Full wwPDB X-ray Structure Validation Report (i)

Oct 23, 2021 – 09:27 AM EDT

PDB ID	:	1F91
Title	:	BETA-KETOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I IN COMPLEX WITH C10 FATTY ACID SUBSTRATE
Authors	:	Olsen, J.G.; Kadziola, A.; Wettstein-Knowles, P.V.; Siggaard-Andersen, M.; Larsen, S.
Deposited on	:	2000-07-06
Resolution	:	2.40 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 following versions of software and data (see references (i)) were used in the production of this report:

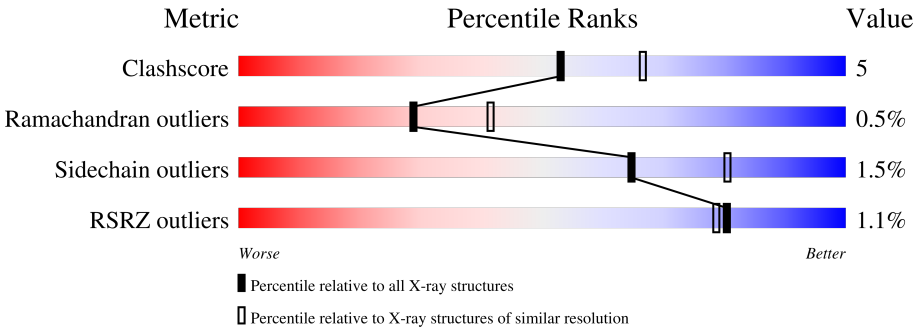
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.40 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))
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	406	% 89% 11%
1	B	406	94% 5% •
1	C	406	% 90% 9% •
1	D	406	2% 87% 12% •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 12400 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.

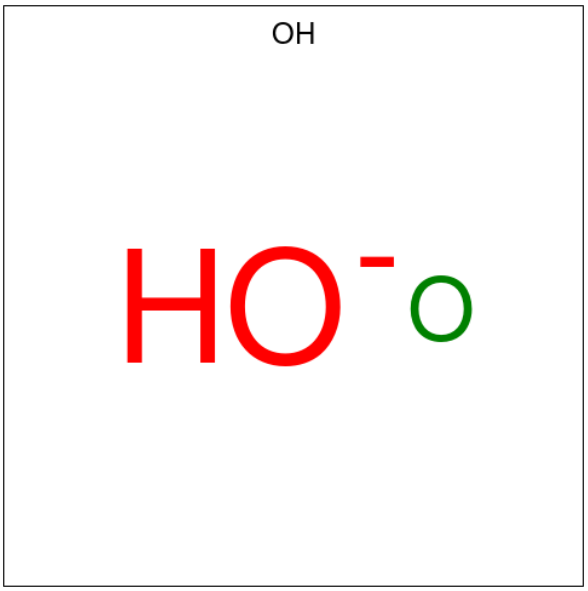
- Molecule 1 is a protein called BETA-KETOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	406	2983	1855	519	587	22	0	0	0
1	B	406	2983	1855	519	587	22	0	0	0
1	C	406	2983	1855	519	587	22	0	0	0
1	D	406	2983	1855	519	587	22	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

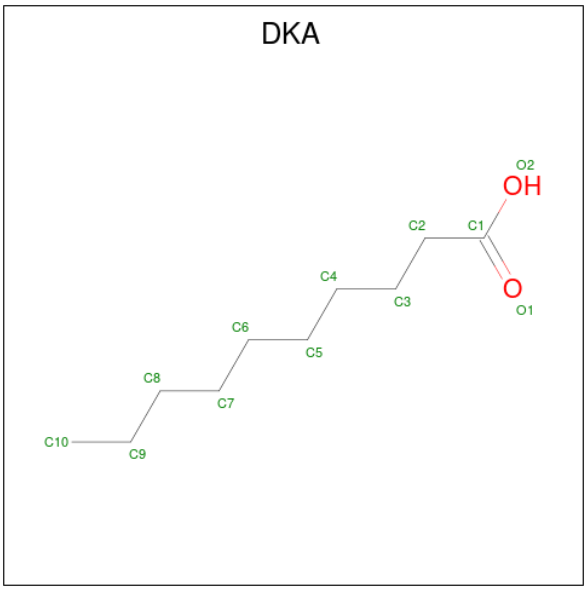
Chain	Residue	Modelled	Actual	Comment	Reference
A	4	VAL	ALA	conflict	UNP P0A953
A	163	SER	CYS	engineered mutation	UNP P0A953
B	4	VAL	ALA	conflict	UNP P0A953
B	163	SER	CYS	engineered mutation	UNP P0A953
C	4	VAL	ALA	conflict	UNP P0A953
C	163	SER	CYS	engineered mutation	UNP P0A953
D	4	VAL	ALA	conflict	UNP P0A953
D	163	SER	CYS	engineered mutation	UNP P0A953

