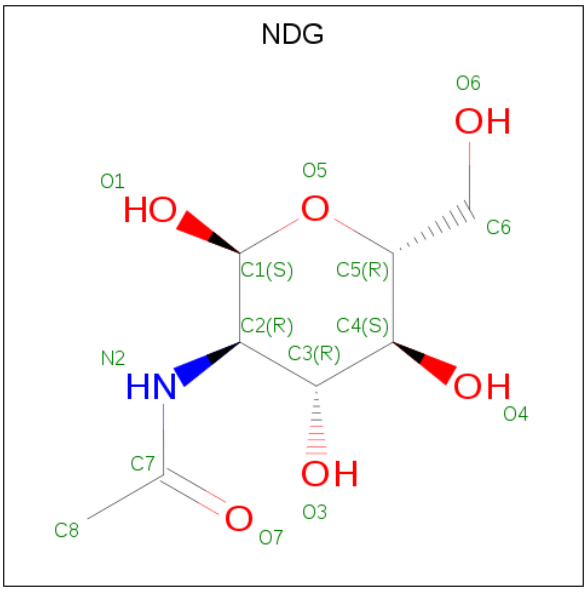
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	cloning artifact	UNP P36894
B	0	SER	-	cloning artifact	UNP P36894
E	-1	GLY	-	cloning artifact	UNP P36894
E	0	SER	-	cloning artifact	UNP P36894

- Molecule 3 is a protein called Activin receptor type 2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	92	Total	C	N	O	S	21	0	0
			758	471	129	147	11			
3	F	93	Total	C	N	O	S	21	0	0
			767	476	130	150	11			

- Molecule 4 is 2-acetamido-2-deoxy-alpha-D-glucopyranose (three-letter code: NDG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C N O 15 8 1 6	0	0
4	C	1	Total C N O 15 8 1 6	0	0
4	F	1	Total C N O 15 8 1 6	0	0
4	F	1	Total C N O 15 8 1 6	0	0

- Molecule 5 is water.

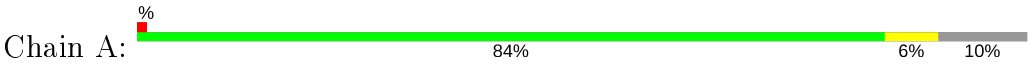
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	89	Total O 89 89	0	0
5	B	47	Total O 47 47	0	0
5	C	19	Total O 19 19	0	0
5	D	75	Total O 75 75	0	0
5	E	67	Total O 67 67	0	0
5	F	30	Total O 30 30	0	0

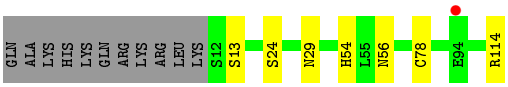
3 Residue-property plots

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: Bone morphogenetic protein 2

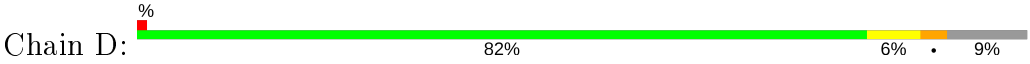
Chain A:

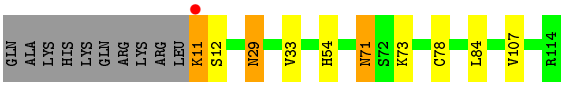




- Molecule 1: Bone morphogenetic protein 2

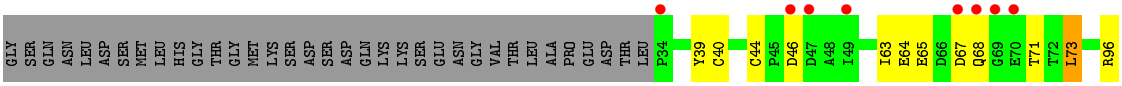
Chain D:

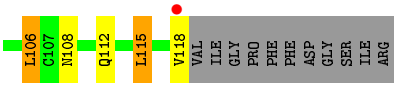




- Molecule 2: Bone morphogenetic protein receptor type IA

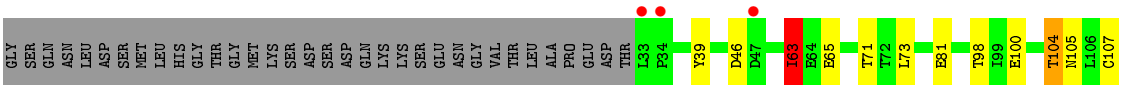
Chain B:

