Full wwPDB X-ray Structure Validation Report (i)

Sep 9, 2023 – 11:34 PM EDT

PDB ID	:	4IOU
Title	:	Crystal structure of the HIV-1 Vif binding, catalytically active domain of APOBEC3F
Authors	:	Bohn, M.; Shandilya, S.M.D.; Schiffer, C.A.
Deposited on	:	2013-01-08
Resolution	:	2.75 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 (1)) were used in the production of this report:

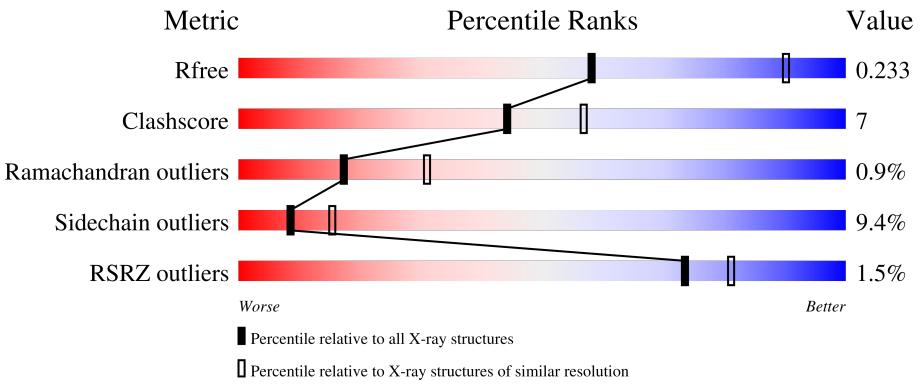
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.75 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}	130704	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	199	.% 66% 22% • 11%
1	B	199	2% 73% 15% • 10%
1	C	199	2% 73% 14% • • 11%
1	D	199	2% 71% 16% • • 10%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5668 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 DNA dC->dU-editing enzyme APOBEC-3F.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	178	1393	904	224	256	9	0	0	0
			Total	C	N	O	S			
1	B	179	1431	926	232	264	9	0	1	0
			Total	C	N	O	S			
1	C	177	1358	888	216	245	9	0	0	0
			Total	C	N	O	S			
1	D	179	1394	902	230	253	9	0	0	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	175	GLY	-	expression tag	UNP Q8IUX4
A	176	PRO	-	expression tag	UNP Q8IUX4
A	177	LEU	-	expression tag	UNP Q8IUX4
A	178	GLY	-	expression tag	UNP Q8IUX4
A	179	SER	-	expression tag	UNP Q8IUX4
A	180	PRO	-	expression tag	UNP Q8IUX4
A	181	GLY	-	expression tag	UNP Q8IUX4
A	182	ILE	-	expression tag	UNP Q8IUX4
A	183	PRO	-	expression tag	UNP Q8IUX4
A	184	GLY	-	expression tag	UNP Q8IUX4
A	196	ASP	TYR	engineered mutation	UNP Q8IUX4
A	247	GLY	HIS	engineered mutation	UNP Q8IUX4
A	248	ARG	CYS	engineered mutation	UNP Q8IUX4
A	259	ALA	CYS	engineered mutation	UNP Q8IUX4
A	302	LYS	PHE	engineered mutation	UNP Q8IUX4
A	310	ASP	TRP	engineered mutation	UNP Q8IUX4
A	314	ALA	TYR	engineered mutation	UNP Q8IUX4
A	315	ALA	GLN	engineered mutation	UNP Q8IUX4
A	355	ASP	LYS	engineered mutation	UNP Q8IUX4
A	358	ASP	LYS	engineered mutation	UNP Q8IUX4
A	363	ASP	PHE	engineered mutation	UNP Q8IUX4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	175	GLY	-	expression tag	UNP Q8IUX4
B	176	PRO	-	expression tag	UNP Q8IUX4
B	177	LEU	-	expression tag	UNP Q8IUX4
B	178	GLY	-	expression tag	UNP Q8IUX4
B	179	SER	-	expression tag	UNP Q8IUX4
B	180	PRO	-	expression tag	UNP Q8IUX4
B	181	GLY	-	expression tag	UNP Q8IUX4
B	182	ILE	-	expression tag	UNP Q8IUX4
