Full wwPDB X-ray Structure Validation Report (i)

Sep 20, 2023 – 06:30 AM EDT

PDB ID	:	5ERO
Title	:	Crystal structure of elongation domain of Phomopsis amygdali fusicoccadiene synthase complexed with cobalt ions and pamidronate
Authors	:	Chen, M.; Christianson, D.W.
Deposited on	:	2015-11-14
Resolution	:	2.55 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

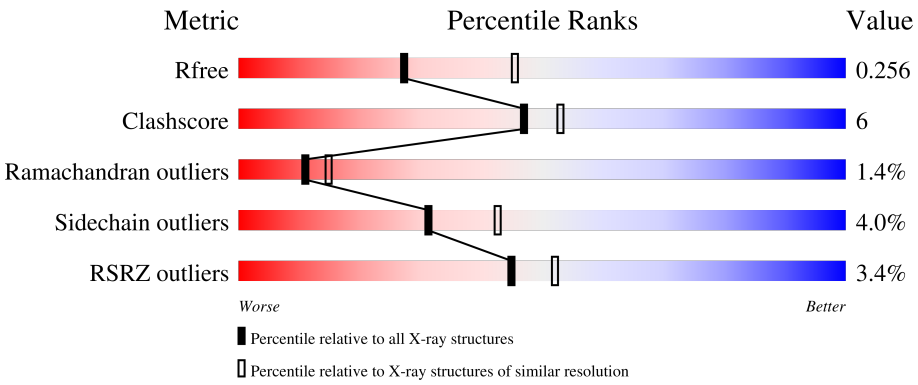
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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 <=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	349	2%, 70%, 14%, •, 14%
1	B	349	3%, 74%, 11%, •, 14%
1	C	349	4%, 70%, 13%, •, 14%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7395 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 Fusicoccadiene synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	301	2418	1533	422	448	15	0	0	0
1	B	300	2407	1526	418	448	15	0	0	0
1	C	299	2386	1513	409	449	15	0	0	0

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	371	MET	-	initiating methionine	UNP A2PZA5
A	372	GLY	-	expression tag	UNP A2PZA5
A	373	SER	-	expression tag	UNP A2PZA5
A	374	SER	-	expression tag	UNP A2PZA5
A	375	HIS	-	expression tag	UNP A2PZA5
A	376	HIS	-	expression tag	UNP A2PZA5
A	377	HIS	-	expression tag	UNP A2PZA5
A	378	HIS	-	expression tag	UNP A2PZA5
A	379	HIS	-	expression tag	UNP A2PZA5
A	380	HIS	-	expression tag	UNP A2PZA5
A	381	SER	-	expression tag	UNP A2PZA5
A	382	SER	-	expression tag	UNP A2PZA5
A	383	GLY	-	expression tag	UNP A2PZA5
A	384	LEU	-	expression tag	UNP A2PZA5
A	385	VAL	-	expression tag	UNP A2PZA5
A	386	PRO	-	expression tag	UNP A2PZA5
A	387	ARG	-	expression tag	UNP A2PZA5
A	388	GLY	-	expression tag	UNP A2PZA5
B	371	MET	-	initiating methionine	UNP A2PZA5
B	372	GLY	-	expression tag	UNP A2PZA5
B	373	SER	-	expression tag	UNP A2PZA5
B	374	SER	-	expression tag	UNP A2PZA5
B	375	HIS	-	expression tag	UNP A2PZA5