- Molecule 2 is HYDROXIDE ION (three-letter code: OH) (formula: HO).



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

- Molecule 3 is DECANOIC ACID (three-letter code: DKA) (formula: $C_{10}H_{20}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	11	10	1	0	0
3	B	1	11	10	1	0	0
3	C	1	11	10	1	0	0
3	D	1	11	10	1	0	0

- Molecule 4 is water.

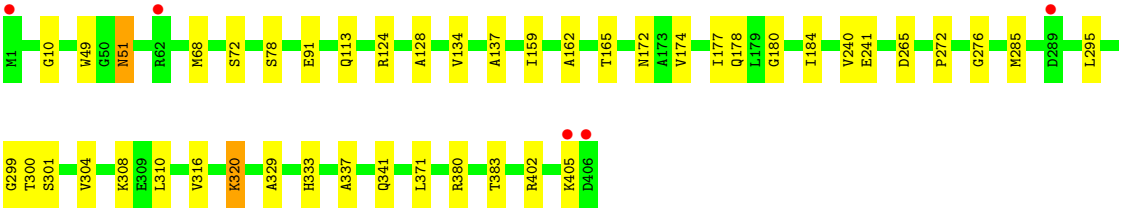
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	98	98	98	0	0
4	B	107	107	107	0	0
4	C	118	118	118	0	0
4	D	97	97	97	0	0

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.

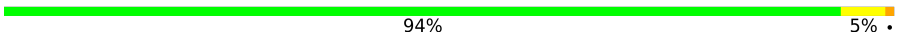
• Molecule 1: BETA-KETOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I

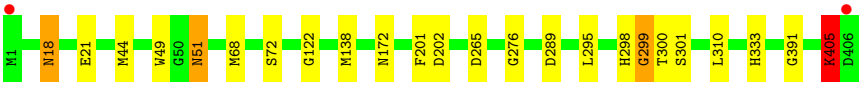
Chain A:



• Molecule 1: BETA-KETOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I

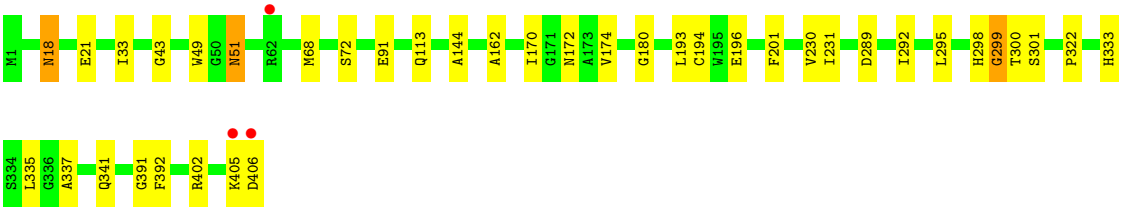
Chain B:





• Molecule 1: BETA-KETOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I

Chain C:



• Molecule 1: BETA-KETOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I

Chain D:

M285
G299
T300
S301
V304
K308
E309
L310
I313
V316
F317
G318
D319
K320
K328
H333
S334
E342
E362
A369
G370
L371
T378
D379
R380
T383
G393
R402
K405
D406

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	59.50Å 141.50Å 213.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	500.00 – 2.40 29.80 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (500.00-2.40) 99.1 (29.80-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.59 (at 2.39Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.174 , 0.209 0.172 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	29.0	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 38.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	12400	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% 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: OH, DKA

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	0/3031	0.60	0/4093
1	B	0.38	0/3031	0.61	0/4093
1	C	0.38	0/3031	0.61	0/4093
1	D	0.39	0/3031	0.61	0/4093
All	All	0.38	0/12124	0.61	0/16372

There are no bond length outliers.

