



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:42 PM GMT

PDB ID : 1UUP
Title : CRYSTAL STRUCTURE OF A DIMERIC FORM OF STREPTOCOCCAL
PYROGENIC EXOTOXIN A (SPEA1).
Authors : Baker, M.D.; Gendlina, I.; Collins, C.M.; Acharya, K.R.
Deposited on : 2004-01-08
Resolution : 2.60 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
<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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

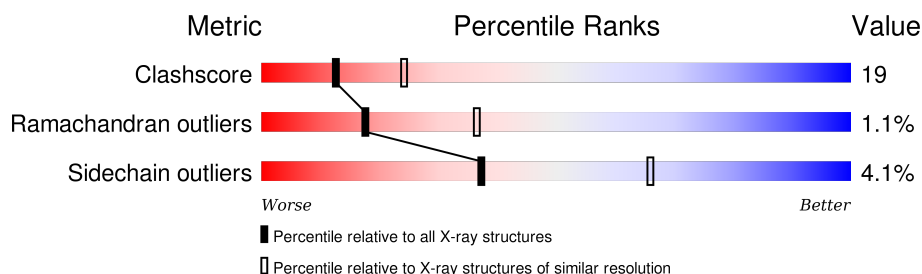
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	221	
1	B	221	
1	C	221	
1	D	221	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7388 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 EXOTOXIN TYPE A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1812	1158	291	357	6			
1	B	221	Total	C	N	O	S	0	0	0
			1812	1158	291	357	6			
1	C	221	Total	C	N	O	S	0	0	0
			1812	1158	291	357	6			
1	D	221	Total	C	N	O	S	0	0	0
			1812	1158	291	357	6			

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

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

- Molecule 3 is water.

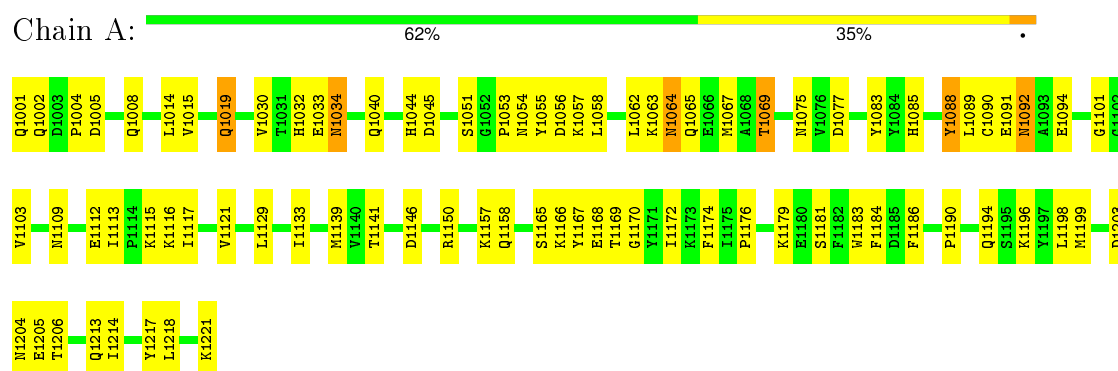
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	36	Total	O	0	0
			36	36		
3	B	27	Total	O	0	0
			27	27		
3	C	37	Total	O	0	0
			37	37		
3	D	36	Total	O	0	0
			36	36		

3 Residue-property plots

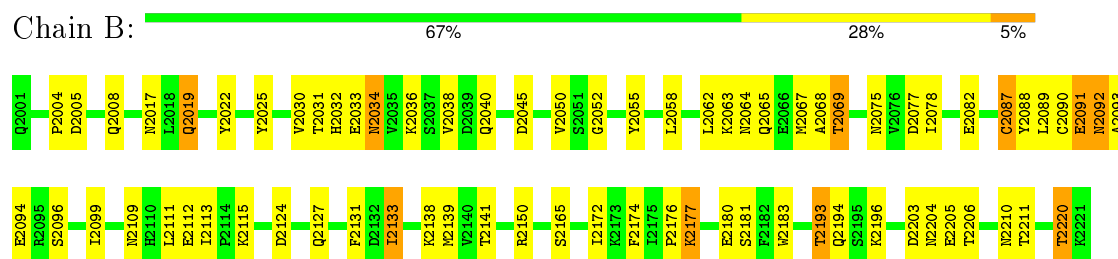
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