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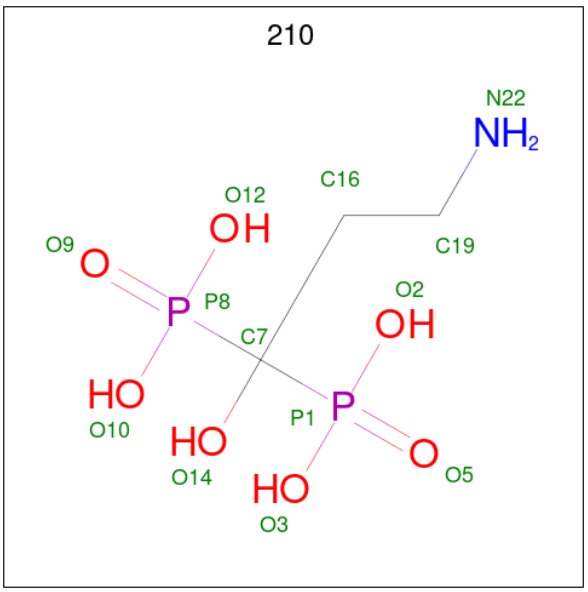
Chain	Residue	Modelled	Actual	Comment	Reference
B	376	HIS	-	expression tag	UNP A2PZA5
B	377	HIS	-	expression tag	UNP A2PZA5
B	378	HIS	-	expression tag	UNP A2PZA5
B	379	HIS	-	expression tag	UNP A2PZA5
B	380	HIS	-	expression tag	UNP A2PZA5
B	381	SER	-	expression tag	UNP A2PZA5
B	382	SER	-	expression tag	UNP A2PZA5
B	383	GLY	-	expression tag	UNP A2PZA5
B	384	LEU	-	expression tag	UNP A2PZA5
B	385	VAL	-	expression tag	UNP A2PZA5
B	386	PRO	-	expression tag	UNP A2PZA5
B	387	ARG	-	expression tag	UNP A2PZA5
B	388	GLY	-	expression tag	UNP A2PZA5
C	371	MET	-	initiating methionine	UNP A2PZA5
C	372	GLY	-	expression tag	UNP A2PZA5
C	373	SER	-	expression tag	UNP A2PZA5
C	374	SER	-	expression tag	UNP A2PZA5
C	375	HIS	-	expression tag	UNP A2PZA5
C	376	HIS	-	expression tag	UNP A2PZA5
C	377	HIS	-	expression tag	UNP A2PZA5
C	378	HIS	-	expression tag	UNP A2PZA5
C	379	HIS	-	expression tag	UNP A2PZA5
C	380	HIS	-	expression tag	UNP A2PZA5
C	381	SER	-	expression tag	UNP A2PZA5
C	382	SER	-	expression tag	UNP A2PZA5
C	383	GLY	-	expression tag	UNP A2PZA5
C	384	LEU	-	expression tag	UNP A2PZA5
C	385	VAL	-	expression tag	UNP A2PZA5
C	386	PRO	-	expression tag	UNP A2PZA5
C	387	ARG	-	expression tag	UNP A2PZA5
C	388	GLY	-	expression tag	UNP A2PZA5

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Co		
2	A	4	4	4	0	0
2	B	4	4	4	0	0
2	C	4	4	4	0	0

- Molecule 3 is PAMIDRONATE (three-letter code: 210) (formula: $C_3H_{11}NO_7P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	13	3	1	7	2	0	0
			Total	C	N	O	P		
3	B	1	13	3	1	7	2	0	0
			Total	C	N	O	P		
3	C	1	13	3	1	7	2	0	0

- Molecule 4 is water.

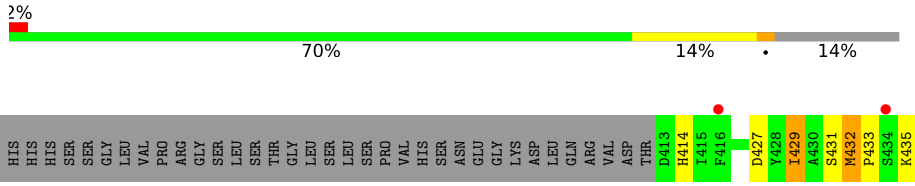
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	65	65	65	0	0
			Total	O		
4	B	52	52	52	0	0
			Total	O		
4	C	16	16	16	0	0

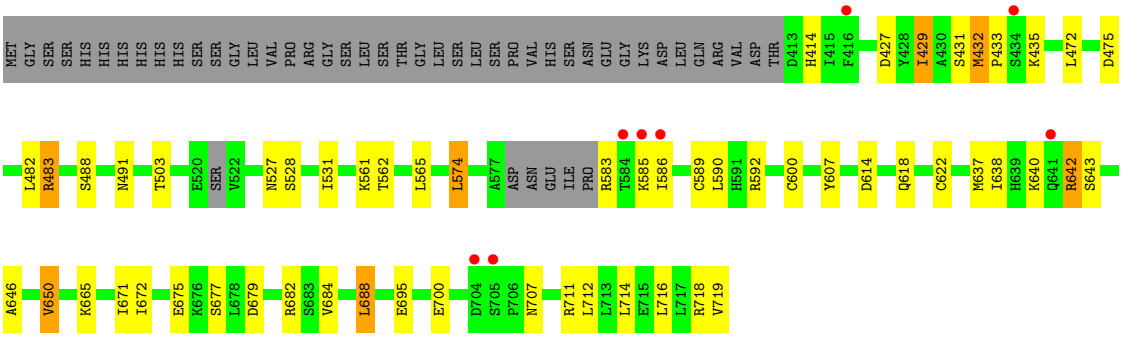
3 Residue-property plots (i)

