Full wwPDB X-ray Structure Validation Report (i)

Oct 30, 2023 – 01:55 PM JST

PDB ID	:	5B37
Title	:	Crystal structure of L-tryptophan dehydrogenase from Nostoc punctiforme
Authors	:	Wakamatsu, T.; Sakuraba, H.; Kitamura, M.; Hakumai, Y.; Ohnishi, K.; Ashiuchi, M.; Ohshima, T.
Deposited on	:	2016-02-11
Resolution	:	3.40 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:

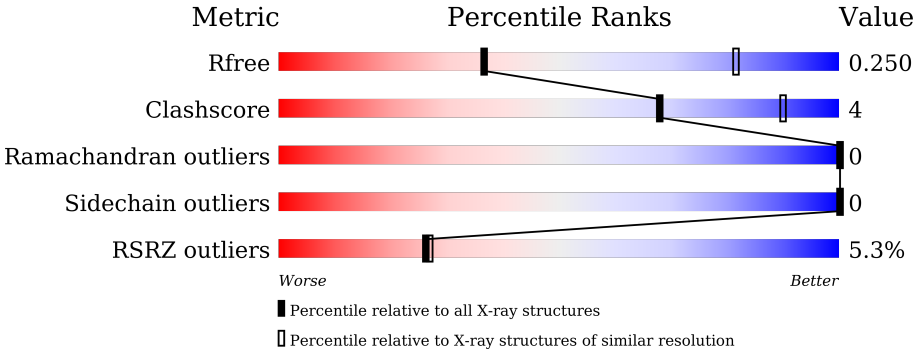
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.40 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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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	361	5% 83% 8% 9%
1	B	361	7% 88% 6% 7%
1	C	361	5% 83% 10% 8%
1	D	361	5% 84% 7% 9%
1	E	361	4% 84% 9% 7%
1	F	361	4% 83% 10% 7%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 15403 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 Tryptophan dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	330	2542	1608	443	481	10	0	0	0
1	B	336	2587	1634	452	491	10	0	0	0
1	C	333	2571	1626	451	484	10	0	0	0
1	D	328	2516	1589	442	475	10	0	0	0
1	E	335	2583	1632	454	487	10	0	0	0
1	F	334	2576	1626	452	488	10	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	354	LEU	-	expression tag	UNP W8CV45
A	355	GLU	-	expression tag	UNP W8CV45
A	356	HIS	-	expression tag	UNP W8CV45
A	357	HIS	-	expression tag	UNP W8CV45
A	358	HIS	-	expression tag	UNP W8CV45
A	359	HIS	-	expression tag	UNP W8CV45
A	360	HIS	-	expression tag	UNP W8CV45
A	361	HIS	-	expression tag	UNP W8CV45
B	354	LEU	-	expression tag	UNP W8CV45
B	355	GLU	-	expression tag	UNP W8CV45
B	356	HIS	-	expression tag	UNP W8CV45
B	357	HIS	-	expression tag	UNP W8CV45
B	358	HIS	-	expression tag	UNP W8CV45
B	359	HIS	-	expression tag	UNP W8CV45
B	360	HIS	-	expression tag	UNP W8CV45
B	361	HIS	-	expression tag	UNP W8CV45
C	354	LEU	-	expression tag	UNP W8CV45