B	183	PRO	-	expression tag	UNP Q8IUX4
B	184	GLY	-	expression tag	UNP Q8IUX4
B	196	ASP	TYR	engineered mutation	UNP Q8IUX4
B	247	GLY	HIS	engineered mutation	UNP Q8IUX4
B	248	ARG	CYS	engineered mutation	UNP Q8IUX4
B	259	ALA	CYS	engineered mutation	UNP Q8IUX4
B	302	LYS	PHE	engineered mutation	UNP Q8IUX4
B	310	ASP	TRP	engineered mutation	UNP Q8IUX4
B	314	ALA	TYR	engineered mutation	UNP Q8IUX4
B	315	ALA	GLN	engineered mutation	UNP Q8IUX4
B	355	ASP	LYS	engineered mutation	UNP Q8IUX4
B	358	ASP	LYS	engineered mutation	UNP Q8IUX4
B	363	ASP	PHE	engineered mutation	UNP Q8IUX4
C	175	GLY	-	expression tag	UNP Q8IUX4
C	176	PRO	-	expression tag	UNP Q8IUX4
C	177	LEU	-	expression tag	UNP Q8IUX4
C	178	GLY	-	expression tag	UNP Q8IUX4
C	179	SER	-	expression tag	UNP Q8IUX4
C	180	PRO	-	expression tag	UNP Q8IUX4
C	181	GLY	-	expression tag	UNP Q8IUX4
C	182	ILE	-	expression tag	UNP Q8IUX4
C	183	PRO	-	expression tag	UNP Q8IUX4
C	184	GLY	-	expression tag	UNP Q8IUX4
C	196	ASP	TYR	engineered mutation	UNP Q8IUX4
C	247	GLY	HIS	engineered mutation	UNP Q8IUX4
C	248	ARG	CYS	engineered mutation	UNP Q8IUX4
C	259	ALA	CYS	engineered mutation	UNP Q8IUX4
C	302	LYS	PHE	engineered mutation	UNP Q8IUX4
C	310	ASP	TRP	engineered mutation	UNP Q8IUX4
C	314	ALA	TYR	engineered mutation	UNP Q8IUX4
C	315	ALA	GLN	engineered mutation	UNP Q8IUX4
C	355	ASP	LYS	engineered mutation	UNP Q8IUX4
C	358	ASP	LYS	engineered mutation	UNP Q8IUX4
C	363	ASP	PHE	engineered mutation	UNP Q8IUX4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	175	GLY	-	expression tag	UNP Q8IUX4
D	176	PRO	-	expression tag	UNP Q8IUX4
D	177	LEU	-	expression tag	UNP Q8IUX4
D	178	GLY	-	expression tag	UNP Q8IUX4
D	179	SER	-	expression tag	UNP Q8IUX4
D	180	PRO	-	expression tag	UNP Q8IUX4
D	181	GLY	-	expression tag	UNP Q8IUX4
D	182	ILE	-	expression tag	UNP Q8IUX4
D	183	PRO	-	expression tag	UNP Q8IUX4
D	184	GLY	-	expression tag	UNP Q8IUX4
D	196	ASP	TYR	engineered mutation	UNP Q8IUX4
D	247	GLY	HIS	engineered mutation	UNP Q8IUX4
D	248	ARG	CYS	engineered mutation	UNP Q8IUX4
D	259	ALA	CYS	engineered mutation	UNP Q8IUX4
D	302	LYS	PHE	engineered mutation	UNP Q8IUX4
D	310	ASP	TRP	engineered mutation	UNP Q8IUX4
D	314	ALA	TYR	engineered mutation	UNP Q8IUX4
D	315	ALA	GLN	engineered mutation	UNP Q8IUX4
D	355	ASP	LYS	engineered mutation	UNP Q8IUX4
D	358	ASP	LYS	engineered mutation	UNP Q8IUX4
D	363	ASP	PHE	engineered mutation	UNP Q8IUX4