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: Fusicoccadiene synthase

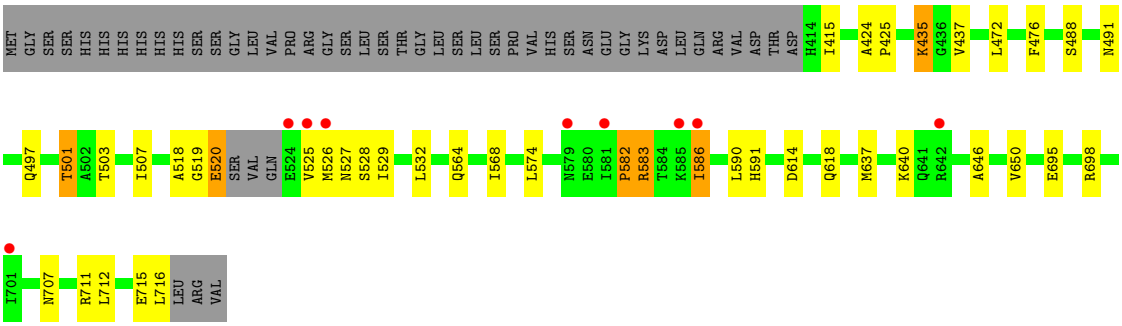
Chain A:





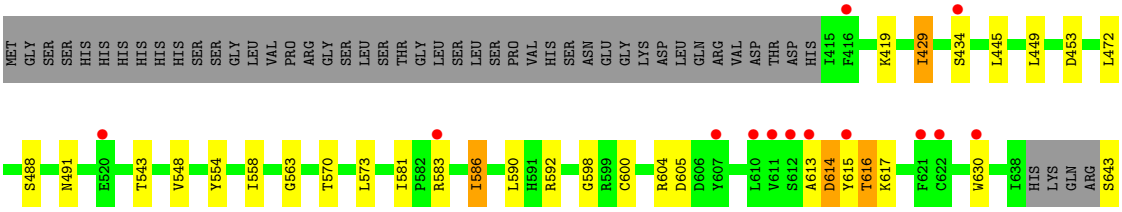
• Molecule 1: Fusicoccadiene synthase

Chain B:



• Molecule 1: Fusicoccadiene synthase

Chain C:



H644
M645
E663
F667
I671
I672
E673
S677
L678
D679
R682
H689
L692
R693
A694
E695
R698
L703
N707
R711
L714
E715
L716
L717
ARG
VAL

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	103.58Å 216.12Å 129.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.85 – 2.55 49.85 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.85-2.55) 94.4 (49.85-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.81 (at 2.54Å)	Xtriage
Refinement program	PHENIX dev_1839	Depositor
R, R_{free}	0.214 , 0.256 0.214 , 0.256	Depositor DCC
R_{free} test set	2391 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	46.6	Xtriage
Anisotropy	0.504	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 46.8	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	0.94	EDS
Total number of atoms	7395	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 210, CO

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	0.22	0/2460	0.39	0/3315
1	B	0.22	0/2451	0.40	0/3306
1	C	0.22	0/2428	0.41	0/3276
All	All	0.22	0/7339	0.40	0/9897

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	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	432	MET	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	2418	0	2431	32	0
1	B	2407	0	2409	27	0
1	C	2386	0	2386	32	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
3	A	13	0	7	2	0
3	B	13	0	7	0	0
3	C	13	0	7	0	0
4	A	65	0	0	1	0
4	B	52	0	0	0	0
4	C	16	0	0	2	0
All	All	7395	0	7247	90	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 6.

