W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 11, 2023 – 10:03 am GMT

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PDB ID	:	5MA5
Title	:	GFP-binding DARPin fusion gc_K11
Authors	:	Hansen, S.; Stueber, J.; Ernst, P.; Koch, A.; Bojar, D.; Batyuk, A.; Plueckthun, A.
Deposited on	:	2016-11-03
Resolution	:	1.85 Å(reported)

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 1.85 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.
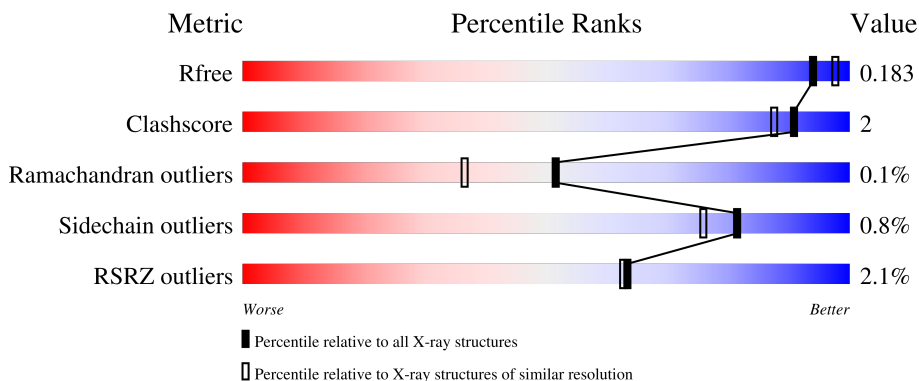
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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	B	243	88% 5% 6%
1	D	243	% 91% · 7%
2	A	302	% 95% · ·
2	C	302	6% 92% · 5%

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 16887 atoms, of which 7946 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 Green fluorescent protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	228	Total 3697	C 1189	H 1826	N 317	O 359	S 6	0	8	0
1	D	227	Total 3580	C 1155	H 1765	N 306	O 348	S 6	0	0	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	GLY	-	expression tag	UNP P42212
B	-3	PRO	-	expression tag	UNP P42212
B	-2	GLY	-	expression tag	UNP P42212
B	-1	SER	-	expression tag	UNP P42212
B	0	MET	-	expression tag	UNP P42212
B	1	VAL	-	expression tag	UNP P42212
B	64	LEU	PHE	conflict	UNP P42212
B	66	CRO	SER	chromophore	UNP P42212
B	66	CRO	TYR	chromophore	UNP P42212
B	66	CRO	GLY	chromophore	UNP P42212
B	231	LEU	HIS	conflict	UNP P42212
B	239	GLN	-	expression tag	UNP P42212
B	240	ALA	-	expression tag	UNP P42212
D	-4	GLY	-	expression tag	UNP P42212
D	-3	PRO	-	expression tag	UNP P42212
D	-2	GLY	-	expression tag	UNP P42212
D	-1	SER	-	expression tag	UNP P42212
D	0	MET	-	expression tag	UNP P42212
D	1	VAL	-	expression tag	UNP P42212
D	64	LEU	PHE	conflict	UNP P42212
D	66	CRO	SER	chromophore	UNP P42212
D	66	CRO	TYR	chromophore	UNP P42212
D	66	CRO	GLY	chromophore	UNP P42212
D	231	LEU	HIS	conflict	UNP P42212
D	239	GLN	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
D	240	ALA	-	expression tag	UNP P42212

- Molecule 2 is a protein called K11.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	A	298	Total	C	H	N	O	S	0	4	0
			4399	1404	2173	383	437	2			
2	C	288	Total	C	H	N	O	S	0	2	0
			4304	1377	2128	372	425	2			