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
2	A	1	1	1	0	0
2	B	1	1	1	0	0
2	C	1	1	1	0	0
2	D	1	1	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	19	19	19	0	0
3	B	27	27	27	0	0
3	C	23	23	23	0	0

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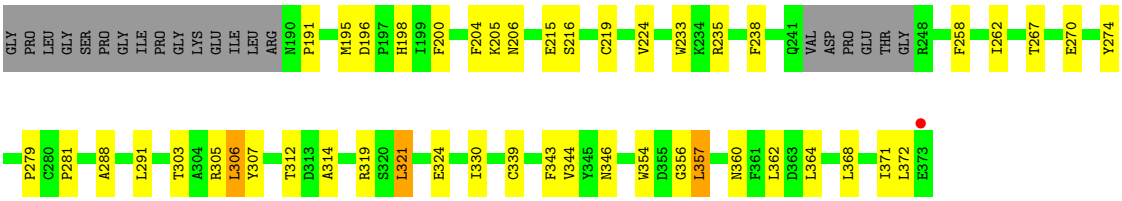
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	D	19	19	19	0	0

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.

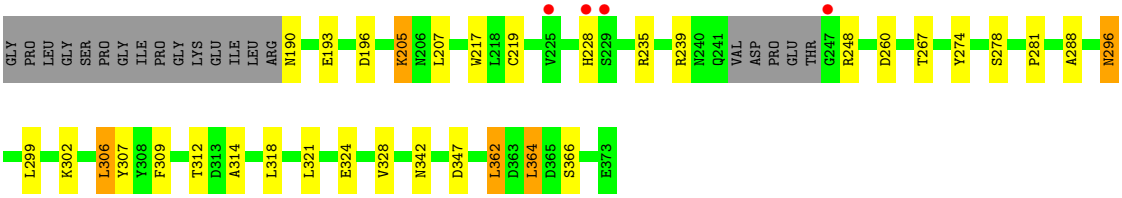
• Molecule 1: DNA dC->dU-editing enzyme APOBEC-3F

Chain A:



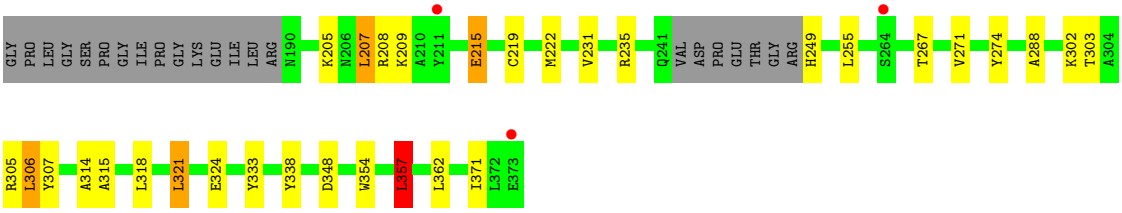
• Molecule 1: DNA dC->dU-editing enzyme APOBEC-3F

Chain B:



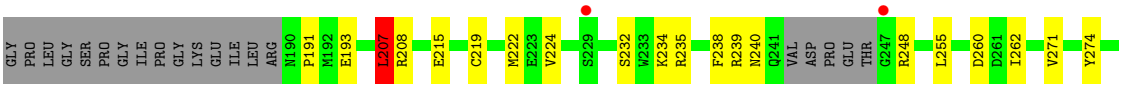
• Molecule 1: DNA dC->dU-editing enzyme APOBEC-3F

