wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 05:16 AM GMT

PDB ID	:	2Q2Q
Title	:	Structure of D-3-Hydroxybutyrate Dehydrogenase from Pseudomonas putida
Authors	:	Paithankar, K.S.; Feller, C.; Kuettner, E.B.; Keim, A.; Grunow, M.; Strater, N.
Deposited on	:	2007-05-29
Resolution	:	2.02 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

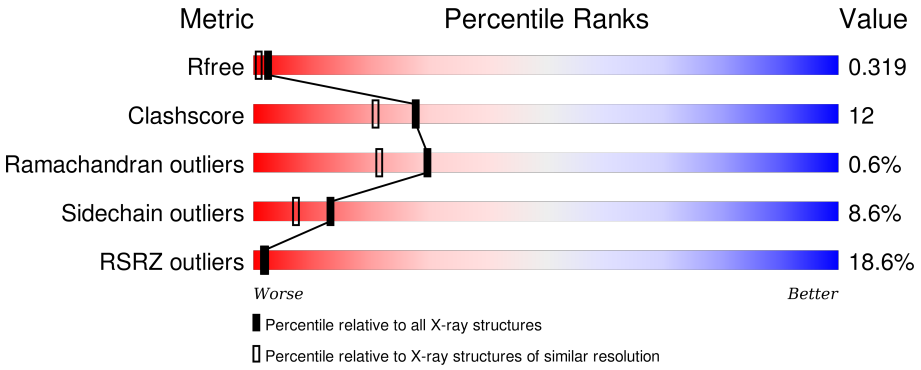
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.02 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	7858 (2.04-2.00)
Clashscore	102246	9060 (2.04-2.00)
Ramachandran outliers	100387	8952 (2.04-2.00)
Sidechain outliers	100360	8951 (2.04-2.00)
RSRZ outliers	91569	7873 (2.04-2.00)

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 <=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	255	18% 71% 24%
1	B	255	12% 76% 20%
1	C	255	26% 67% 24% 5% 5%
1	D	255	19% 73% 22% 5%
1	E	255	17% 68% 24% 5%

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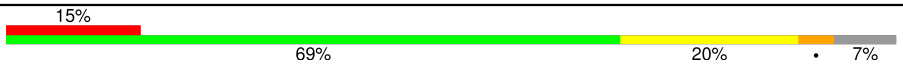
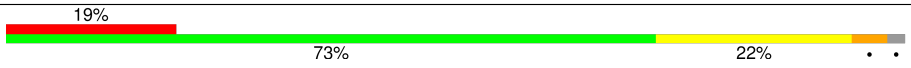
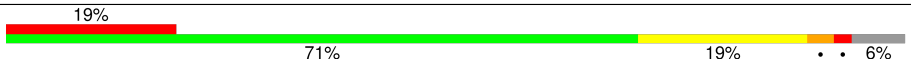
Mol	Chain	Length	Quality of chain
1	F	255	
1	G	255	
1	H	255	