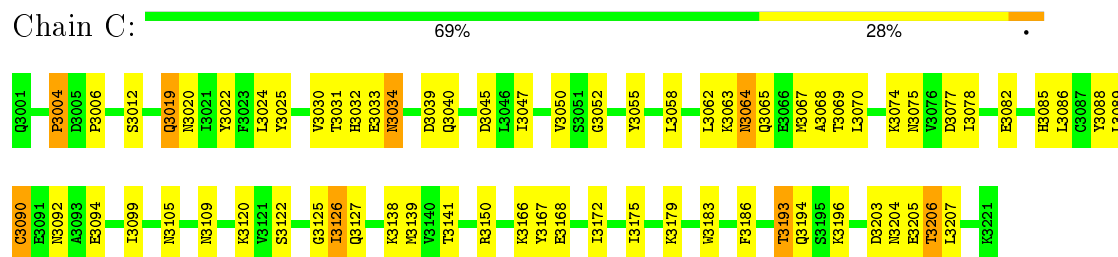
• Molecule 1: EXOTOXIN TYPE A



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• Molecule 1: EXOTOXIN TYPE A



E4082	E4001
C4087	P4004
Y4088	
L4089	Q4008
C4090	L4009
E4091	H4010
M4092	R4011
A4093	
E4094	L4014
R4095	V4015
	K4016
I4099	M4017
	L4018
T4104	Q4019
N4109	Y4022
K4115	E4026
I4133	V4030
	T4031
K4138	
M4139	M4034
V4140	V4035
T4141	K4036
E4144	D4039
	Q4040
K4148	L4041
K4151	H4044
Y4152	D4045
	L4046
D4155	I4047
N4156	
	G4052
T4161	
N4162	Y4055
G4163	D4056
K4166	E4061
	L4062
G4170	K4063
	M4064
K4177	Q4065
M4178	E4066
	M4067
F4182	A4068
M4183	T4069
	L4070
F4187	
	D4073
E4191	K4074
F4192	M4075
T4193	V4076
	E4077
K4196	I4078
	Y4079
N4204	
E4205	
T4206	
N4210	
Y4217	
K4221	

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	53.30 Å 127.20 Å 148.00 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	89.0 (20.00-2.60)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.215 , 0.282	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7388	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

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	0.42	0/1854	0.65	0/2510
1	B	0.38	0/1854	0.66	0/2510
1	C	0.40	0/1854	0.64	0/2510
1	D	0.38	0/1854	0.62	0/2510
All	All	0.40	0/7416	0.64	0/10040

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	1812	0	1752	75	0
1	B	1812	0	1752	65	0
1	C	1812	0	1752	63	0
1	D	1812	0	1752	82	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	36	0	0	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	27	0	0	2	0
3	C	37	0	0	7	0
3	D	36	0	0	0	0
All	All	7388	0	7008	277	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 19.