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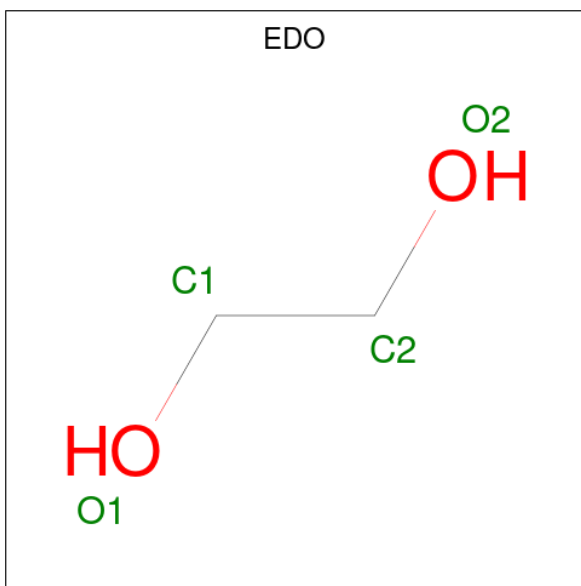
EDO

O2

OH

C1

C2

HO

O1

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	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 CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).

CIT

O5

O2

OH

C2

C1

C6

C3

HO

O6

C4

O1

HO

O7

C5

O3

OH

O4

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			18	6	5	7		
4	A	1	Total	C	H	O	0	0
			18	6	5	7		
4	C	1	Total	C	H	O	0	0
			18	6	5	7		
4	C	1	Total	C	H	O	0	0
			18	6	5	7		

- Molecule 5 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C_3H_8O).

IPA

C3

C2

C1

OH

O2
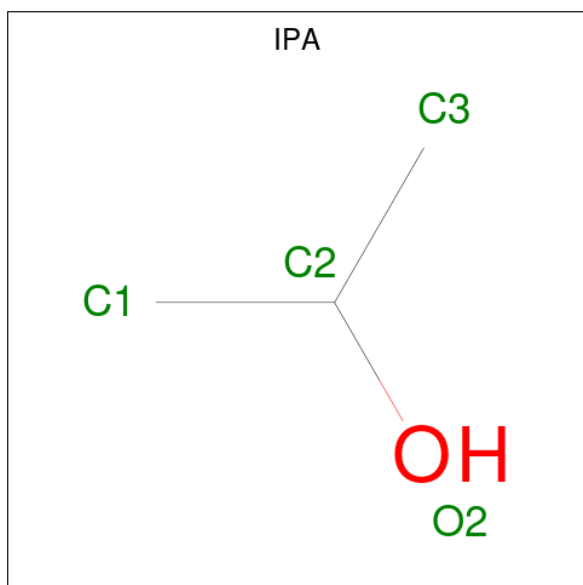
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total 12	C 3	H 8	O 1	0	0
5	A	1	Total 12	C 3	H 8	O 1	0	0

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total 1	Na 1	0	0
6	C	1	Total 1	Na 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	223	Total 223	O 223	0	0
7	A	294	Total 294	O 294	0	0
7	D	125	Total 125	O 125	0	0
7	C	137	Total 137	O 137	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.

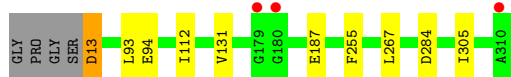• Molecule 1: Green fluorescent protein

Chain B:
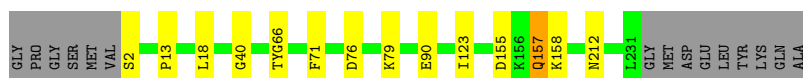
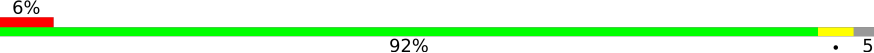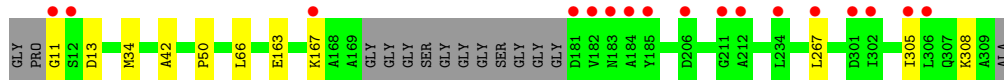• Molecule 1: Green fluorescent protein

Chain D:

• Molecule 2: K11

Chain A:

• Molecule 2: K11

Chain C:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	58.71Å 60.28Å 90.24Å 86.94° 79.13° 89.35°	Depositor
Resolution (Å)	44.25 – 1.85 44.25 – 1.85	Depositor EDS
% Data completeness (in resolution range)	89.5 (44.25-1.85) 89.5 (44.25-1.85)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.72 (at 1.86Å)	Xtriage
Refinement program	PHENIX (1.11_2567: ???)	Depositor
R, R_{free}	0.154 , 0.184 0.153 , 0.183	Depositor DCC
R_{free} test set	4615 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	27.1	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 44.0	EDS
L-test for twinning[2]	$< \lvert L \rvert > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	16887	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.73% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< \lvert L \rvert >$, $< L^2 >$ 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: CRO, EDO, CIT, NA, IPA

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	B	0.41	0/1901	0.64	0/2566
1	D	0.36	0/1833	0.57	0/2477
2	A	0.39	0/2279	0.57	0/3101
2	C	0.32	0/2220	0.48	0/3022
All	All	0.37	0/8233	0.57	0/11166

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 ⓘ

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	B	1871	1826	1814	10	0
1	D	1815	1765	1764	3	0
2	A	2226	2173	2154	8	0
2	C	2176	2128	2121	5	0
3	B	4	6	6	0	0
3	C	4	6	6	0	0
3	D	4	6	6	0	0
4	A	26	10	9	0	0
4	C	26	10	9	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	8	16	16	2	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
7	A	294	0	0	3	0
7	B	223	0	0	3	0
7	C	137	0	0	2	0
7	D	125	0	0	0	0
All	All	8941	7946	7905	28	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 2.

The worst 5 of 28 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:A:94:GLU:OE1	7:A:501:HOH:O	1.97	0.82
1:B:2:SER:N	7:B:402:HOH:O	2.15	0.78
1:B:90:GLU:OE1	7:B:401:HOH:O	2.01	0.77
2:A:13:ASP:N	7:A:503:HOH:O	2.19	0.74
2:A:267:LEU:HD11	2:A:305:ILE:HD12	1.74	0.70

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	B	231/243 (95%)	227 (98%)	4 (2%)	0	100	100
1	D	222/243 (91%)	219 (99%)	3 (1%)	0	100	100
2	A	300/302 (99%)	296 (99%)	4 (1%)	0	100	100
2	C	286/302 (95%)	280 (98%)	5 (2%)	1 (0%)	41	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1039/1090 (95%)	1022 (98%)	16 (2%)	1 (0%)	51	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	308	LYS

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	B	205/210 (98%)	200 (98%)	5 (2%)	49	33
1	D	198/210 (94%)	197 (100%)	1 (0%)	88	86
2	A	222/221 (100%)	221 (100%)	1 (0%)	88	86
2	C	219/221 (99%)	218 (100%)	1 (0%)	88	86
All	All	844/862 (98%)	836 (99%)	8 (1%)	81	72

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	13	ASP
1	D	76	ASP
1	B	157[B]	GLN
1	B	157[A]	GLN
2	A	13	ASP

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	$\#|Z| > 2$
1	CRO	D	66	1	23,23,24	2.43	6 (26%)	30,32,34	3.19	11 (36%)
1	CRO	B	66	1	23,23,24	2.11	7 (30%)	30,32,34	2.12	8 (26%)

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
1	CRO	D	66	1	-	0/12/31/32	0/2/2/2
1	CRO	B	66	1	-	0/12/31/32	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	66	CRO	C1-N2	6.86	1.42	1.32
1	D	66	CRO	CA2-C2	5.80	1.54	1.48
1	B	66	CRO	C1-N2	5.34	1.40	1.32
1	B	66	CRO	CA2-C2	4.91	1.53	1.48
1	D	66	CRO	C1-N3	4.48	1.44	1.37

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(º)	Ideal(º)
1	D	66	CRO	CA2-C2-N3	9.32	107.78	103.37
1	D	66	CRO	O2-C2-CA2	-8.80	126.02	130.96
1	D	66	CRO	C2-N3-C1	-6.88	104.49	107.97
1	B	66	CRO	CA2-C2-N3	6.24	106.32	103.37
1	B	66	CRO	C2-N3-C1	-4.68	105.60	107.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	66	CRO	1	0