2 Entry composition (i)

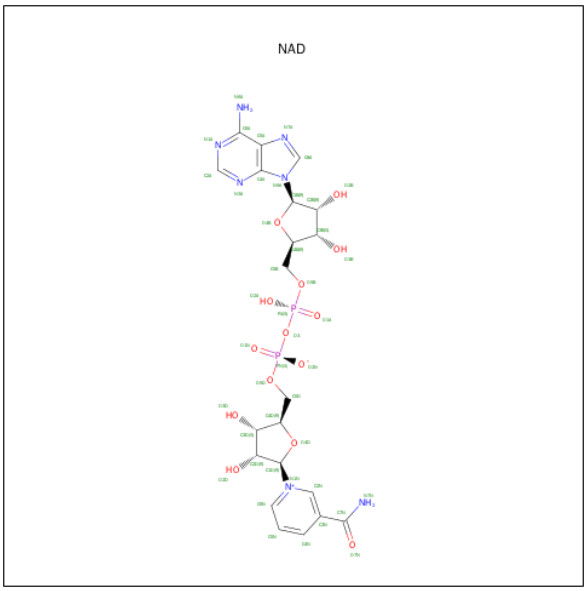
There are 3 unique types of molecules in this entry. The entry contains 15261 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Beta-D-hydroxybutyrate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1843	1171	330	338	4			
1	B	252	Total	C	N	O	S	0	0	0
			1852	1176	332	340	4			
1	C	243	Total	C	N	O	S	0	0	0
			1784	1137	319	324	4			
1	D	255	Total	C	N	O	S	0	0	0
			1869	1185	336	344	4			
1	E	249	Total	C	N	O	S	0	0	0
			1833	1165	329	335	4			
1	F	238	Total	C	N	O	S	0	0	0
			1742	1110	311	317	4			
1	G	251	Total	C	N	O	S	0	0	0
			1845	1173	331	337	4			
1	H	240	Total	C	N	O	S	0	0	0
			1758	1120	314	320	4			

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	61	Total	O	0	0
			61	61		
3	B	83	Total	O	0	0
			83	83		
3	C	37	Total	O	0	0
			37	37		
3	D	70	Total	O	0	0
			70	70		
3	E	55	Total	O	0	0
			55	55		
3	F	50	Total	O	0	0
			50	50		

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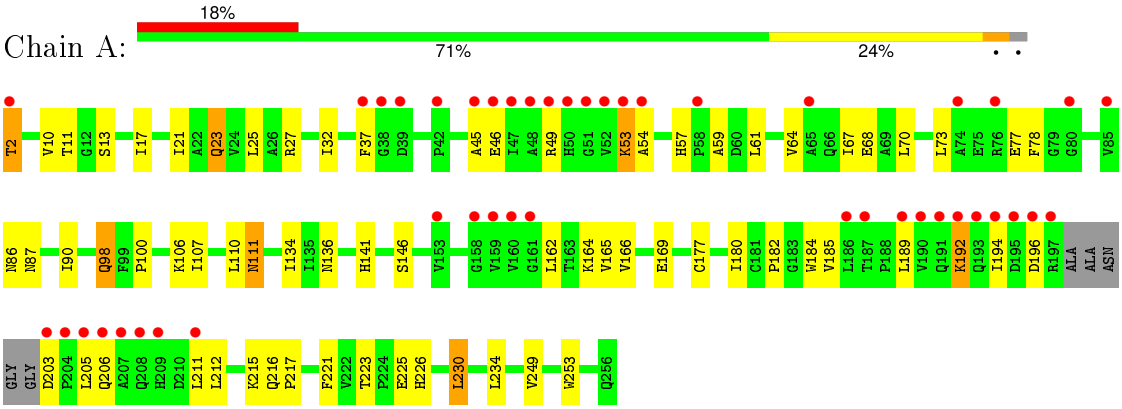
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	71	Total O 71 71	0	0
3	H	44	Total O 44 44	0	0

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.

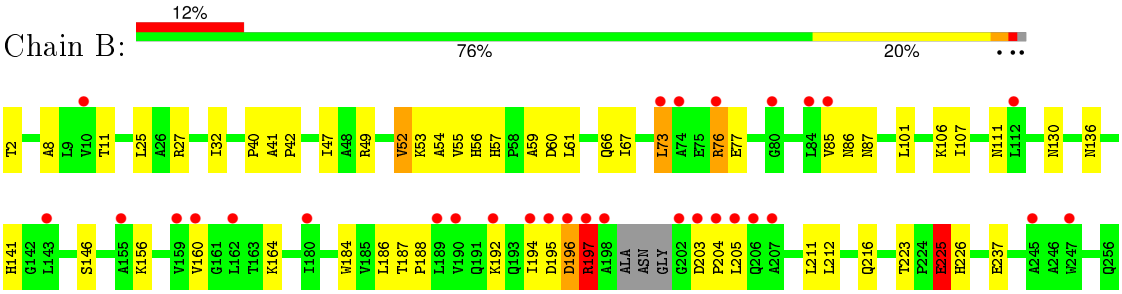
- Molecule 1: Beta-D-hydroxybutyrate dehydrogenase

