



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:16 AM GMT

PDB ID : 3OBV
Title : Autoinhibited Formin mDia1 Structure
Authors : Tomchick, D.R.; Rosen, M.K.; Otomo, T.
Deposited on : 2010-08-09
Resolution : 2.75 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

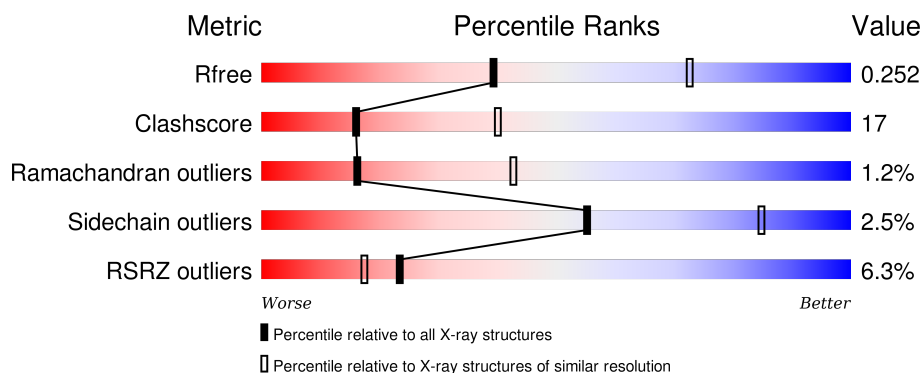
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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}	91344	3340 (2.80-2.72)
Clashscore	102246	3829 (2.80-2.72)
Ramachandran outliers	100387	3767 (2.80-2.72)
Sidechain outliers	100360	3770 (2.80-2.72)
RSRZ outliers	91569	3352 (2.80-2.72)

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. 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	327	<div> <div>2%</div> <div>77%</div> <div>21%</div> <div>••</div> </div>
1	B	327	<div> <div>6%</div> <div>70%</div> <div>26%</div> <div>••</div> </div>
1	C	327	<div> <div>2%</div> <div>77%</div> <div>20%</div> <div>••</div> </div>
1	D	327	<div> <div>%</div> <div>71%</div> <div>27%</div> <div>•</div> </div>
2	E	457	<div> <div>7%</div> <div>63%</div> <div>27%</div> <div>• 8%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	457	
2	G	457	
2	H	457	

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
3	SUC	A	2001	X	-	-	-
3	SUC	A	2005	X	-	-	X
3	SUC	B	2002	X	-	-	-
3	SUC	B	2006	X	-	-	-
3	SUC	C	2004	X	-	-	X
3	SUC	C	2008	X	-	-	X
3	SUC	D	2003	X	-	-	-
3	SUC	D	2007	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24400 atoms, of which 176 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.

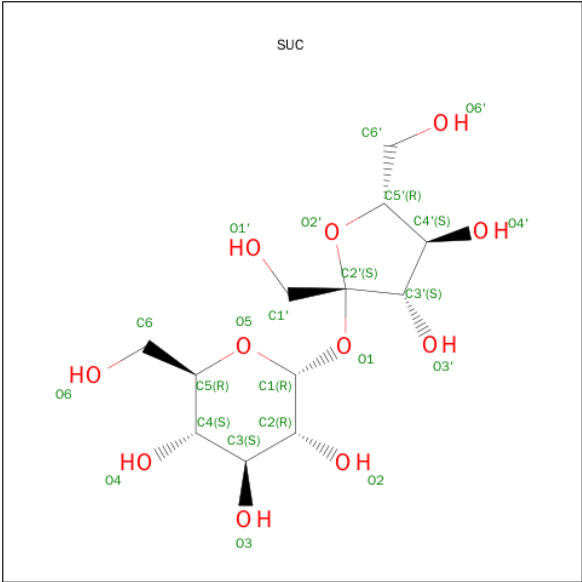
- Molecule 1 is a protein called Protein diaphanous homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	322	Total	C	N	O	S	0	0	0
			2589	1625	445	497	22			
1	B	319	Total	C	N	O	S	0	0	0
			2571	1617	443	489	22			
1	C	322	Total	C	N	O	S	0	0	0
			2589	1625	445	497	22			
1	D	327	Total	C	N	O	S	0	0	0
			2632	1651	453	506	22			

- Molecule 2 is a protein called Protein diaphanous homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	419	Total	C	N	O	S	0	0	0
			3410	2154	579	656	21			
2	F	419	Total	C	N	O	S	0	0	0
			3414	2155	582	656	21			
2	G	420	Total	C	N	O	S	0	0	0
			3421	2160	583	657	21			
2	H	419	Total	C	N	O	S	0	0	0
			3414	2156	582	655	21			

- Molecule 3 is SUGAR (SUCROSE) (three-letter code: SUC) (formula: C₁₂H₂₂O₁₁).