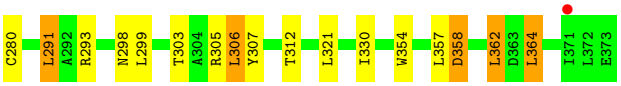
Chain C:



• Molecule 1: DNA dC->dU-editing enzyme APOBEC-3F

Chain D:




C280
L291
A292
R293
N298
L299
T303
A304
R305
L306
Y307
T312
L321
I330
W354
L357
D358
L362
D363
L364
I371
L372
E373

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	50.79Å 66.91Å 75.64Å 110.75° 94.41° 108.83°	Depositor
Resolution (Å)	36.46 – 2.75 36.89 – 2.75	Depositor EDS
% Data completeness (in resolution range)	96.0 (36.46-2.75) 92.9 (36.89-2.75)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.22 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309, REFMAC 5.7.0025	Depositor
R, R_{free}	0.193 , 0.233 0.193 , 0.233	Depositor DCC
R_{free} test set	1099 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	43.8	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 65.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5668	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.00% 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: ZN

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	0.24	0/1441	0.42	0/1972
1	B	0.24	0/1484	0.41	0/2027
1	C	0.24	0/1406	0.42	1/1929 (0.1%)
1	D	0.24	0/1441	0.42	1/1970 (0.1%)
All	All	0.24	0/5772	0.42	2/7898 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	207	LEU	CA-CB-CG	5.24	127.35	115.30
1	C	357	LEU	CA-CB-CG	5.04	126.90	115.30

There are no chirality outliers.

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	1393	0	1205	22	0
1	B	1431	0	1259	16	1
1	C	1358	0	1156	15	1
1	D	1394	0	1211	18	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	19	0	0	0	0
3	B	27	0	0	0	0
3	C	23	0	0	2	0
3	D	19	0	0	1	0
All	All	5668	0	4831	69	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 7.