All (90) 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:642:ARG:NH1	1:A:675:GLU:OE2	2.20	0.74
1:B:574:LEU:HG	1:B:583:ARG:HD2	1.70	0.72
1:C:672:ILE:HG23	1:C:677:SER:HB2	1.74	0.69
1:B:582:PRO:HD2	1:B:586:ILE:HD11	1.77	0.66
1:A:561:LYS:HG3	1:A:562:THR:HG23	1.78	0.65
1:C:592:ARG:NH1	1:C:695:GLU:OE2	2.27	0.65
1:A:592:ARG:NH1	1:A:695:GLU:OE1	2.31	0.64
1:C:679:ASP:OD1	1:C:682:ARG:NH2	2.30	0.64
1:A:482:LEU:HD21	1:C:663:GLU:HG3	1.79	0.64
1:A:637:MET:HE1	1:A:671:ILE:HG22	1.81	0.63
1:B:488:SER:OG	1:B:491:ASN:ND2	2.33	0.62
1:C:673:GLU:HA	1:C:678:LEU:HD11	1.81	0.61
1:B:529:ILE:HA	1:B:532:LEU:HD23	1.83	0.60
1:B:525:VAL:HG11	1:B:568:ILE:HG23	1.83	0.60
1:A:622:CYS:HB2	1:A:665:LYS:HD3	1.84	0.59
1:A:637:MET:HE3	1:A:675:GLU:HG3	1.85	0.57
1:A:679:ASP:OD1	1:A:682:ARG:NH2	2.32	0.57
1:C:445:LEU:HD22	1:C:570:THR:HG22	1.86	0.57
1:B:637:MET:HA	1:B:640:LYS:HE3	1.88	0.56
1:B:528:SER:OG	1:B:564:GLN:OE1	2.24	0.56
1:C:600:CYS:SG	1:C:604:ARG:NH2	2.78	0.56
1:B:519:GLY:HA3	1:B:520:GLU:HG2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:488:SER:OG	1:A:491:ASN:ND2	2.41	0.53
1:A:700:GLU:OE1	1:A:711:ARG:NH1	2.42	0.53
1:C:488:SER:OG	1:C:491:ASN:ND2	2.40	0.53
1:B:526:MET:O	1:B:529:ILE:N	2.27	0.53
1:C:614:ASP:O	1:C:616:THR:N	2.32	0.53
1:C:429:ILE:HG12	1:C:472:LEU:HD21	1.91	0.50
1:A:475:ASP:OD1	1:A:483:ARG:NH2	2.45	0.50
1:B:526:MET:O	1:B:528:SER:N	2.45	0.50
1:B:646:ALA:O	1:B:650:VAL:HG23	2.11	0.50
1:B:519:GLY:HA3	1:B:520:GLU:C	2.32	0.49
1:C:613:ALA:HA	1:C:614:ASP:C	2.32	0.49
1:B:564:GLN:O	1:B:568:ILE:HG13	2.13	0.49
1:C:586:ILE:HG23	1:C:590:LEU:HD13	1.95	0.49
1:C:445:LEU:HD23	1:C:573:LEU:HD12	1.94	0.49
3:A:804:210:N22	3:A:804:210:O14	2.46	0.48
1:A:503:THR:HG23	1:B:503:THR:HG23	1.95	0.48
1:A:646:ALA:O	1:A:650:VAL:HG22	2.13	0.48
1:C:419:LYS:NZ	4:C:905:HOH:O	2.46	0.47
1:C:554:TYR:CZ	1:C:558:ILE:HD11	2.49	0.47
1:B:497:GLN:O	1:B:501:THR:HG23	2.15	0.47
1:A:607:TYR:OH	1:A:682:ARG:NH1	2.46	0.47
1:C:614:ASP:O	1:C:617:LYS:N	2.46	0.47
1:A:700:GLU:OE2	1:A:707:ASN:N	2.42	0.46
1:C:605:ASP:OD1	4:C:901:HOH:O	2.20	0.46
1:A:483:ARG:NH2	4:A:904:HOH:O	2.47	0.46
1:C:429:ILE:H	1:C:429:ILE:HG13	1.41	0.46
1:C:586:ILE:HD11	1:C:703:LEU:HG	1.97	0.46
1:C:695:GLU:OE2	1:C:698:ARG:NH1	2.44	0.46
1:A:637:MET:HA	1:A:640:LYS:HB2	1.98	0.45
1:B:503:THR:O	1:B:507:ILE:HG12	2.15	0.45
1:A:483:ARG:NH1	3:A:804:210:O2	2.41	0.45
1:C:643:SER:O	1:C:644:HIS:ND1	2.49	0.45
1:C:692:LEU:HB3	1:C:714:LEU:HD11	1.98	0.45
1:B:525:VAL:HA	1:B:526:MET:C	2.37	0.44
1:A:574:LEU:HD23	1:A:574:LEU:HA	1.82	0.44
1:A:583:ARG:O	1:A:585:LYS:N	2.50	0.44
1:B:586:ILE:HG22	1:B:590:LEU:HG	1.98	0.44
1:A:427:ASP:O	1:A:431:SER:HB3	2.18	0.43
1:C:449:LEU:HA	1:C:581:ILE:HD13	2.00	0.43
1:C:689:HIS:HB3	1:C:693:ARG:HH12	1.84	0.43
1:B:424:ALA:HB3	1:B:425:PRO:HD3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:672:ILE:HG23	1:A:677:SER:OG	2.19	0.43
1:C:548:VAL:HG22	1:C:630:TRP:CH2	2.54	0.43
1:C:586:ILE:HD13	1:C:586:ILE:HA	1.80	0.43
1:A:600:CYS:SG	1:A:688:LEU:HB3	2.59	0.43
1:B:415:ILE:H	1:B:415:ILE:HD12	1.84	0.42
1:C:678:LEU:H	1:C:678:LEU:HD12	1.84	0.42
1:A:586:ILE:O	1:A:590:LEU:HD12	2.19	0.42
1:B:695:GLU:OE2	1:B:698:ARG:NH1	2.52	0.42
1:C:563:GLY:HA2	1:C:598:GLY:HA3	2.01	0.42
1:C:707:ASN:O	1:C:711:ARG:HG3	2.20	0.42
1:A:429:ILE:H	1:A:429:ILE:HG13	1.45	0.41
1:C:604:ARG:NE	1:C:716:LEU:O	2.53	0.41
1:C:667:PHE:CE2	1:C:671:ILE:HD11	2.56	0.41
1:A:688:LEU:HD12	1:A:688:LEU:HA	1.92	0.41
1:B:425:PRO:HD2	1:B:501:THR:HG21	2.03	0.41
1:A:565:LEU:HD12	1:A:565:LEU:HA	1.89	0.41
1:A:684:VAL:HG12	1:A:688:LEU:HD22	2.02	0.41
1:A:614:ASP:O	1:A:618:GLN:HG2	2.20	0.41
1:B:707:ASN:O	1:B:711:ARG:HG3	2.21	0.41
1:B:574:LEU:HD12	1:B:574:LEU:HA	1.91	0.41
1:C:667:PHE:O	1:C:671:ILE:HG13	2.21	0.41
1:A:527:ASN:O	1:A:531:ILE:HG13	2.20	0.41
1:B:435:LYS:HG3	1:B:437:VAL:HG23	2.03	0.40
1:B:614:ASP:O	1:B:618:GLN:HG2	2.21	0.40
1:B:640:LYS:HE3	1:B:640:LYS:HB2	1.92	0.40
1:A:429:ILE:HG12	1:A:472:LEU:HD21	2.03	0.40
1:A:638:ILE:HD13	1:A:638:ILE:HA	1.94	0.40