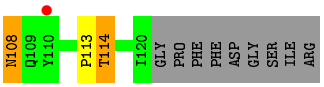




- Molecule 2: Bone morphogenetic protein receptor type IA

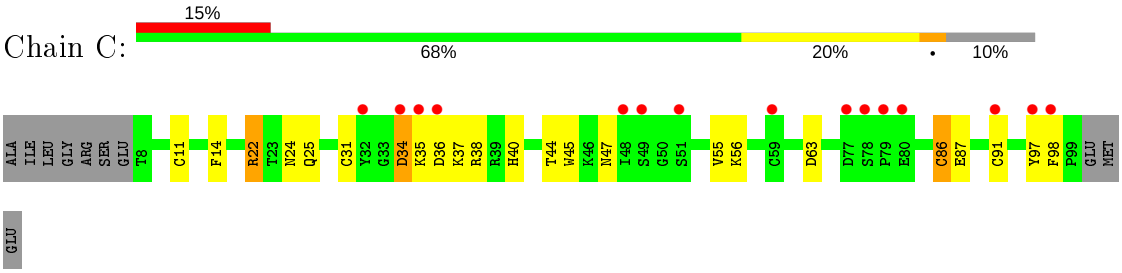
Chain E:





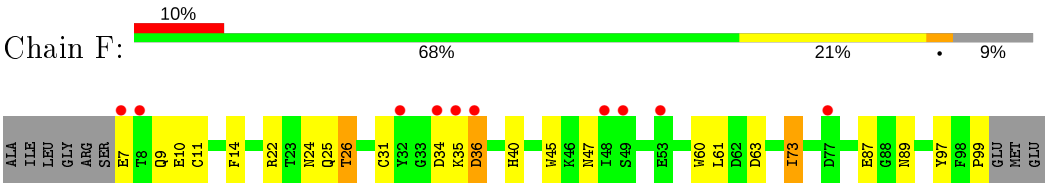
- Molecule 3: Activin receptor type 2A

Chain C:



- Molecule 3: Activin receptor type 2A

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	104.03Å 104.03Å 362.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.20 38.26 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.20) 99.4 (38.26-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.17 (at 2.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.222 , 0.259 0.234 , 0.263	Depositor DCC
R_{free} test set	3057 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	38.1	Xtriage
Anisotropy	0.195	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 44.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4862	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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

5.1 Standard geometry

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

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	0.56	1/828 (0.1%)	0.59	0/1129
1	D	0.54	1/837 (0.1%)	0.59	0/1140
2	B	0.49	0/667	0.74	0/903
2	E	0.54	0/690	0.71	1/936 (0.1%)
3	C	1.23	2/777 (0.3%)	1.64	4/1047 (0.4%)
3	F	1.11	4/786 (0.5%)	1.52	8/1059 (0.8%)
All	All	0.81	8/4585 (0.2%)	1.06	13/6214 (0.2%)

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
3	F	1	0

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	22	ARG	NE-CZ	26.11	1.67	1.33
3	F	22	ARG	NE-CZ	21.14	1.60	1.33
3	C	22	ARG	CZ-NH1	-15.49	1.12	1.33
3	F	22	ARG	CZ-NH2	-14.97	1.13	1.33
1	A	78	CYS	CB-SG	-8.22	1.68	1.82

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	22	ARG	NE-CZ-NH2	-36.21	102.19	120.30
3	F	22	ARG	NE-CZ-NH1	-31.78	104.41	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	22	ARG	NH1-CZ-NH2	24.28	146.11	119.40
3	C	22	ARG	NE-CZ-NH1	-21.96	109.32	120.30
3	F	22	ARG	NH1-CZ-NH2	20.25	141.67	119.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	F	73	ILE	CB

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	805	0	762	4	0
1	D	814	0	775	6	0
2	B	654	0	610	8	0
2	E	677	0	638	9	0
3	C	758	0	684	21	1
3	F	767	0	688	16	1
4	C	30	0	24	7	0
4	F	30	0	24	5	0
5	A	89	0	0	2	0
5	B	47	0	0	1	0
5	C	19	0	0	0	0
5	D	75	0	0	4	0
5	E	67	0	0	1	0
5	F	30	0	0	0	0
All	All	4862	0	4205	64	1

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 8.