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Chain	Residue	Modelled	Actual	Comment	Reference
C	355	GLU	-	expression tag	UNP W8CV45
C	356	HIS	-	expression tag	UNP W8CV45
C	357	HIS	-	expression tag	UNP W8CV45
C	358	HIS	-	expression tag	UNP W8CV45
C	359	HIS	-	expression tag	UNP W8CV45
C	360	HIS	-	expression tag	UNP W8CV45
C	361	HIS	-	expression tag	UNP W8CV45
D	354	LEU	-	expression tag	UNP W8CV45
D	355	GLU	-	expression tag	UNP W8CV45
D	356	HIS	-	expression tag	UNP W8CV45
D	357	HIS	-	expression tag	UNP W8CV45
D	358	HIS	-	expression tag	UNP W8CV45
D	359	HIS	-	expression tag	UNP W8CV45
D	360	HIS	-	expression tag	UNP W8CV45
D	361	HIS	-	expression tag	UNP W8CV45
E	354	LEU	-	expression tag	UNP W8CV45
E	355	GLU	-	expression tag	UNP W8CV45
E	356	HIS	-	expression tag	UNP W8CV45
E	357	HIS	-	expression tag	UNP W8CV45
E	358	HIS	-	expression tag	UNP W8CV45
E	359	HIS	-	expression tag	UNP W8CV45
E	360	HIS	-	expression tag	UNP W8CV45
E	361	HIS	-	expression tag	UNP W8CV45
F	354	LEU	-	expression tag	UNP W8CV45
F	355	GLU	-	expression tag	UNP W8CV45
F	356	HIS	-	expression tag	UNP W8CV45
F	357	HIS	-	expression tag	UNP W8CV45
F	358	HIS	-	expression tag	UNP W8CV45
F	359	HIS	-	expression tag	UNP W8CV45
F	360	HIS	-	expression tag	UNP W8CV45
F	361	HIS	-	expression tag	UNP W8CV45

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	2	2	2	0	0
			Total	O		
2	B	3	3	3	0	0
			Total	O		
2	C	6	6	6	0	0
			Total	O		
2	D	6	6	6	0	0

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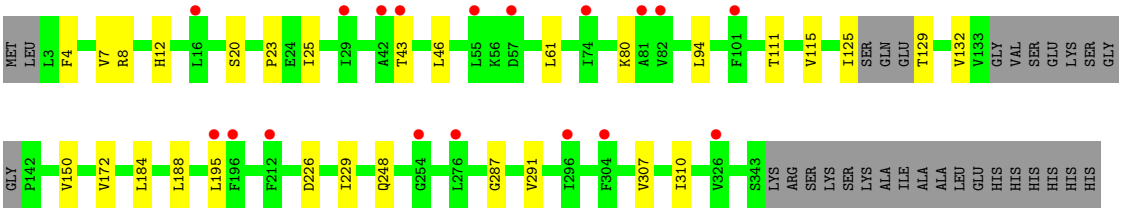
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	E	2	2	2	0	0
			Total	O		
2	F	9	9	9	0	0

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.

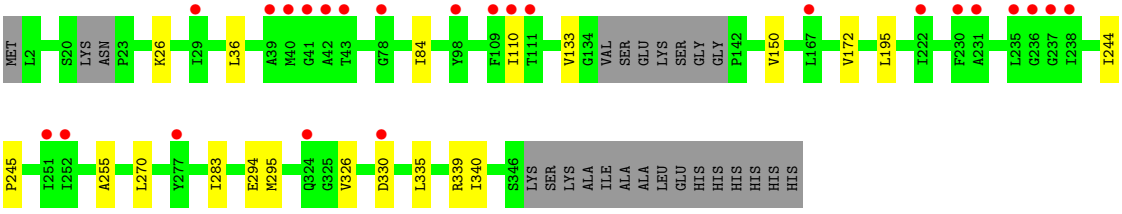
• Molecule 1: Tryptophan dehydrogenase

Chain A:



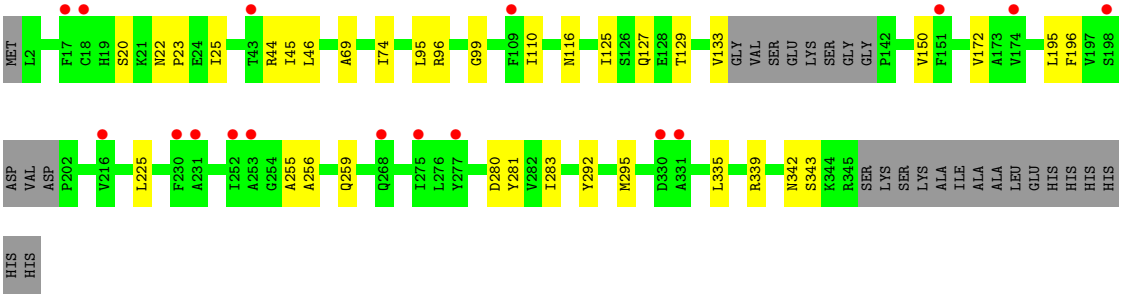
• Molecule 1: Tryptophan dehydrogenase

Chain B:



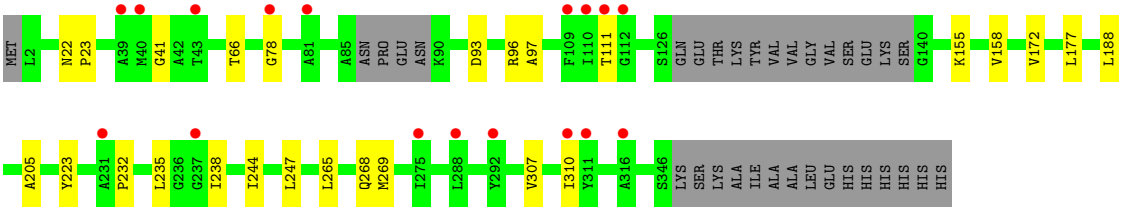
• Molecule 1: Tryptophan dehydrogenase

Chain C:



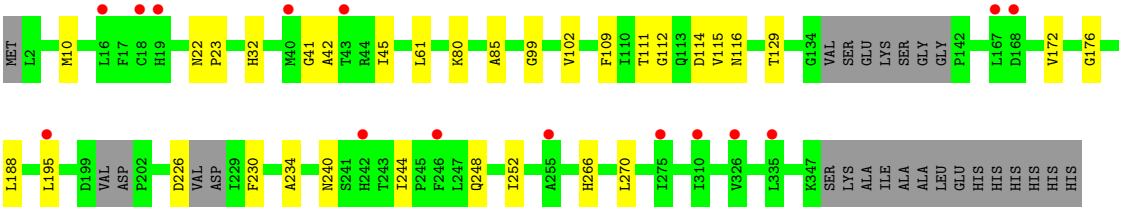
• Molecule 1: Tryptophan dehydrogenase

Chain D:



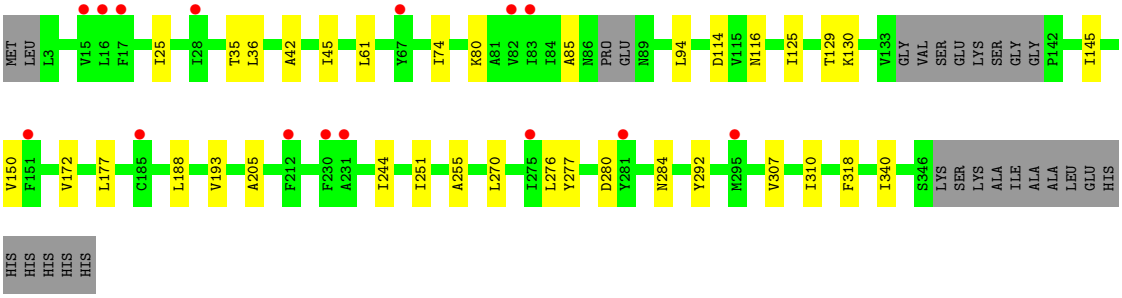
• Molecule 1: Tryptophan dehydrogenase

Chain E:



• Molecule 1: Tryptophan dehydrogenase

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	63.71Å 337.77Å 63.65Å 90.00° 120.03° 90.00°	Depositor
Resolution (Å)	50.00 – 3.40 49.53 – 3.39	Depositor EDS
% Data completeness (in resolution range)	98.2 (50.00-3.40) 98.3 (49.53-3.39)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.24 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.203 , 0.254 0.203 , 0.250	Depositor DCC
R_{free} test set	1494 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å^2)	73.8	Xtriage
Anisotropy	0.292	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 47.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.398 for -h-l,k,h 0.398 for l,k,-h-l 0.417 for -h-l,-k,l 0.408 for l,-k,h 0.408 for h,-k,-h-l	Xtriage
Reported twinning fraction	0.180 for H, K, L 0.144 for -H, -K, H+L 0.194 for H+L, -K, -L 0.167 for L, K, -H-L 0.159 for -H-L, K, H 0.157 for L, -K, H	Depositor
Outliers	0 of 31703 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	15403	wwPDB-VP
Average B, all atoms (Å^2)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% 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)