All (277) 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:2063:LYS:H	1:B:2067:MET:HE2	1.04	1.09
1:C:3062:LEU:HB3	1:C:3067:MET:HE2	1.33	1.03
1:B:2115:LYS:HE2	1:B:2210:ASN:HA	1.43	1.00
1:A:1063:LYS:H	1:A:1067:MET:HE2	1.31	0.95
1:D:4062:LEU:HB3	1:D:4067:MET:HE2	1.47	0.94
1:B:2092:ASN:HD22	1:B:2092:ASN:H	1.16	0.93
1:B:2088:TYR:HE1	1:B:2090:CYS:HB3	1.31	0.92
1:B:2063:LYS:N	1:B:2067:MET:HE2	1.86	0.90
1:B:2109:ASN:HD21	1:B:2139:MET:H	1.13	0.90
1:A:1062:LEU:HB3	1:A:1067:MET:HE2	1.53	0.89
1:A:1109:ASN:HD21	1:A:1139:MET:H	1.20	0.88
1:D:4193:THR:HG22	1:D:4196:LYS:H	1.38	0.86
3:A:2003:HOH:O	1:D:4094:GLU:HG3	1.75	0.86
1:D:4011:ARG:HB2	1:D:4014:LEU:HD13	1.55	0.85
1:D:4063:LYS:H	1:D:4067:MET:HE2	1.39	0.84
1:D:4063:LYS:H	1:D:4067:MET:CE	1.94	0.80
1:B:2193:THR:HG22	1:B:2196:LYS:H	1.46	0.79
1:A:1103:VAL:H	1:A:1204:ASN:HD21	1.29	0.79
1:C:3019:GLN:HE21	1:C:3019:GLN:H	1.32	0.78
1:A:1034:ASN:ND2	1:A:1075:ASN:HB3	1.98	0.78
1:C:3033:GLU:HG2	3:C:2005:HOH:O	1.84	0.78
1:A:1063:LYS:H	1:A:1067:MET:CE	2.00	0.75
1:B:2089:LEU:HG	1:D:4088:TYR:OH	1.87	0.75
1:D:4062:LEU:HD22	1:D:4067:MET:HE3	1.68	0.74
1:D:4017:ASN:HA	1:D:4019:GLN:HE22	1.52	0.74
1:C:3109:ASN:HD21	1:C:3139:MET:H	1.36	0.73
1:C:3019:GLN:NE2	1:C:3019:GLN:H	1.86	0.73
1:D:4019:GLN:NE2	1:D:4019:GLN:H	1.89	0.71
1:D:4088:TYR:HD1	1:D:4090:CYS:H	1.39	0.70
1:C:3069:THR:HG23	3:C:2006:HOH:O	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4010:HIS:HD2	1:D:4187:PHE:O	1.73	0.70
1:B:2019:GLN:H	1:B:2019:GLN:NE2	1.89	0.70
1:A:1005:ASP:HB3	1:A:1008:GLN:HB2	1.74	0.69
1:A:1116:LYS:HE2	3:A:2024:HOH:O	1.92	0.69
1:A:1067:MET:HE3	1:A:1204:ASN:HB2	1.73	0.69
1:A:1069:THR:HG21	3:A:2012:HOH:O	1.91	0.69
1:A:1019:GLN:NE2	1:A:1019:GLN:H	1.91	0.69
1:B:2065:GLN:O	1:B:2069:THR:HG23	1.92	0.68
1:A:1121:VAL:HB	1:A:1129:LEU:HB3	1.75	0.68
1:D:4133:ILE:HD12	1:D:4148:LYS:HB3	1.76	0.68
1:D:4089:LEU:O	1:D:4090:CYS:HB2	1.93	0.67
1:C:3193:THR:HG21	3:C:2030:HOH:O	1.93	0.67
1:C:3120:LYS:HD3	1:C:3127:GLN:HE22	1.60	0.67
1:D:4040:GLN:HG3	1:D:4045:ASP:O	1.96	0.66
1:C:3090:CYS:HB3	1:C:3092:ASN:OD1	1.96	0.65
1:C:3085:HIS:O	1:C:3086:LEU:HB2	1.95	0.65
1:C:3063:LYS:H	1:C:3067:MET:HE2	1.61	0.65
1:D:4089:LEU:HD12	1:D:4089:LEU:N	2.12	0.65
1:B:2019:GLN:H	1:B:2019:GLN:HE21	1.44	0.64
1:C:3109:ASN:ND2	1:C:3138:LYS:HB2	2.12	0.64
1:B:2092:ASN:HD22	1:B:2092:ASN:N	1.88	0.64
1:A:1063:LYS:N	1:A:1067:MET:HE2	2.10	0.64
1:D:4030:VAL:HG13	1:D:4055:TYR:OH	1.97	0.64
1:C:3089:LEU:N	1:C:3089:LEU:HD12	2.12	0.64
1:B:2040:GLN:HG3	1:B:2045:ASP:O	1.98	0.63
1:A:1088:TYR:HE1	1:A:1090:CYS:HB2	1.64	0.63
1:D:4193:THR:CG2	1:D:4196:LYS:H	2.12	0.63
1:D:4017:ASN:HA	1:D:4019:GLN:NE2	2.14	0.63
1:C:3206:THR:HG21	3:C:2015:HOH:O	1.98	0.63
1:B:2091:GLU:CD	1:B:2091:GLU:H	2.00	0.62
1:A:1062:LEU:HD22	1:A:1067:MET:HE3	1.80	0.62
1:A:1019:GLN:HE21	1:A:1019:GLN:H	1.47	0.62
1:A:1033:GLU:O	1:A:1077:ASP:OD1	2.16	0.62
1:C:3175:ILE:N	1:C:3175:ILE:HD12	2.14	0.62
1:C:3193:THR:HG22	1:C:3196:LYS:H	1.64	0.62