There are no bond angle outliers.

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	2983	0	2942	32	0
1	B	2983	0	2942	23	0
1	C	2983	0	2942	39	0
1	D	2983	0	2942	39	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	11	0	19	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	11	0	19	2	0
3	C	11	0	19	6	0
3	D	11	0	19	3	0
4	A	98	0	0	3	0
4	B	107	0	0	2	0
4	C	118	0	0	7	0
4	D	97	0	0	2	0
All	All	12400	0	11844	128	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 5.

All (128) 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:405:LYS:HD2	1:C:405:LYS:H	1.21	1.00
1:B:51:ASN:H	1:B:51:ASN:HD22	1.14	0.92
1:C:51:ASN:HD22	1:C:51:ASN:H	1.18	0.92
1:D:405:LYS:HD2	1:D:405:LYS:O	1.71	0.90
1:A:51:ASN:H	1:A:51:ASN:HD22	1.21	0.86
1:D:51:ASN:H	1:D:51:ASN:HD22	1.18	0.86
1:C:405:LYS:HD2	1:C:405:LYS:N	1.93	0.84
1:C:162:ALA:HB1	3:C:903:DKA:H41	1.70	0.73
1:C:18:ASN:ND2	1:C:21:GLU:H	1.88	0.72
1:B:18:ASN:ND2	1:B:21:GLU:H	1.86	0.72
1:B:405:LYS:HD2	4:B:980:HOH:O	1.91	0.71
1:D:51:ASN:H	1:D:51:ASN:ND2	1.88	0.71
1:C:231:ILE:HD11	4:C:993:HOH:O	1.93	0.69
1:A:51:ASN:H	1:A:51:ASN:ND2	1.91	0.69
1:D:310:LEU:HD22	1:D:371:LEU:HD12	1.75	0.68
1:B:18:ASN:HD22	1:B:18:ASN:C	1.97	0.67
1:D:51:ASN:HD22	1:D:51:ASN:N	1.85	0.66
1:C:18:ASN:C	1:C:18:ASN:HD22	1.98	0.65
1:A:124:ARG:HB2	1:A:128:ALA:HB2	1.80	0.64
1:A:320:LYS:O	1:A:320:LYS:HD2	1.96	0.64
1:C:33:ILE:HD12	1:C:230:VAL:HG11	1.79	0.63
1:A:51:ASN:HD22	1:A:51:ASN:N	1.88	0.63
1:C:18:ASN:HD21	1:C:21:GLU:H	1.46	0.62
1:A:304:VAL:O	1:A:308:LYS:HG2	2.01	0.61
1:A:177:ILE:HD12	1:A:240:VAL:HG12	1.82	0.60
1:D:378:THR:HG21	1:D:380:ARG:HH21	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:335:LEU:HD11	4:C:993:HOH:O	2.01	0.60
1:C:391:GLY:HA2	3:C:903:DKA:O1	2.01	0.60
1:B:51:ASN:H	1:B:51:ASN:ND2	1.92	0.60
1:C:51:ASN:H	1:C:51:ASN:ND2	1.95	0.59
1:D:192:GLU:HG2	4:D:912:HOH:O	2.02	0.59
1:C:405:LYS:O	1:C:406:ASP:HB3	2.03	0.58
1:D:300:THR:O	1:D:301:SER:HB3	2.02	0.58
1:C:405:LYS:H	1:C:405:LYS:CD	2.05	0.57
1:D:285:MET:CE	1:D:316:VAL:HG11	2.34	0.57
1:C:402:ARG:NH1	4:C:1012:HOH:O	2.37	0.57
1:D:378:THR:HG21	1:D:380:ARG:NH2	2.18	0.57