Chain A:



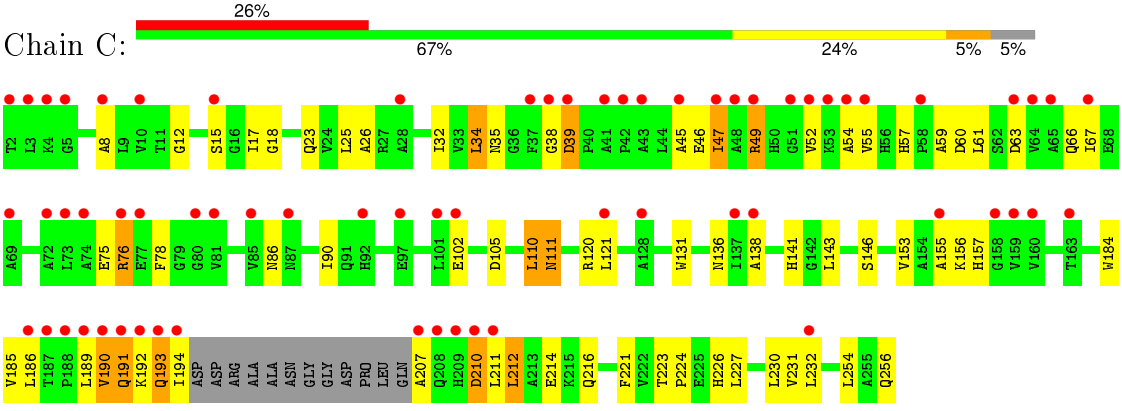
- Molecule 1: Beta-D-hydroxybutyrate dehydrogenase

Chain B:



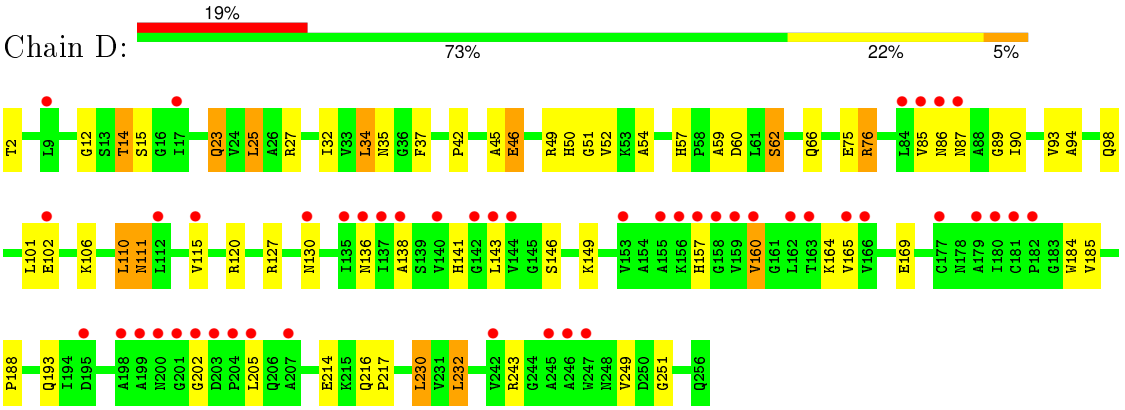
- Molecule 1: Beta-D-hydroxybutyrate dehydrogenase

Chain C:



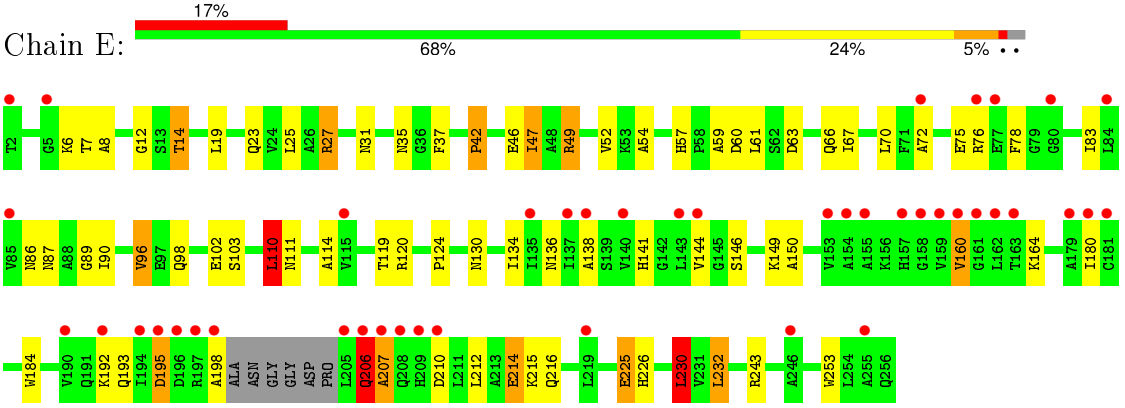
- Molecule 1: Beta-D-hydroxybutyrate dehydrogenase

Chain D:



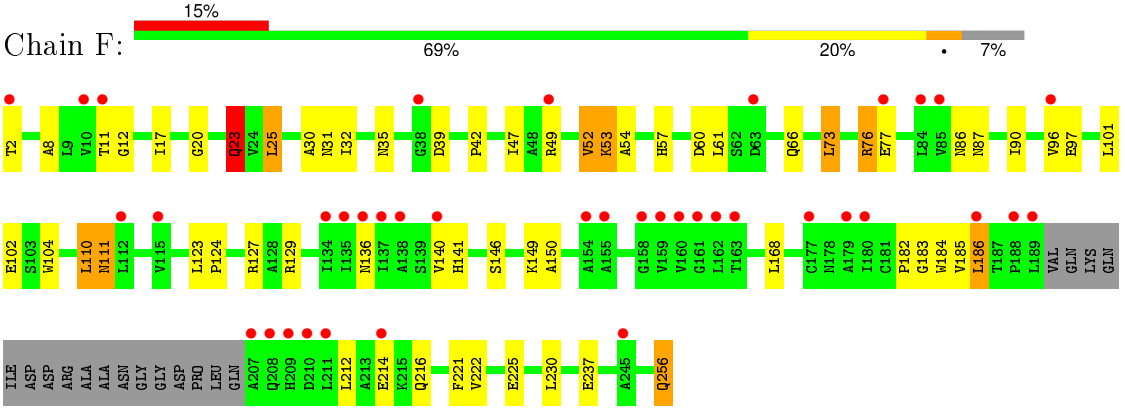
• Molecule 1: Beta-D-hydroxybutyrate dehydrogenase

Chain E:



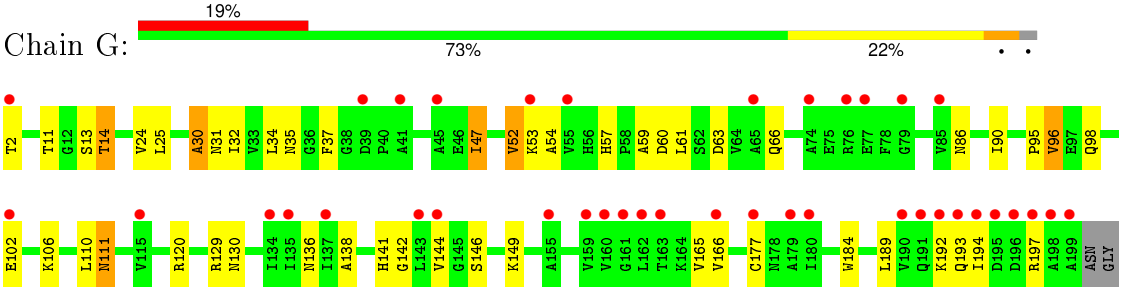
• Molecule 1: Beta-D-hydroxybutyrate dehydrogenase