All (69) 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:D:215:GLU:OE2	1:D:239:ARG:NH2	2.25	0.68
1:D:222:MET:HG3	1:D:271:VAL:HG22	1.74	0.67
1:C:235:ARG:NH1	1:C:338:TYR:OH	2.30	0.64
1:B:205:LYS:HG2	1:B:207:LEU:HD22	1.80	0.62
1:C:207:LEU:O	1:C:209:LYS:N	2.34	0.60
1:C:222:MET:HG3	1:C:271:VAL:HG22	1.82	0.60
1:A:233:TRP:HZ3	1:A:235:ARG:HG2	1.67	0.60
1:C:249:HIS:N	3:C:1117:HOH:O	2.34	0.60
1:C:205:LYS:O	1:C:305:ARG:NH2	2.34	0.59
1:C:219:CYS:HB2	1:C:274:TYR:HB2	1.85	0.59
1:A:307:TYR:CZ	1:A:314:ALA:HB1	2.39	0.58
1:A:303:THR:OG1	1:A:305:ARG:O	2.20	0.57
1:B:219:CYS:HB2	1:B:274:TYR:HB2	1.86	0.57
1:D:219:CYS:HB2	1:D:274:TYR:HB2	1.86	0.57
1:A:205:LYS:O	1:A:305:ARG:NH1	2.39	0.56
1:B:281:PRO:HG3	1:B:314:ALA:HA	1.88	0.55
1:A:196:ASP:OD1	1:A:198:HIS:ND1	2.35	0.55
1:C:303:THR:OG1	1:C:305:ARG:O	2.19	0.54
1:B:217:TRP:CE2	1:B:239:ARG:HG3	2.42	0.54
1:B:296:ASN:OD1	1:B:296:ASN:N	2.33	0.53
1:A:195:MET:HE3	1:A:200:PHE:HD1	1.73	0.53
1:B:288:ALA:HB1	1:B:324:GLU:HG3	1.90	0.52
1:A:356:GLY:O	1:A:360:ASN:ND2	2.28	0.50
1:D:358:ASP:N	1:D:358:ASP:OD1	2.45	0.50
1:B:228:HIS:HE1	1:D:298:ASN:HB3	1.78	0.48
1:B:306:LEU:HB3	1:B:307:TYR:H	1.55	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:PRO:HB3	1:A:238:PHE:CZ	2.49	0.47
1:D:303:THR:OG1	1:D:305:ARG:O	2.21	0.47
1:D:224:VAL:HB	1:D:232:SER:HB3	1.95	0.47
1:A:288:ALA:HB1	1:A:324:GLU:HG3	1.97	0.46
1:B:193:GLU:O	1:B:235:ARG:NH1	2.42	0.46
1:D:193:GLU:O	1:D:235:ARG:NH1	2.25	0.46
1:C:274:TYR:CE2	1:C:302:LYS:HD3	2.51	0.45
1:A:281:PRO:HG3	1:A:314:ALA:HA	1.99	0.45
1:A:319:ARG:NE	1:A:371:ILE:O	2.44	0.45
1:D:207:LEU:H	1:D:207:LEU:HD12	1.81	0.45
1:C:307:TYR:CZ	1:C:314:ALA:HB1	2.52	0.45
1:A:354:TRP:CE2	1:A:357:LEU:HD22	2.52	0.45
1:C:288:ALA:HB1	1:C:324:GLU:HG3	1.99	0.45
1:A:258:PHE:HA	1:A:262:ILE:HD13	2.00	0.44
1:A:339:CYS:HA	1:A:343:PHE:HD2	1.83	0.44
1:B:274:TYR:CE2	1:B:302:LYS:HD2	2.52	0.43
1:B:306:LEU:HD12	1:B:306:LEU:HA	1.87	0.43
1:D:330:ILE:HG21	1:D:364:LEU:HB3	2.00	0.43
1:B:235:ARG:NH1	1:B:342:ASN:O	2.48	0.43
1:C:315:ALA:HB1	1:C:371:ILE:HG23	2.01	0.42
1:D:293:ARG:NH1	3:D:1110:HOH:O	2.48	0.42
1:C:354:TRP:CE2	1:C:357:LEU:HD22	2.54	0.42
1:A:219:CYS:HB2	1:A:274:TYR:HB2	2.01	0.42
1:B:364:LEU:HD12	1:B:364:LEU:HA	1.87	0.42
1:D:291:LEU:HD12	1:D:291:LEU:HA	1.88	0.42
1:A:344:VAL:O	1:A:346:ASN:ND2	2.53	0.42
1:B:217:TRP:CZ2	1:B:239:ARG:HG3	2.55	0.42
1:C:215:GLU:O	3:C:1107:HOH:O	2.21	0.42
1:D:362:LEU:HD13	1:D:362:LEU:HA	1.91	0.42
1:D:234:LYS:HE2	1:D:262:ILE:HD12	2.02	0.42
1:C:321:LEU:HD12	1:C:321:LEU:HA	1.92	0.41
1:A:321:LEU:HD12	1:A:321:LEU:HA	1.87	0.41
1:B:362:LEU:HD12	1:B:362:LEU:HA	1.85	0.41
1:D:354:TRP:CE2	1:D:357:LEU:HD12	2.55	0.41
1:A:279:PRO:O	1:A:307:TYR:OH	2.19	0.41
1:D:306:LEU:HB3	1:D:307:TYR:H	1.48	0.41
1:A:206:ASN:OD1	1:A:354:TRP:NE1	2.42	0.41
1:D:306:LEU:HD12	1:D:306:LEU:HA	1.81	0.41
1:A:270:GLU:HG2	1:B:309:PHE:HD2	1.86	0.40
1:D:191:PRO:HB3	1:D:238:PHE:CE2	2.57	0.40
1:A:200:PHE:O	1:A:204:PHE:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:ILE:HG12	1:A:368:LEU:HD22	2.03	0.40
1:C:306:LEU:HB3	1:C:307:TYR:H	1.57	0.40