The worst 5 of 64 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)
3:C:24:ASN:HD21	4:C:402:NDG:C1	1.60	1.13
3:C:97:TYR:C	3:C:98:PHE:HD1	1.62	1.02
2:E:104:THR:HG22	2:E:107:CYS:HB3	1.38	1.02
3:C:24:ASN:ND2	4:C:402:NDG:C1	2.23	1.01
3:C:97:TYR:O	3:C:98:PHE:HD1	1.47	0.95

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:22:ARG:NH2	3:F:10:GLU:OE2[6_664]	2.06	0.14

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	101/114 (89%)	97 (96%)	4 (4%)	0	100	100
1	D	102/114 (90%)	101 (99%)	1 (1%)	0	100	100
2	B	83/131 (63%)	77 (93%)	6 (7%)	0	100	100
2	E	86/131 (66%)	81 (94%)	5 (6%)	0	100	100
3	C	90/102 (88%)	84 (93%)	4 (4%)	2 (2%)	6	4
3	F	91/102 (89%)	84 (92%)	6 (7%)	1 (1%)	14	12
All	All	553/694 (80%)	524 (95%)	26 (5%)	3 (0%)	29	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	36	ASP
3	C	36	ASP
3	C	34	ASP

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	92/102 (90%)	91 (99%)	1 (1%)	73 85
1	D	93/102 (91%)	88 (95%)	5 (5%)	22 26
2	B	76/115 (66%)	68 (90%)	8 (10%)	7 6
2	E	79/115 (69%)	71 (90%)	8 (10%)	7 7
3	C	85/93 (91%)	84 (99%)	1 (1%)	71 83
3	F	86/93 (92%)	82 (95%)	4 (5%)	26 33
All	All	511/620 (82%)	484 (95%)	27 (5%)	22 27

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	29	ASN
2	E	46	ASP
3	F	26	THR
1	D	33	VAL
2	B	71	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	54	HIS
1	D	71	ASN
3	F	24	ASN
1	D	17	HIS
3	F	40	HIS

5.3.3 RNA

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	NDG	F	401	-	15,15,15	1.04	1 (6%)	21,21,21	1.48	3 (14%)
4	NDG	C	403	-	15,15,15	0.43	0	21,21,21	1.33	1 (4%)
4	NDG	F	400	-	15,15,15	0.64	0	21,21,21	1.82	5 (23%)
4	NDG	C	402	-	15,15,15	0.64	0	21,21,21	1.84	4 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NDG	F	401	-	-	2/6/26/26	0/1/1/1
4	NDG	C	403	-	-	2/6/26/26	0/1/1/1
4	NDG	F	400	-	-	4/6/26/26	0/1/1/1
4	NDG	C	402	-	1/1/6/7	2/6/26/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	401	NDG	O6-C6	3.50	1.57	1.42

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	402	NDG	O5-C1-C2	6.32	115.87	109.52
4	C	403	NDG	O5-C1-C2	4.48	114.02	109.52
4	F	400	NDG	O5-C1-C2	4.38	113.92	109.52
4	F	400	NDG	C4-C3-C2	4.18	116.46	110.34
4	F	401	NDG	C4-C3-C2	3.24	115.09	110.34

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	C	402	NDG	C1

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	401	NDG	C8-C7-N2-C2
4	F	401	NDG	O7-C7-N2-C2
4	C	403	NDG	C8-C7-N2-C2
4	C	403	NDG	O7-C7-N2-C2
4	F	400	NDG	C8-C7-N2-C2

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	401	NDG	4	0
4	C	403	NDG	4	0
4	F	400	NDG	1	0
4	C	402	NDG	3	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

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	103/114 (90%)	0.23	1 (0%) 82 81	18, 29, 45, 55	0
1	D	104/114 (91%)	0.12	1 (0%) 82 81	19, 29, 46, 54	0
2	B	85/131 (64%)	0.46	9 (10%) 6 5	22, 35, 54, 59	0
2	E	88/131 (67%)	0.20	4 (4%) 33 32	21, 32, 48, 52	0
3	C	92/102 (90%)	0.85	15 (16%) 1 1	28, 54, 67, 69	6 (6%)
3	F	93/102 (91%)	0.64	10 (10%) 5 5	27, 48, 60, 62	6 (6%)
All	All	565/694 (81%)	0.41	40 (7%) 16 14	18, 35, 61, 69	12 (2%)

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	36	ASP	6.4
3	C	49	SER	5.9
2	E	33	LEU	5.8
3	C	48	ILE	5.1
3	F	49	SER	5.0

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 monosaccharides in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
4	NDG	F	400	15/15	0.26	0.28	73,75,76,76	0
4	NDG	C	402	15/15	0.76	0.20	56,61,62,62	0
4	NDG	F	401	15/15	0.80	0.20	80,81,81,81	0
4	NDG	C	403	15/15	0.82	0.20	83,83,84,84	0

6.5 Other polymers

There are no such residues in this entry.