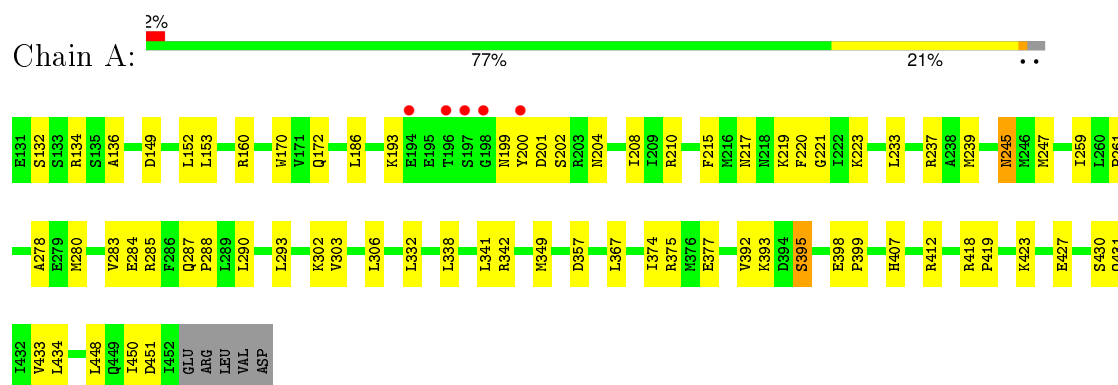


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			45	12	22	11		
3	B	1	Total	C	H	O	0	0
			45	12	22	11		
3	D	1	Total	C	H	O	0	0
			45	12	22	11		
3	C	1	Total	C	H	O	0	0
			45	12	22	11		
3	A	1	Total	C	H	O	0	0
			45	12	22	11		
3	B	1	Total	C	H	O	0	0
			45	12	22	11		
3	D	1	Total	C	H	O	0	0
			45	12	22	11		
3	C	1	Total	C	H	O	0	0
			45	12	22	11		

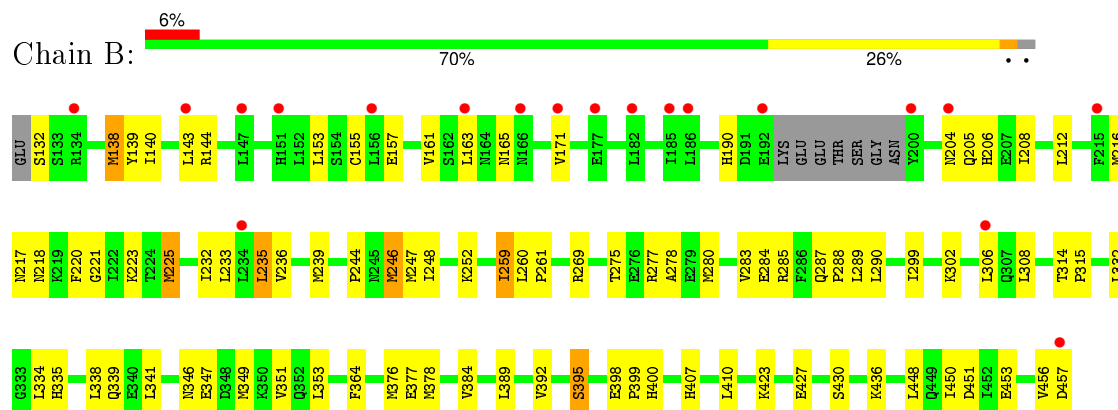
3 Residue-property plots [i](#)

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.

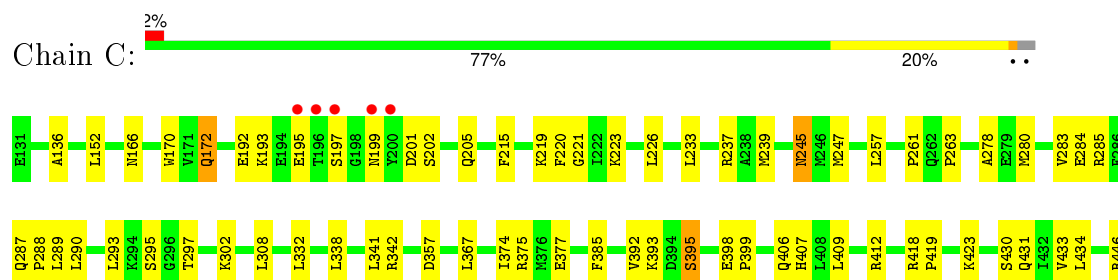
• Molecule 1: Protein diaphanous homolog 1