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)
1:B:260:ASP:OD2	1:C:333:TYR:OH[1_444]	2.10	0.10

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	174/199 (87%)	166 (95%)	7 (4%)	1 (1%)	25	42
1	B	176/199 (88%)	170 (97%)	5 (3%)	1 (1%)	25	42
1	C	173/199 (87%)	163 (94%)	8 (5%)	2 (1%)	13	23
1	D	175/199 (88%)	166 (95%)	7 (4%)	2 (1%)	14	25
All	All	698/796 (88%)	665 (95%)	27 (4%)	6 (1%)	17	31

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	248	ARG
1	C	208	ARG
1	D	208	ARG
1	C	207	LEU
1	D	248	ARG
1	A	306	LEU

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	136/176 (77%)	124 (91%)	12 (9%)	10 17
1	B	145/176 (82%)	129 (89%)	16 (11%)	6 10
1	C	127/176 (72%)	117 (92%)	10 (8%)	12 22
1	D	135/176 (77%)	122 (90%)	13 (10%)	8 14
All	All	543/704 (77%)	492 (91%)	51 (9%)	8 15

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	215	GLU
1	A	216	SER
1	A	224	VAL
1	A	267	THR
1	A	291	LEU
1	A	306	LEU
1	A	312	THR
1	A	321	LEU
1	A	357	LEU
1	A	362	LEU
1	A	364	LEU
1	A	372	LEU
1	B	190	ASN
1	B	196	ASP
1	B	205	LYS
1	B	267	THR
1	B	278	SER
1	B	296	ASN
1	B	299	LEU
1	B	306	LEU
1	B	312	THR
1	B	318	LEU
1	B	321	LEU
1	B	328	VAL

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Mol	Chain	Res	Type
1	B	347	ASP
1	B	362	LEU
1	B	364	LEU
1	B	366	SER
1	C	215	GLU
1	C	231	VAL
1	C	255	LEU
1	C	267	THR
1	C	306	LEU
1	C	318	LEU
1	C	321	LEU
1	C	348	ASP
1	C	357	LEU
1	C	362	LEU
1	D	207	LEU
1	D	240	ASN
1	D	255	LEU
1	D	260	ASP
1	D	280	CYS
1	D	291	LEU
1	D	299	LEU
1	D	306	LEU
1	D	312	THR
1	D	321	LEU
1	D	358	ASP
1	D	362	LEU
1	D	364	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	228	HIS
1	B	369	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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

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	178/199 (89%)	-0.08	1 (0%)	89	92	27, 42, 58, 63	0
1	B	179/199 (89%)	-0.03	4 (2%)	62	70	17, 35, 56, 73	0
1	C	177/199 (88%)	-0.02	3 (1%)	70	78	22, 39, 60, 72	0
1	D	179/199 (89%)	-0.09	3 (1%)	70	78	22, 35, 53, 61	0
All	All	713/796 (89%)	-0.06	11 (1%)	73	81	17, 38, 58, 73	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	211	TYR	4.0
1	B	228	HIS	3.1
1	D	247	GLY	2.9
1	B	247	GLY	2.8
1	B	229	SER	2.8
1	C	373	GLU	2.8
1	D	229	SER	2.8
1	D	371	ILE	2.3
1	B	225	VAL	2.1
1	C	264	SER	2.1
1	A	373	GLU	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	ZN	B	1001	1/1	0.91	0.11	49,49,49,49	0
2	ZN	D	1001	1/1	0.94	0.10	45,45,45,45	0
2	ZN	C	1001	1/1	0.95	0.04	50,50,50,50	0
2	ZN	A	1001	1/1	0.98	0.08	61,61,61,61	0

6.5 Other polymers (i)

There are no such residues in this entry.