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	295/349 (84%)	280 (95%)	12 (4%)	3 (1%)	15	22
1	B	296/349 (85%)	280 (95%)	11 (4%)	5 (2%)	9	11
1	C	295/349 (84%)	281 (95%)	10 (3%)	4 (1%)	11	15
All	All	886/1047 (85%)	841 (95%)	33 (4%)	12 (1%)	11	15

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	432	MET
1	A	433	PRO
1	B	527	ASN
1	C	614	ASP
1	A	643	SER
1	B	435	LYS
1	C	615	TYR
1	B	518	ALA
1	C	434	SER
1	C	616	THR
1	B	582	PRO
1	B	715	GLU

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	267/310 (86%)	252 (94%)	15 (6%)	21	28
1	B	265/310 (86%)	256 (97%)	9 (3%)	37	50
1	C	264/310 (85%)	256 (97%)	8 (3%)	41	55
All	All	796/930 (86%)	764 (96%)	32 (4%)	31	43

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	414	HIS

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Mol	Chain	Res	Type
1	A	429	ILE
1	A	435	LYS
1	A	483	ARG
1	A	528	SER
1	A	574	LEU
1	A	589	CYS
1	A	642	ARG
1	A	650	VAL
1	A	688	LEU
1	A	712	LEU
1	A	714	LEU
1	A	716	LEU
1	A	718	ARG
1	A	719	VAL
1	B	472	LEU
1	B	476	PHE
1	B	501	THR
1	B	520	GLU
1	B	583	ARG
1	B	586	ILE
1	B	591	HIS
1	B	712	LEU
1	B	716	LEU
1	C	429	ILE
1	C	453	ASP
1	C	543	THR
1	C	583	ARG
1	C	586	ILE
1	C	645	MET
1	C	678	LEU
1	C	716	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	512	GLN