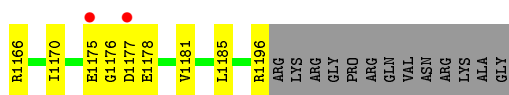


• Molecule 1: Protein diaphanous homolog 1



• Molecule 1: Protein diaphanous homolog 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.93Å 208.52Å 131.52Å 90.00° 102.74° 90.00°	Depositor
Resolution (Å)	29.95 – 2.75 48.54 – 2.75	Depositor EDS
% Data completeness (in resolution range)	95.8 (29.95-2.75) 95.8 (48.54-2.75)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.77Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.6.4_486)	Depositor
R, R_{free}	0.199 , 0.261 0.187 , 0.252	Depositor DCC
R_{free} test set	1797 reflections (1.47%)	DCC
Wilson B-factor (Å ²)	74.7	Xtriage
Anisotropy	0.373	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 72.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 122379 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	24400	wwPDB-VP
Average B, all atoms (Å ²)	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: SUC

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	0.50	0/2626	0.68	1/3536 (0.0%)
1	B	0.46	0/2607	0.62	0/3510
1	C	0.55	0/2626	0.73	0/3536
1	D	0.50	0/2669	0.65	0/3594
2	E	0.39	0/3462	0.55	0/4641
2	F	0.44	2/3466 (0.1%)	0.56	0/4645
2	G	0.39	0/3473	0.55	0/4655
2	H	0.45	2/3466 (0.1%)	0.58	0/4644
All	All	0.46	4/24395 (0.0%)	0.61	1/32761 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	932	GLN	CD-NE2	-7.82	1.13	1.32
2	F	932	GLN	CD-NE2	-7.53	1.14	1.32
2	F	932	GLN	CD-OE1	-6.13	1.10	1.24
2	H	932	GLN	CD-OE1	-6.08	1.10	1.24

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	448	LEU	CB-CG-CD1	-5.92	100.94	111.00

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	A	2589	0	2594	73	0
1	B	2571	0	2584	93	0
1	C	2589	0	2594	75	0
1	D	2632	0	2637	92	0
2	E	3410	0	3416	134	0
2	F	3414	0	3420	163	0
2	G	3421	0	3429	133	0
2	H	3414	0	3425	153	0
3	A	46	44	32	5	0
3	B	46	44	32	1	0
3	C	46	44	32	8	0
3	D	46	44	34	6	0
All	All	24224	176	24229	819	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 17.

The worst 5 of 819 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:G:771:VAL:H	2:G:775:LEU:HD12	1.13	1.10
2:F:771:VAL:H	2:F:775:LEU:HD12	1.14	1.07
1:D:375:ARG:HH22	3:D:2007:SUC:H61	1.12	1.07
2:H:771:VAL:H	2:H:775:LEU:HD12	1.12	1.06
2:E:771:VAL:H	2:E:775:LEU:HD12	1.19	1.05

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	320/327 (98%)	311 (97%)	9 (3%)	0	100	100
1	B	315/327 (96%)	300 (95%)	15 (5%)	0	100	100
1	C	320/327 (98%)	309 (97%)	11 (3%)	0	100	100
1	D	325/327 (99%)	313 (96%)	12 (4%)	0	100	100
2	E	415/457 (91%)	375 (90%)	33 (8%)	7 (2%)	11	32
2	F	415/457 (91%)	368 (89%)	37 (9%)	10 (2%)	7	22
2	G	416/457 (91%)	376 (90%)	32 (8%)	8 (2%)	10	28
2	H	415/457 (91%)	366 (88%)	39 (9%)	10 (2%)	7	22
All	All	2941/3136 (94%)	2718 (92%)	188 (6%)	35 (1%)	16	43

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	773	GLU
2	E	996	ALA
2	F	773	GLU
2	G	773	GLU
2	H	773	GLU

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	292/297 (98%)	289 (99%)	3 (1%)	82	95
1	B	290/297 (98%)	279 (96%)	11 (4%)	40	73
1	C	292/297 (98%)	287 (98%)	5 (2%)	68	90
1	D	297/297 (100%)	287 (97%)	10 (3%)	44	76
2	E	378/410 (92%)	368 (97%)	10 (3%)	54	84
2	F	378/410 (92%)	370 (98%)	8 (2%)	61	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	G	379/410 (92%)	369 (97%)	10 (3%)	54	84
2	H	378/410 (92%)	367 (97%)	11 (3%)	50	81
All	All	2684/2828 (95%)	2616 (98%)	68 (2%)	55	85