3:C:903:DKA:H82	1:D:138:MET:HB3	1.87	0.56
1:D:113:GLN:HG3	1:D:137:ALA:HB1	1.88	0.56
1:D:304:VAL:O	1:D:308:LYS:HG2	2.05	0.56
1:A:285:MET:CE	1:A:316:VAL:HG11	2.36	0.56
1:A:300:THR:O	1:A:301:SER:HB3	2.06	0.55
1:A:113:GLN:HG3	1:A:137:ALA:HB1	1.87	0.55
1:C:51:ASN:HD22	1:C:51:ASN:N	1.97	0.55
1:B:68:MET:HE2	1:B:72:SER:HB3	1.89	0.55
3:A:901:DKA:H91	1:B:138:MET:HB3	1.89	0.54
1:C:91:GLU:CD	1:C:91:GLU:H	2.11	0.54
1:A:172:ASN:HD21	1:B:172:ASN:HD21	1.56	0.53
1:C:289:ASP:N	4:C:1012:HOH:O	2.41	0.52
1:B:300:THR:O	1:B:301:SER:HB3	2.10	0.52
1:B:391:GLY:HA2	3:B:902:DKA:O1	2.09	0.52
1:A:329:ALA:HB3	4:A:910:HOH:O	2.09	0.52
1:D:320:LYS:O	1:D:320:LYS:HD2	2.10	0.51
1:C:68:MET:HE2	1:C:72:SER:HB3	1.92	0.51
1:B:18:ASN:HD21	1:B:21:GLU:H	1.55	0.51
1:D:201:PHE:HE1	3:D:904:DKA:H31	1.76	0.51
1:C:292:ILE:O	1:C:322:PRO:HB3	2.12	0.50
1:D:68:MET:HE2	1:D:72:SER:HB3	1.92	0.50
1:D:124:ARG:HB2	1:D:128:ALA:HB2	1.92	0.49
1:D:285:MET:HE3	1:D:316:VAL:HG11	1.93	0.49
1:C:162:ALA:HB1	3:C:903:DKA:C4	2.41	0.49
1:A:124:ARG:HD3	1:C:43:GLY:HA2	1.94	0.49
1:A:184:ILE:HG12	1:A:241:GLU:HG3	1.94	0.49
1:A:285:MET:HE1	1:A:316:VAL:HG11	1.95	0.49
1:B:51:ASN:HD22	1:B:51:ASN:N	1.94	0.49
1:C:405:LYS:O	1:C:406:ASP:CB	2.61	0.48
1:C:180:GLY:HA2	4:C:985:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:335:LEU:CD1	4:C:993:HOH:O	2.61	0.48
1:A:265:ASP:OD1	1:A:276:GLY:HA3	2.14	0.48
1:C:193:LEU:HD12	4:C:987:HOH:O	2.14	0.48
1:D:383:THR:O	1:D:402:ARG:HG3	2.13	0.48
1:C:300:THR:O	1:C:301:SER:HB3	2.13	0.48
1:D:217:LYS:HE2	1:D:362:GLU:OE1	2.14	0.47
1:A:159:ILE:O	1:A:165:THR:HG23	2.14	0.47
1:C:170:ILE:O	1:C:174:VAL:HG23	2.15	0.47
1:D:159:ILE:O	1:D:165:THR:HG23	2.14	0.47
1:A:174:VAL:O	1:A:178:GLN:HG3	2.15	0.47
1:D:285:MET:HE1	1:D:316:VAL:HG11	1.97	0.46
1:B:265:ASP:OD1	1:B:276:GLY:HA3	2.16	0.46
1:A:68:MET:HE2	1:A:72:SER:HB3	1.96	0.46
1:A:134:VAL:HB	4:A:997:HOH:O	2.15	0.46
1:D:174:VAL:O	1:D:178:GLN:HG3	2.16	0.46
1:D:265:ASP:OD1	1:D:276:GLY:HA3	2.15	0.46
1:A:320:LYS:O	1:A:320:LYS:CD	2.64	0.46
1:D:300:THR:O	1:D:301:SER:CB	2.64	0.46
1:D:162:ALA:HA	3:D:904:DKA:H62	1.97	0.45