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)

Of 15 ligands modelled in this entry, 12 are monoatomic - leaving 3 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	210	B	804	2	12,12,12	2.35	2 (16%)	17,20,20	1.14	1 (5%)
3	210	A	804	2	12,12,12	2.22	3 (25%)	17,20,20	1.06	0
3	210	C	804	2	12,12,12	2.05	2 (16%)	17,20,20	1.07	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	210	B	804	2	-	4/22/22/22	-
3	210	A	804	2	-	3/22/22/22	-
3	210	C	804	2	-	4/22/22/22	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	804	210	P1-C7	-4.99	1.81	1.85
3	A	804	210	P8-C7	-4.89	1.81	1.85
3	B	804	210	P8-C7	-4.89	1.81	1.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	804	210	P8-C7	-4.47	1.82	1.85
3	A	804	210	P1-C7	-4.38	1.82	1.85
3	C	804	210	P1-C7	-4.22	1.82	1.85
3	A	804	210	P1-O3	-2.03	1.51	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	804	210	O3-P1-O2	2.16	114.09	107.99

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	804	210	C19-C16-C7-P1
3	B	804	210	C19-C16-C7-P1
3	B	804	210	C19-C16-C7-P8
3	B	804	210	C19-C16-C7-O14
3	C	804	210	C19-C16-C7-P1
3	C	804	210	C19-C16-C7-P8
3	C	804	210	C19-C16-C7-O14
3	A	804	210	C19-C16-C7-P8
3	A	804	210	C19-C16-C7-O14
3	B	804	210	C16-C7-P1-O5
3	C	804	210	O14-C7-P1-O5

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	804	210	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	301/349 (86%)	-0.05	8 (2%)	54	61	27, 46, 93, 119	0
1	B	300/349 (85%)	-0.06	9 (3%)	50	57	27, 48, 88, 114	0
1	C	299/349 (85%)	0.22	14 (4%)	31	38	31, 58, 93, 118	0
All	All	900/1047 (85%)	0.04	31 (3%)	45	52	27, 51, 93, 119	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	581	ILE	5.1
1	C	613	ALA	4.7
1	A	434	SER	4.5
1	C	621	PHE	4.5
1	B	525	VAL	4.1
1	C	610	LEU	3.8
1	C	434	SER	3.7
1	C	520	GLU	3.6
1	B	585	LYS	3.4
1	A	416	PHE	3.1
1	B	579	ASN	3.1
1	C	630	TRP	3.0
1	B	524	GLU	2.9
1	C	611	VAL	2.9
1	B	526	MET	2.8
1	C	607	TYR	2.9
1	B	701	ILE	2.8
1	A	586	ILE	2.8
1	C	671	ILE	2.7
1	C	612	SER	2.7
1	A	584	THR	2.7
1	A	705	SER	2.4
1	A	704	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	585	LYS	2.4
1	C	622	CYS	2.4
1	A	641	GLN	2.3
1	C	583	ARG	2.2
1	C	615	TYR	2.2
1	B	642	ARG	2.1
1	B	586	ILE	2.1
1	C	416	PHE	2.0

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
2	CO	A	805	1/1	0.88	0.63	182,182,182,182	0
2	CO	C	805	1/1	0.89	0.44	176,176,176,176	0
3	210	C	804	13/13	0.93	0.15	75,84,96,98	0
2	CO	B	805	1/1	0.95	0.15	61,61,61,61	0
2	CO	C	802	1/1	0.96	0.12	71,71,71,71	0
3	210	A	804	13/13	0.98	0.16	38,41,68,75	0
2	CO	C	801	1/1	0.99	0.09	71,71,71,71	0
2	CO	A	803	1/1	0.99	0.12	37,37,37,37	0
2	CO	C	803	1/1	0.99	0.11	54,54,54,54	0
2	CO	A	801	1/1	0.99	0.12	38,38,38,38	0
2	CO	B	803	1/1	0.99	0.10	40,40,40,40	0
3	210	B	804	13/13	0.99	0.12	28,42,49,54	0
2	CO	A	802	1/1	0.99	0.13	40,40,40,40	0
2	CO	B	802	1/1	1.00	0.12	44,44,44,44	0
2	CO	B	801	1/1	1.00	0.09	37,37,37,37	0

6.5 Other polymers (i)

There are no such residues in this entry.