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	0.38	0/2584	0.62	0/3499
1	B	0.38	0/2629	0.61	0/3557
1	C	0.38	0/2613	0.62	0/3534
1	D	0.40	0/2556	0.64	1/3457 (0.0%)
1	E	0.38	0/2624	0.61	0/3545
1	F	0.39	0/2617	0.62	0/3540
All	All	0.39	0/15623	0.62	1/21132 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	22	ASN	C-N-CD	5.26	139.46	128.40

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	2542	0	2558	19	0
1	B	2587	0	2604	14	0
1	C	2571	0	2598	21	0
1	D	2516	0	2538	17	0
1	E	2583	0	2609	20	0
1	F	2576	0	2595	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2	0	0	0	0
2	B	3	0	0	0	0
2	C	6	0	0	0	0
2	D	6	0	0	0	0
2	E	2	0	0	0	0
2	F	9	0	0	0	0
All	All	15403	0	15502	117	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 4.

All (117) 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:B:172:VAL:HG13	1:B:195:LEU:HD23	1.66	0.76
1:F:172:VAL:HG11	1:F:188:LEU:HD13	1.67	0.75
1:A:172:VAL:HG13	1:A:195:LEU:HD23	1.70	0.73
1:E:172:VAL:HG13	1:E:195:LEU:HD23	1.74	0.69
1:D:155:LYS:HA	1:D:158:VAL:HG22	1.76	0.66
1:D:232:PRO:HB3	1:D:238:ILE:HD13	1.78	0.65
1:A:7:VAL:HG13	1:A:12:HIS:HB2	1.79	0.64
1:D:244:ILE:HD13	1:D:269:MET:HB3	1.78	0.64
1:D:93:ASP:OD1	1:D:96:ARG:NH2	2.31	0.64
1:F:150:VAL:HG21	1:F:255:ALA:HB2	1.81	0.63
1:F:280:ASP:O	1:F:284:ASN:ND2	2.34	0.60
1:D:235:LEU:O	1:D:238:ILE:HD11	2.01	0.60
1:A:307:VAL:O	1:A:310:ILE:HD12	2.02	0.59
1:C:280:ASP:OD1	1:C:281:TYR:N	2.37	0.58
1:E:172:VAL:CG1	1:E:195:LEU:HD23	2.34	0.57
1:D:66:THR:HG23	1:D:78:GLY:HA3	1.86	0.57
1:C:256:ALA:HB3	1:C:259:GLN:HG2	1.87	0.57
1:B:150:VAL:HG21	1:B:255:ALA:HB2	1.86	0.56
1:F:125:ILE:HG22	1:F:129:THR:HG21	1.88	0.56
1:F:244:ILE:HD11	1:F:270:LEU:HG	1.88	0.56
1:A:25:ILE:CG2	1:A:94:LEU:HG	2.36	0.55
1:A:25:ILE:HG21	1:A:94:LEU:HG	1.89	0.54
1:C:99:GLY:O	1:C:129:THR:HB	2.07	0.54
1:D:41:GLY:O	1:D:111:THR:HA	2.08	0.54
1:D:23:PRO:HG3	1:D:97:ALA:HB2	1.90	0.53
1:F:45:ILE:HG23	1:F:116:ASN:HB3	1.90	0.53
1:A:61:LEU:HD13	1:A:80:LYS:HE2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:244:ILE:HD11	1:E:270:LEU:HG	1.89	0.53
1:F:25:ILE:HG12	1:F:94:LEU:HD12	1.91	0.52
1:C:69:ALA:O	1:C:74:ILE:HG22	2.10	0.52
1:A:46:LEU:HD21	1:A:115:VAL:HG11	1.91	0.52
1:B:26:LYS:HG2	1:B:84:ILE:HD13	1.91	0.51
1:D:23:PRO:HG3	1:D:97:ALA:CB	2.41	0.51