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	C	401	-	3,3,3	0.49	0	2,2,2	0.15	0
4	CIT	C	402	6	12,12,12	0.98	0	17,17,17	1.56	2 (11%)
4	CIT	A	401	6	12,12,12	1.06	0	17,17,17	1.79	6 (35%)
4	CIT	A	402	-	12,12,12	0.97	0	17,17,17	1.57	2 (11%)
5	IPA	A	404	-	3,3,3	0.68	0	3,3,3	0.23	0
3	EDO	D	301	-	3,3,3	0.45	0	2,2,2	0.31	0
3	EDO	B	301	-	3,3,3	0.49	0	2,2,2	0.29	0
5	IPA	A	403	-	3,3,3	0.53	0	3,3,3	0.19	0
4	CIT	C	403	-	12,12,12	0.97	0	17,17,17	2.17	6 (35%)

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	401	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CIT	C	402	6	-	0/16/16/16	-
4	CIT	A	401	6	-	0/16/16/16	-
4	CIT	A	402	-	-	9/16/16/16	-
3	EDO	D	301	-	-	0/1/1/1	-
3	EDO	B	301	-	-	1/1/1/1	-
4	CIT	C	403	-	-	8/16/16/16	-

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	403	CIT	O6-C6-C3	6.22	123.85	113.05
4	A	402	CIT	O6-C6-C3	3.95	119.92	113.05
4	A	401	CIT	O6-C6-C3	3.94	119.90	113.05
4	C	402	CIT	O6-C6-C3	3.72	119.51	113.05
4	A	401	CIT	C2-C3-C6	-2.91	103.85	110.11

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	402	CIT	C1-C2-C3-O7
4	A	402	CIT	C1-C2-C3-C4
4	A	402	CIT	C1-C2-C3-C6
4	A	402	CIT	C2-C3-C6-O5
4	A	402	CIT	C2-C3-C6-O6

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	403	IPA	2	0
4	C	403	CIT	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 ⓘ

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	B	227/243 (93%)	-0.40	0	100	100	18, 27, 55, 74	0
1	D	226/243 (93%)	-0.03	2 (0%)	84	84	30, 40, 68, 97	0
2	A	298/302 (98%)	-0.54	3 (1%)	82	82	20, 30, 54, 92	0
2	C	288/302 (95%)	-0.06	17 (5%)	22	22	25, 50, 89, 120	0
All	All	1039/1090 (95%)	-0.26	22 (2%)	63	63	18, 36, 74, 120	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	182	VAL	5.8
2	C	211	GLY	4.3
2	A	179	GLY	4.0
2	C	185	TYR	3.6
2	C	181	ASP	3.4

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

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
1	CRO	B	66	22/23	0.97	0.14	19,22,27,29	0
1	CRO	D	66	22/23	0.97	0.16	28,34,41,42	0

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, 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	CIT	A	402	13/13	0.62	0.19	67,74,89,93	0
4	CIT	C	403	13/13	0.72	0.21	84,94,114,116	0
5	IPA	A	404	4/4	0.86	0.22	43,52,55,58	0
5	IPA	A	403	4/4	0.87	0.19	46,56,60,62	0
4	CIT	A	401	13/13	0.90	0.10	34,43,53,53	0
3	EDO	C	401	4/4	0.93	0.14	56,67,67,68	0
3	EDO	D	301	4/4	0.94	0.10	61,74,78,80	0
4	CIT	C	402	13/13	0.95	0.08	32,39,53,53	0
3	EDO	B	301	4/4	0.97	0.07	50,60,62,62	0
6	NA	A	405	1/1	0.97	0.06	37,37,37,37	0
6	NA	C	404	1/1	0.98	0.05	35,35,35,35	0

6.5 Other polymers ⓘ

There are no such residues in this entry.