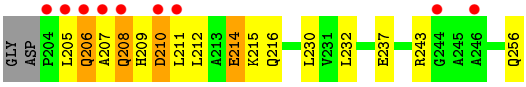
Chain F:



• Molecule 1: Beta-D-hydroxybutyrate dehydrogenase

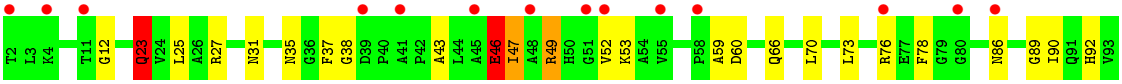
Chain G:

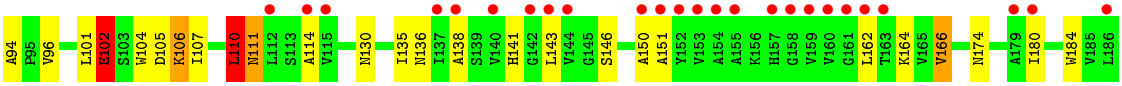


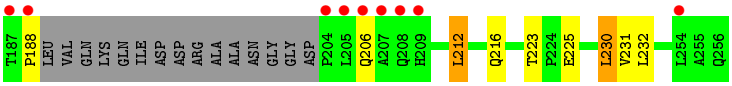


• Molecule 1: Beta-D-hydroxybutyrate dehydrogenase

Chain H:







4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	261.46Å 59.91Å 116.52Å 90.00° 113.70° 90.00°	Depositor
Resolution (Å)	30.00 – 2.02 29.96 – 2.02	Depositor EDS
% Data completeness (in resolution range)	96.4 (30.00-2.02) 96.4 (29.96-2.02)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.27 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.199 , 0.274 0.255 , 0.319	Depositor DCC
R_{free} test set	5241 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	36.6	Xtriage
Anisotropy	0.515	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 57.4	EDS
Estimated twinning fraction	0.009 for -h-2*l,-k,l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.36$	Xtriage
Outliers	0 of 104909 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	15261	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.55 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.5024e-04.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: NAD

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	1.20	4/1879 (0.2%)	0.99	1/2560 (0.0%)
1	B	1.20	5/1888 (0.3%)	1.04	5/2572 (0.2%)
1	C	1.06	2/1819 (0.1%)	1.00	2/2478 (0.1%)
1	D	1.39	12/1906 (0.6%)	1.16	15/2598 (0.6%)
1	E	1.37	8/1868 (0.4%)	1.18	11/2544 (0.4%)
1	F	1.33	8/1777 (0.5%)	1.05	5/2422 (0.2%)
1	G	1.33	14/1881 (0.7%)	1.13	10/2562 (0.4%)
1	H	1.32	8/1794 (0.4%)	1.11	7/2445 (0.3%)
All	All	1.28	61/14812 (0.4%)	1.08	56/20181 (0.3%)

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	E	0	2
1	H	0	2
All	All	0	4

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	206	GLN	CD-OE1	15.60	1.58	1.24
1	G	209	HIS	CE1-NE2	14.02	1.65	1.32
1	E	206	GLN	CD-NE2	13.54	1.66	1.32
1	D	75	GLU	CG-CD	12.25	1.70	1.51
1	G	209	HIS	CG-ND1	10.21	1.61	1.38