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	1092	SER
2	G	831	GLU
2	H	1020	PHE
2	F	1159	ARG
1	C	245	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	932	GLN
1	C	431	GLN
2	H	886	GLN
1	C	165	ASN
1	C	172	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 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	SUC	A	2001	-	24,24,24	1.06	2 (8%)	36,36,36	2.88	16 (44%)
3	SUC	A	2005	-	24,24,24	1.06	2 (8%)	36,36,36	3.15	18 (50%)
3	SUC	B	2002	-	24,24,24	1.08	2 (8%)	36,36,36	2.75	14 (38%)
3	SUC	B	2006	-	24,24,24	1.20	3 (12%)	36,36,36	2.65	13 (36%)
3	SUC	C	2004	-	24,24,24	1.13	2 (8%)	36,36,36	2.78	13 (36%)
3	SUC	C	2008	-	24,24,24	1.16	2 (8%)	36,36,36	2.90	18 (50%)
3	SUC	D	2003	-	24,24,24	1.12	2 (8%)	36,36,36	2.27	9 (25%)
3	SUC	D	2007	-	24,24,24	1.26	3 (12%)	36,36,36	2.58	12 (33%)

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	SUC	A	2001	-	4/4/9/9	0/12/51/51	0/2/2/2
3	SUC	A	2005	-	5/5/9/9	0/12/51/51	0/2/2/2
3	SUC	B	2002	-	4/4/9/9	0/12/51/51	0/2/2/2
3	SUC	B	2006	-	4/4/9/9	0/12/51/51	0/2/2/2
3	SUC	C	2004	-	4/4/9/9	0/12/51/51	0/2/2/2
3	SUC	C	2008	-	5/5/9/9	0/12/51/51	0/2/2/2
3	SUC	D	2003	-	4/4/9/9	0/12/51/51	0/2/2/2
3	SUC	D	2007	-	5/5/9/9	0/12/51/51	0/2/2/2

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2008	SUC	O3-C3	-2.94	1.35	1.43
3	D	2007	SUC	O3-C3	-2.93	1.36	1.43
3	C	2004	SUC	O3-C3	-2.82	1.36	1.43
3	B	2006	SUC	O3-C3	-2.77	1.36	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2002	SUC	O3-C3	-2.77	1.36	1.43

The worst 5 of 113 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2005	SUC	C1-O5-C5	-4.09	105.81	113.75
3	A	2001	SUC	C1-O5-C5	-2.85	108.21	113.75
3	C	2004	SUC	C2'-O1-C1	-2.34	111.37	117.53
3	C	2008	SUC	C2'-O1-C1	-2.31	111.45	117.53
3	D	2003	SUC	C1-O5-C5	-2.27	109.34	113.75

5 of 35 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	D	2007	SUC	C2
3	D	2007	SUC	C3
3	D	2007	SUC	C4'
3	D	2007	SUC	C5'
3	D	2007	SUC	C4

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2001	SUC	1	0
3	A	2005	SUC	4	0
3	B	2006	SUC	1	0
3	C	2004	SUC	2	0
3	C	2008	SUC	6	0
3	D	2003	SUC	1	0
3	D	2007	SUC	5	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	A	322/327 (98%)	0.20	5 (1%) 74 70	53, 74, 117, 180	0
1	B	319/327 (97%)	0.36	19 (5%) 25 19	54, 88, 139, 197	0
1	C	322/327 (98%)	0.20	5 (1%) 74 70	48, 70, 108, 191	0
1	D	327/327 (100%)	0.21	2 (0%) 90 88	52, 81, 127, 185	0
2	E	419/457 (91%)	0.52	34 (8%) 15 9	62, 110, 160, 200	0
2	F	419/457 (91%)	0.90	76 (18%) 2 1	59, 107, 173, 214	0
2	G	420/457 (91%)	0.51	26 (6%) 24 18	68, 111, 159, 201	0
2	H	419/457 (91%)	0.45	19 (4%) 37 30	62, 105, 166, 205	0
All	All	2967/3136 (94%)	0.44	186 (6%) 23 17	48, 96, 157, 214	0

The worst 5 of 186 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	900	LEU	10.6
2	F	906	PHE	9.7
2	F	835	LEU	7.7
2	F	897	TYR	7.3
2	F	868	VAL	6.6

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 [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. 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	SUC	C	2008	23/23	0.83	0.31	4.59	185,223,266,269	0
3	SUC	C	2004	23/23	0.85	0.22	2.63	173,194,225,251	0
3	SUC	A	2005	23/23	0.89	0.28	2.06	181,204,237,254	0
3	SUC	D	2007	23/23	0.89	0.26	1.96	173,208,239,286	0
3	SUC	D	2003	23/23	0.86	0.21	1.18	153,178,208,214	0
3	SUC	B	2006	23/23	0.89	0.23	0.74	179,215,269,298	0
3	SUC	A	2001	23/23	0.89	0.20	0.68	162,187,209,217	0
3	SUC	B	2002	23/23	0.87	0.19	0.40	147,171,192,200	0

6.5 Other polymers [i](#)

There are no such residues in this entry.