1:E:41:GLY:O	1:E:111:THR:HA	2.11	0.51
1:F:307:VAL:O	1:F:310:ILE:HD12	2.11	0.51
1:A:226:ASP:HA	1:A:248:GLN:HB2	1.93	0.50
1:A:111:THR:CG2	1:A:132:VAL:HG12	2.41	0.50
1:E:45:ILE:HD11	1:E:85:ALA:HB3	1.93	0.50
1:C:45:ILE:HG23	1:C:116:ASN:CB	2.42	0.50
1:A:43:THR:OG1	1:A:111:THR:OG1	2.29	0.50
1:D:172:VAL:HG11	1:D:188:LEU:HD13	1.93	0.49
1:C:96:ARG:HD3	1:C:127:GLN:HE21	1.77	0.49
1:E:42:ALA:HA	1:E:112:GLY:H	1.78	0.49
1:A:125:ILE:HG22	1:A:129:THR:HG21	1.93	0.49
1:C:45:ILE:HG23	1:C:116:ASN:HB2	1.94	0.49
1:E:176:GLY:HA3	1:E:234:ALA:HB2	1.95	0.48
1:F:270:LEU:HD13	1:F:277:TYR:HB2	1.95	0.48
1:A:150:VAL:HG13	1:A:184:LEU:HD13	1.95	0.48
1:B:244:ILE:N	1:B:245:PRO:HD2	2.29	0.48
1:F:125:ILE:HG22	1:F:129:THR:CG2	2.44	0.47
1:D:235:LEU:O	1:D:238:ILE:CG1	2.63	0.47
1:F:276:LEU:HD11	1:F:318:PHE:CD1	2.48	0.47
1:F:172:VAL:HG12	1:F:193:VAL:HG12	1.96	0.47
1:C:74:ILE:HD11	1:C:292:TYR:CD2	2.49	0.47
1:C:335:LEU:HD21	1:C:339:ARG:NH1	2.30	0.47
1:B:110:ILE:HG21	1:B:295:MET:SD	2.55	0.47
1:F:45:ILE:HD11	1:F:85:ALA:HB3	1.97	0.47
1:A:20:SER:HB3	1:A:23:PRO:HG2	1.98	0.46
1:E:10:MET:O	1:E:32:HIS:NE2	2.47	0.46
1:B:326:VAL:HG22	1:B:330:ASP:HB2	1.97	0.46
1:D:232:PRO:HB3	1:D:238:ILE:CD1	2.46	0.46
1:B:335:LEU:HD21	1:B:339:ARG:NH1	2.32	0.45
1:E:115:VAL:HG12	1:E:116:ASN:ND2	2.31	0.45
1:F:36:LEU:HD11	1:F:340:ILE:HG12	1.98	0.45
1:F:35:THR:HB	1:F:36:LEU:HD12	1.99	0.45
1:B:36:LEU:HD12	1:B:36:LEU:N	2.32	0.44
1:E:109:PHE:CE2	1:E:111:THR:HG23	2.53	0.44
1:A:7:VAL:CG1	1:A:12:HIS:HB2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:VAL:CG1	1:B:195:LEU:HD23	2.41	0.44
1:F:61:LEU:HD13	1:F:80:LYS:HE2	2.00	0.44
1:F:251:ILE:HG22	1:F:276:LEU:HB3	1.99	0.43
1:C:150:VAL:HG21	1:C:255:ALA:HB2	2.00	0.43
1:C:196:PHE:CG	1:C:225:LEU:HD13	2.53	0.43
1:D:177:LEU:CD1	1:D:205:ALA:HA	2.49	0.43
1:D:223:TYR:O	1:D:247:LEU:HD23	2.18	0.43
1:D:235:LEU:O	1:D:238:ILE:CD1	2.67	0.43
1:E:61:LEU:HD13	1:E:80:LYS:HE2	2.01	0.43
1:C:20:SER:HB3	1:C:25:ILE:HG22	1.99	0.43
1:E:45:ILE:HG23	1:E:116:ASN:HB2	2.01	0.43
1:C:133:VAL:HG11	1:C:295:MET:HG3	2.01	0.43
1:E:99:GLY:O	1:E:129:THR:HB	2.19	0.42
1:F:45:ILE:HG23	1:F:116:ASN:CB	2.49	0.42
1:B:244:ILE:HD11	1:B:270:LEU:HG	2.01	0.42
1:C:22:ASN:HB3	1:C:23:PRO:HD3	2.01	0.42
1:C:110:ILE:HG21	1:C:295:MET:SD	2.59	0.42
1:C:172:VAL:HB	1:C:195:LEU:HD23	2.01	0.42