1:B:44:MET:HB3	1:B:202:ASP:OD2	2.17	0.45
1:B:18:ASN:ND2	1:B:18:ASN:C	2.69	0.45
1:A:337:ALA:O	1:A:341:GLN:HG3	2.17	0.45
1:C:172:ASN:HD21	1:D:172:ASN:HD21	1.65	0.45
1:A:295:LEU:C	1:A:295:LEU:HD23	2.37	0.45
1:B:201:PHE:HE1	3:B:902:DKA:H31	1.82	0.45
1:D:27:ARG:NE	4:D:957:HOH:O	2.47	0.44
1:D:10:GLY:HA3	1:D:78:SER:O	2.18	0.44
1:D:91:GLU:H	1:D:91:GLU:CD	2.20	0.44
1:A:285:MET:HE3	1:A:316:VAL:HG11	2.00	0.43
1:C:194:CYS:HB2	1:C:196:GLU:OE2	2.18	0.43
1:D:272:PRO:HG2	1:D:308:LYS:HG3	2.01	0.43
1:A:272:PRO:HG2	1:A:308:LYS:HG3	2.01	0.43
1:C:295:LEU:HD23	1:C:295:LEU:C	2.39	0.43
1:D:328:LYS:HZ2	1:D:342:GLU:CD	2.23	0.42
1:C:298:HIS:O	1:C:299:GLY:C	2.57	0.42
1:D:309:GLU:O	1:D:313:ILE:HG13	2.19	0.42
1:A:310:LEU:HD22	1:A:371:LEU:HD12	2.00	0.42
1:D:201:PHE:CE1	3:D:904:DKA:H31	2.54	0.42
1:B:289:ASP:OD2	1:B:289:ASP:N	2.53	0.42
1:D:220:ARG:NH1	1:D:223:ASP:OD2	2.44	0.42
1:D:320:LYS:NZ	1:D:320:LYS:HB3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:GLU:H	1:A:91:GLU:CD	2.23	0.41
1:C:337:ALA:O	1:C:341:GLN:HG3	2.20	0.41
1:B:122:GLY:HA3	4:B:971:HOH:O	2.19	0.41
1:A:162:ALA:HA	3:A:901:DKA:H62	2.02	0.41
1:B:295:LEU:HD23	1:B:295:LEU:C	2.41	0.41
1:B:298:HIS:O	1:B:299:GLY:C	2.58	0.41
1:C:144:ALA:HB1	1:D:393:GLY:HA3	2.03	0.41
1:C:392:PHE:CG	3:C:903:DKA:H32	2.55	0.41
1:A:180:GLY:HA2	4:A:963:HOH:O	2.21	0.41
3:A:901:DKA:H91	1:B:138:MET:CB	2.51	0.41
1:C:193:LEU:HD12	1:C:193:LEU:HA	1.94	0.41
1:A:383:THR:O	1:A:402:ARG:HG3	2.20	0.41
1:D:232:ALA:O	1:D:334:SER:HA	2.21	0.41
1:B:300:THR:O	1:B:301:SER:CB	2.69	0.41
1:A:320:LYS:HD2	1:A:320:LYS:C	2.41	0.40
1:B:310:LEU:HD23	1:B:310:LEU:HA	1.88	0.40
1:C:113:GLN:CD	1:D:110:PRO:HB3	2.41	0.40
1:C:18:ASN:ND2	1:C:18:ASN:C	2.70	0.40
1:C:201:PHE:HZ	3:C:903:DKA:H51	1.86	0.40
1:A:10:GLY:HA3	1:A:78:SER:O	2.21	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	404/406 (100%)	384 (95%)	18 (4%)	2 (0%)	29	41
1	B	404/406 (100%)	390 (96%)	12 (3%)	2 (0%)	29	41
1	C	404/406 (100%)	386 (96%)	17 (4%)	1 (0%)	47	62
1	D	404/406 (100%)	386 (96%)	15 (4%)	3 (1%)	22	32
All	All	1616/1624 (100%)	1546 (96%)	62 (4%)	8 (0%)	29	41