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	243	ARG	NE-CZ-NH2	-13.92	113.34	120.30
1	E	243	ARG	NE-CZ-NH1	12.62	126.61	120.30
1	G	129	ARG	NE-CZ-NH2	-9.81	115.40	120.30
1	C	63	ASP	CB-CG-OD2	8.27	125.74	118.30
1	E	63	ASP	CB-CG-OD1	7.68	125.21	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	206	GLN	Sidechain
1	E	207	ALA	Peptide
1	H	38	GLY	Peptide
1	H	49	ARG	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	1843	0	1865	57	0
1	B	1852	0	1873	35	0
1	C	1784	0	1814	56	0
1	D	1869	0	1888	43	0
1	E	1833	0	1859	51	0
1	F	1742	0	1765	46	0
1	G	1845	0	1872	33	0
1	H	1758	0	1781	38	0
2	C	44	0	26	1	0
2	D	44	0	26	2	0
2	E	44	0	26	4	0
2	F	44	0	26	3	0
2	G	44	0	26	2	0
2	H	44	0	26	1	0
3	A	61	0	0	2	0
3	B	83	0	0	2	0
3	C	37	0	0	1	0
3	D	70	0	0	4	0
3	E	55	0	0	1	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	50	0	0	1	0
3	G	71	0	0	1	1
3	H	44	0	0	2	0
All	All	15261	0	14873	350	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 12.

The worst 5 of 350 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:C:32:ILE:HG22	1:C:34:LEU:HD13	1.27	1.08
1:F:186:LEU:HD23	1:F:186:LEU:H	1.19	1.07
1:C:32:ILE:HG22	1:C:34:LEU:CD1	1.90	1.01
1:E:184:TRP:H	1:E:216:GLN:HE22	1.09	1.00
1:C:32:ILE:CG2	1:C:34:LEU:CD1	2.39	0.99

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)
3:E:336:HOH:O	3:G:332:HOH:O[2_555]	1.98	0.22

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	246/255 (96%)	237 (96%)	9 (4%)	0	100 100
1	B	248/255 (97%)	230 (93%)	15 (6%)	3 (1%)	16 8
1	C	239/255 (94%)	224 (94%)	13 (5%)	2 (1%)	24 15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	D	253/255 (99%)	244 (96%)	8 (3%)	1 (0%)	39 32
1	E	245/255 (96%)	233 (95%)	11 (4%)	1 (0%)	39 32
1	F	234/255 (92%)	226 (97%)	8 (3%)	0	100 100
1	G	247/255 (97%)	237 (96%)	7 (3%)	3 (1%)	16 8
1	H	236/255 (92%)	220 (93%)	14 (6%)	2 (1%)	24 15
All	All	1948/2040 (96%)	1851 (95%)	85 (4%)	12 (1%)	30 21

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	39	ASP
1	H	46	GLU
1	H	47	ILE
1	G	207	ALA
1	B	196	ASP

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	188/189 (100%)	175 (93%)	13 (7%)	19 12
1	B	188/189 (100%)	175 (93%)	13 (7%)	19 12
1	C	181/189 (96%)	159 (88%)	22 (12%)	6 3
1	D	189/189 (100%)	174 (92%)	15 (8%)	15 9
1	E	186/189 (98%)	166 (89%)	20 (11%)	8 4
1	F	176/189 (93%)	161 (92%)	15 (8%)	13 7
1	G	187/189 (99%)	169 (90%)	18 (10%)	10 5
1	H	178/189 (94%)	168 (94%)	10 (6%)	26 19
All	All	1473/1512 (97%)	1347 (91%)	126 (9%)	13 7

5 of 126 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	102	GLU
1	E	75	GLU
1	H	23	GLN
1	D	111	ASN
1	E	6	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	136	ASN
1	E	66	GLN
1	H	92	HIS
1	D	216	GLN
1	E	111	ASN

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)