1:E:102:VAL:HG23	1:E:109:PHE:CD2	2.55	0.42
1:C:74:ILE:HD11	1:C:292:TYR:CG	2.54	0.42
1:E:226:ASP:OD1	1:E:248:GLN:NE2	2.53	0.42
1:B:150:VAL:HG22	1:B:283:ILE:CG2	2.50	0.42
1:C:342:ASN:OD1	1:C:343:SER:N	2.53	0.42
1:E:22:ASN:CG	1:E:23:PRO:HD3	2.40	0.42
1:F:145:ILE:HD11	1:F:307:VAL:HG21	2.02	0.42
1:F:129:THR:HG23	1:F:130:LYS:N	2.35	0.41
1:A:125:ILE:CG2	1:A:129:THR:HG21	2.50	0.41
1:A:172:VAL:HG23	1:A:229:ILE:HG23	2.01	0.41
1:C:44:ARG:HG2	1:C:46:LEU:HD13	2.01	0.41
1:F:177:LEU:CD1	1:F:205:ALA:HA	2.50	0.41
1:C:150:VAL:HA	1:C:283:ILE:HG23	2.03	0.41
1:A:172:VAL:HG11	1:A:188:LEU:HD13	2.02	0.41
1:D:265:LEU:O	1:D:268:GLN:HG2	2.19	0.41
1:A:287:GLY:O	1:A:291:VAL:HG23	2.21	0.41
1:F:74:ILE:HD11	1:F:292:TYR:HB2	2.02	0.41
1:A:4:PHE:O	1:A:8:ARG:HG2	2.21	0.41
1:B:36:LEU:HD11	1:B:340:ILE:HG12	2.03	0.41
1:B:36:LEU:CD1	1:B:340:ILE:HG12	2.51	0.41
1:E:42:ALA:HB1	1:E:114:ASP:HB2	2.03	0.41
1:E:230:PHE:HB3	1:E:252:ILE:HG22	2.02	0.41
1:F:74:ILE:HD11	1:F:292:TYR:CG	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:VAL:CG2	1:B:294:GLU:HB2	2.51	0.40
1:F:74:ILE:HD11	1:F:292:TYR:CB	2.50	0.40
1:E:172:VAL:HG11	1:E:188:LEU:HD13	2.03	0.40
1:E:240:ASN:HA	1:E:266:HIS:CE1	2.56	0.40
1:D:307:VAL:O	1:D:310:ILE:HG12	2.21	0.40
1:F:36:LEU:HD12	1:F:36:LEU:N	2.35	0.40
1:C:95:LEU:O	1:C:125:ILE:HG22	2.21	0.40
1:F:42:ALA:HB1	1:F:114:ASP:HB2	2.02	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	324/361 (90%)	310 (96%)	14 (4%)	0	100	100
1	B	330/361 (91%)	321 (97%)	9 (3%)	0	100	100
1	C	327/361 (91%)	311 (95%)	16 (5%)	0	100	100
1	D	322/361 (89%)	312 (97%)	10 (3%)	0	100	100
1	E	327/361 (91%)	308 (94%)	19 (6%)	0	100	100
1	F	328/361 (91%)	316 (96%)	12 (4%)	0	100	100
All	All	1958/2166 (90%)	1878 (96%)	80 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	271/296 (92%)	271 (100%)	0	100	100
1	B	276/296 (93%)	276 (100%)	0	100	100
1	C	274/296 (93%)	274 (100%)	0	100	100
1	D	267/296 (90%)	267 (100%)	0	100	100
1	E	275/296 (93%)	275 (100%)	0	100	100
1	F	275/296 (93%)	275 (100%)	0	100	100
All	All	1638/1776 (92%)	1638 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	309	ASN
1	C	127	GLN
1	C	266	HIS
1	C	293	ASN
1	D	341	ASN
1	E	116	ASN
1	E	163	GLN
1	F	191	HIS
1	F	194	GLN
1	F	259	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)