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	299	GLY
1	C	299	GLY
1	A	299	GLY
1	A	405	LYS
1	D	299	GLY
1	B	405	LYS
1	D	405	LYS
1	D	301	SER

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	310/310 (100%)	305 (98%)	5 (2%)	62	79
1	B	310/310 (100%)	305 (98%)	5 (2%)	62	79
1	C	310/310 (100%)	306 (99%)	4 (1%)	69	84
1	D	310/310 (100%)	305 (98%)	5 (2%)	62	79
All	All	1240/1240 (100%)	1221 (98%)	19 (2%)	65	80

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	TRP
1	A	51	ASN
1	A	320	LYS
1	A	333	HIS
1	A	380	ARG
1	B	18	ASN
1	B	49	TRP
1	B	51	ASN
1	B	333	HIS
1	B	405	LYS
1	C	18	ASN
1	C	49	TRP

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Mol	Chain	Res	Type
1	C	51	ASN
1	C	333	HIS
1	D	49	TRP
1	D	51	ASN
1	D	320	LYS
1	D	333	HIS
1	D	405	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	94	GLN
1	A	113	GLN
1	A	172	ASN
1	B	18	ASN
1	B	51	ASN
1	B	94	GLN
1	B	252	HIS
1	C	18	ASN
1	C	51	ASN
1	C	94	GLN
1	D	51	ASN
1	D	94	GLN
1	D	113	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 8 ligands modelled in this entry, 4 are modelled with single atom - leaving 4 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	DKA	D	904	1	10,10,11	0.51	0	9,9,11	0.76	0
3	DKA	C	903	1	10,10,11	0.44	0	9,9,11	0.80	0
3	DKA	B	902	1	10,10,11	0.52	0	9,9,11	0.81	0
3	DKA	A	901	1	10,10,11	0.50	0	9,9,11	0.75	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	DKA	D	904	1	-	1/7/8/9	-
3	DKA	C	903	1	-	2/7/8/9	-
3	DKA	B	902	1	-	2/7/8/9	-
3	DKA	A	901	1	-	0/7/8/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	904	DKA	C5-C6-C7-C8
3	C	903	DKA	C2-C3-C4-C5
3	B	902	DKA	C4-C5-C6-C7
3	C	903	DKA	C1-C2-C3-C4
3	B	902	DKA	C5-C6-C7-C8

There are no ring outliers.

4 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	904	DKA	3	0
3	C	903	DKA	6	0
3	B	902	DKA	2	0
3	A	901	DKA	3	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	406/406 (100%)	-0.41	5 (1%)	79	77	18, 26, 42, 72	0
1	B	406/406 (100%)	-0.51	2 (0%)	91	89	15, 23, 38, 71	0
1	C	406/406 (100%)	-0.56	3 (0%)	87	86	15, 23, 38, 68	0
1	D	406/406 (100%)	-0.30	8 (1%)	65	63	18, 27, 46, 70	0
All	All	1624/1624 (100%)	-0.44	18 (1%)	80	79	15, 25, 42, 72	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	406	ASP	10.2
1	D	406	ASP	8.1
1	C	405	LYS	6.4
1	A	406	ASP	6.1
1	C	406	ASP	5.2
1	A	1	MET	4.7
1	B	1	MET	4.7
1	D	319	ASP	3.8
1	D	405	LYS	3.6
1	D	1	MET	3.3
1	A	62	ARG	3.0
1	C	62	ARG	2.6
1	D	318	GLY	2.5
1	D	225	HIS	2.4
1	D	320	LYS	2.4
1	D	369	ALA	2.2
1	A	405	LYS	2.1
1	A	289	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)

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
3	DKA	B	902	11/12	0.84	0.29	31,32,33,34	0
3	DKA	C	903	11/12	0.84	0.29	30,32,36,37	0
3	DKA	D	904	11/12	0.86	0.26	26,30,33,34	0
3	DKA	A	901	11/12	0.87	0.25	31,35,37,38	0
2	OH	D	504	1/1	0.95	0.32	30,30,30,30	0
2	OH	C	503	1/1	0.96	0.32	27,27,27,27	0
2	OH	B	502	1/1	0.97	0.38	32,32,32,32	0
2	OH	A	501	1/1	0.98	0.28	30,30,30,30	0

6.5 Other polymers (i)

There are no such residues in this entry.