6 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	$\#\|Z\|>2$
2	NAD	C	300	-	38,48,48	1.87	5 (13%)	47,73,73	2.39	8 (17%)
2	NAD	D	300	-	38,48,48	1.48	7 (18%)	47,73,73	2.79	12 (25%)
2	NAD	E	300	-	38,48,48	1.53	5 (13%)	47,73,73	2.60	11 (23%)
2	NAD	F	300	-	38,48,48	1.71	6 (15%)	47,73,73	2.57	8 (17%)
2	NAD	G	300	-	38,48,48	1.62	4 (10%)	47,73,73	1.73	6 (12%)
2	NAD	H	300	-	38,48,48	1.74	7 (18%)	47,73,73	2.71	7 (14%)

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
2	NAD	C	300	-	-	0/22/62/62	0/5/5/5
2	NAD	D	300	-	-	0/22/62/62	0/5/5/5
2	NAD	E	300	-	-	0/22/62/62	0/5/5/5
2	NAD	F	300	-	-	0/22/62/62	0/5/5/5
2	NAD	G	300	-	-	0/22/62/62	0/5/5/5
2	NAD	H	300	-	-	0/22/62/62	0/5/5/5

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	300	NAD	C2N-C3N	-3.06	1.34	1.39
2	D	300	NAD	PA-O2A	-2.10	1.46	1.54
2	C	300	NAD	O4D-C1D	2.02	1.43	1.41
2	H	300	NAD	O4D-C1D	2.11	1.43	1.41
2	F	300	NAD	O4B-C1B	2.18	1.44	1.41

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	300	NAD	N3A-C2A-N1A	-14.74	117.61	128.89
2	C	300	NAD	N3A-C2A-N1A	-11.44	120.13	128.89
2	E	300	NAD	N3A-C2A-N1A	-10.40	120.93	128.89
2	F	300	NAD	N3A-C2A-N1A	-9.98	121.25	128.89
2	D	300	NAD	N3A-C2A-N1A	-8.60	122.31	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	300	NAD	1	0
2	D	300	NAD	2	0
2	E	300	NAD	4	0
2	F	300	NAD	3	0
2	G	300	NAD	2	0
2	H	300	NAD	1	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, 95^{th} 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	250/255 (98%)	0.95	45 (18%)	2 2	36, 42, 52, 60	0
1	B	252/255 (98%)	0.78	30 (11%)	6 6	35, 42, 48, 59	0
1	C	243/255 (95%)	1.34	66 (27%)	1 1	35, 42, 50, 57	0
1	D	255/255 (100%)	0.88	48 (18%)	2 2	37, 42, 50, 59	0
1	E	249/255 (97%)	0.98	44 (17%)	2 2	36, 42, 48, 57	0
1	F	238/255 (93%)	0.94	39 (16%)	2 3	35, 42, 50, 55	0
1	G	251/255 (98%)	1.10	48 (19%)	2 2	35, 42, 49, 56	0
1	H	240/255 (94%)	0.98	48 (20%)	1 1	36, 42, 53, 63	0
All	All	1978/2040 (96%)	0.99	368 (18%)	2 2	35, 42, 50, 63	0

The worst 5 of 368 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	205	LEU	11.2
1	C	190	VAL	10.8
1	G	198	ALA	10.5
1	G	199	ALA	8.7
1	C	2	THR	8.6

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

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, 95^{th} 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
2	NAD	C	300	44/44	0.80	0.16	-0.44	47,62,73,77	0
2	NAD	F	300	44/44	0.90	0.14	-0.51	39,51,56,59	0
2	NAD	D	300	44/44	0.95	0.11	-0.78	25,35,41,44	0
2	NAD	G	300	44/44	0.95	0.09	-1.04	35,42,48,52	0
2	NAD	E	300	44/44	0.95	0.09	-1.11	30,39,45,49	0
2	NAD	H	300	44/44	0.94	0.09	-1.12	33,42,47,51	0

6.5 Other polymers

There are no such residues in this entry.