There are no ligands in this entry.

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	330/361 (91%)	0.37	18 (5%)	25	25	75, 97, 113, 121	0
1	B	336/361 (93%)	0.44	24 (7%)	16	18	77, 98, 114, 124	0
1	C	333/361 (92%)	0.33	17 (5%)	28	28	75, 97, 113, 128	0
1	D	328/361 (90%)	0.39	17 (5%)	27	27	75, 96, 110, 119	0
1	E	335/361 (92%)	0.34	15 (4%)	33	33	79, 97, 114, 124	0
1	F	334/361 (92%)	0.34	15 (4%)	33	33	78, 96, 114, 123	0
All	All	1996/2166 (92%)	0.37	106 (5%)	26	27	75, 97, 113, 128	0

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	237	GLY	8.9
1	B	236	GLY	7.7
1	C	331	ALA	4.7
1	D	40	MET	4.5
1	B	238	ILE	4.5
1	D	111	THR	4.2
1	C	330	ASP	4.1
1	B	42	ALA	4.0
1	B	41	GLY	3.8
1	C	231	ALA	3.7
1	F	231	ALA	3.6
1	E	275	ILE	3.5
1	F	230	PHE	3.4
1	A	57	ASP	3.4
1	B	40	MET	3.4
1	F	17	PHE	3.3
1	F	83	ILE	3.3
1	F	15	VAL	3.3
1	F	82	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	112	GLY	3.2
1	A	212	PHE	3.2
1	A	82	VAL	3.1
1	B	251	ILE	3.1
1	C	230	PHE	3.1
1	D	43	THR	3.0
1	E	255	ALA	3.0
1	C	277	TYR	3.0
1	B	222	ILE	3.0
1	D	110	ILE	3.0
1	A	43	THR	2.9
1	A	254	GLY	2.9
1	A	55	LEU	2.9
1	D	237	GLY	2.9
1	B	43	THR	2.9
1	E	195	LEU	2.9
1	D	78	GLY	2.9
1	C	109	PHE	2.8
1	A	276	LEU	2.8
1	D	310	ILE	2.8
1	C	268	GLN	2.8
1	C	18	CYS	2.8
1	B	235	LEU	2.7
1	D	109	PHE	2.7
1	F	151	PHE	2.7
1	C	198	SER	2.7
1	A	195	LEU	2.6
1	B	111	THR	2.6
1	F	16	LEU	2.6
1	F	28	ILE	2.6
1	F	281	TYR	2.6
1	F	295	MET	2.6
1	B	98	TYR	2.5
1	B	78	GLY	2.5
1	E	242	HIS	2.5
1	D	311	TYR	2.5
1	A	304	PHE	2.5
1	C	252	ILE	2.5
1	E	43	THR	2.5
1	C	151	PHE	2.5
1	F	212	PHE	2.5
1	B	167	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	110	ILE	2.5
1	F	185	CYS	2.4
1	B	29	ILE	2.4
1	E	168	ASP	2.4
1	B	39	ALA	2.4
1	D	288	LEU	2.4
1	A	74	ILE	2.4
1	D	81	ALA	2.4
1	D	316	ALA	2.4
1	E	246	PHE	2.4
1	A	101	PHE	2.3
1	B	109	PHE	2.3
1	A	326	VAL	2.3
1	C	275	ILE	2.3
1	B	252	ILE	2.3
1	D	292	TYR	2.3
1	A	42	ALA	2.3
1	F	275	ILE	2.2
1	A	81	ALA	2.2
1	B	277	TYR	2.2
1	C	253	ALA	2.2
1	C	17	PHE	2.2
1	C	43	THR	2.2
1	D	231	ALA	2.2
1	E	16	LEU	2.2
1	B	230	PHE	2.2
1	E	310	ILE	2.2
1	E	40	MET	2.2
1	E	167	LEU	2.1
1	D	39	ALA	2.1
1	C	174	VAL	2.1
1	C	216	VAL	2.1
1	D	275	ILE	2.1
1	E	18	CYS	2.1
1	A	16	LEU	2.1
1	E	19	HIS	2.1
1	E	335	LEU	2.1
1	A	29	ILE	2.1
1	A	196	PHE	2.1
1	A	296	ILE	2.1
1	B	231	ALA	2.1
1	F	67	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	324	GLN	2.0
1	E	326	VAL	2.0
1	B	330	ASP	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.