1:C:3063:LYS:H	1:C:3067:MET:CE	2.12	0.62
1:B:2082:GLU:HA	1:B:2099:ILE:HG22	1.82	0.62
1:D:4063:LYS:N	1:D:4067:MET:HE2	2.14	0.61
1:C:3125:GLY:O	1:C:3126:ILE:HG13	2.00	0.61
1:A:1139:MET:HG3	3:A:2033:HOH:O	1.99	0.61
1:D:4109:ASN:HD21	1:D:4139:MET:H	1.47	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2033:GLU:O	1:B:2077:ASP:OD1	2.17	0.61
1:D:4141:THR:HA	1:D:4206:THR:HA	1.82	0.61
1:A:1030:VAL:HG11	1:A:1058:LEU:HD22	1.82	0.61
1:D:4016:LYS:HD2	1:D:4191:GLU:OE1	2.01	0.61
1:C:3062:LEU:CB	1:C:3067:MET:HE2	2.21	0.60
1:A:1062:LEU:HD23	1:A:1101:GLY:HA2	1.83	0.60
1:A:1064:ASN:ND2	1:A:1067:MET:H	1.98	0.60
1:A:1109:ASN:ND2	1:A:1139:MET:H	1.98	0.60
1:A:1170:GLY:HA2	1:A:1217:TYR:O	2.01	0.60
1:C:3089:LEU:O	1:C:3090:CYS:HB2	2.00	0.59
1:D:4004:PRO:HA	1:D:4008:GLN:OE1	2.02	0.59
1:B:2088:TYR:CE1	1:B:2090:CYS:HB3	2.24	0.59
1:A:1205:GLU:OE2	1:A:1205:GLU:HA	2.03	0.58
1:C:3004:PRO:HB3	1:C:3183:TRP:CZ2	2.38	0.58
1:A:1085:HIS:ND1	1:D:4094:GLU:OE1	2.37	0.58
1:B:2005:ASP:N	1:B:2008:GLN:OE1	2.36	0.58
1:A:1030:VAL:HG13	1:A:1055:TYR:OH	2.03	0.57
1:B:2094:GLU:OE2	1:C:3085:HIS:HD2	1.87	0.57
1:C:3030:VAL:HG13	1:C:3055:TYR:OH	2.05	0.57
1:B:2177:LYS:HB3	3:B:3018:HOH:O	2.03	0.57
1:B:2092:ASN:H	1:B:2092:ASN:ND2	1.96	0.56
1:C:3062:LEU:HD12	1:C:3068:ALA:HA	1.87	0.56
1:D:4089:LEU:O	1:D:4090:CYS:CB	2.53	0.56
1:B:2124:ASP:OD2	1:B:2220:THR:HG23	2.06	0.56
1:B:2131:PHE:HE1	1:B:2133:ILE:HD13	1.70	0.56
1:C:3012:SER:HB3	3:C:2037:HOH:O	2.05	0.56
1:B:2062:LEU:HB3	1:B:2067:MET:HG2	1.87	0.56
1:A:1067:MET:CE	1:A:1204:ASN:HB2	2.35	0.56
1:D:4151:LYS:HE3	1:D:4155:ASP:OD1	2.06	0.56
1:C:3082:GLU:HA	1:C:3099:ILE:HG22	1.88	0.56
1:C:3067:MET:HE3	1:C:3204:ASN:HB2	1.89	0.55
1:B:2141:THR:HA	1:B:2206:THR:HA	1.87	0.55
1:C:3034:ASN:ND2	1:C:3075:ASN:HB3	2.22	0.55
1:B:2091:GLU:N	1:B:2091:GLU:OE2	2.28	0.55
1:D:4019:GLN:HE21	1:D:4019:GLN:H	1.52	0.55
1:A:1051:SER:CB	1:A:1056:ASP:HA	2.36	0.55
1:B:2194:GLN:HG3	1:C:3094:GLU:OE1	2.07	0.54
1:A:1001:GLN:HG3	1:A:1002:GLN:H	1.73	0.54
1:D:4062:LEU:CB	1:D:4067:MET:HE2	2.31	0.54
1:D:4089:LEU:CD1	1:D:4089:LEU:N	2.71	0.54
1:D:4166:LYS:HD3	1:D:4166:LYS:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3019:GLN:O	1:C:3022:TYR:HB3	2.08	0.53
1:C:3141:THR:HA	1:C:3206:THR:HA	1.91	0.53
1:D:4182:PHE:CZ	1:D:4205:GLU:HG2	2.43	0.53
1:D:4087:CYS:O	1:D:4088:TYR:HB3	2.09	0.53
1:D:4065:GLN:O	1:D:4069:THR:HG23	2.09	0.53
1:D:4026:GLU:HA	1:D:4026:GLU:OE2	2.08	0.53
1:B:2141:THR:HG22	1:B:2206:THR:HG22	1.91	0.52
1:D:4115:LYS:HE2	1:D:4210:ASN:HA	1.91	0.52
1:D:4047:ILE:HD13	1:D:4089:LEU:HD23	1.90	0.52
1:D:4052:GLY:HA3	1:D:4055:TYR:CE2	2.43	0.52
1:A:1088:TYR:CE1	1:A:1090:CYS:HB2	2.43	0.52
1:D:4193:THR:HG22	1:D:4196:LYS:N	2.18	0.52
1:C:3062:LEU:HD22	1:C:3067:MET:HE3	1.92	0.52
1:D:4010:HIS:CD2	1:D:4187:PHE:O	2.60	0.52
1:B:2067:MET:HE3	1:B:2204:ASN:HB2	1.93	0.51
1:A:1062:LEU:CB	1:A:1067:MET:HE2	2.35	0.51
1:A:1176:PRO:HG2	1:A:1179:LYS:O	2.10	0.51
1:D:4070:LEU:O	1:D:4074:LYS:HD2	2.10	0.51
1:A:1064:ASN:C	1:A:1064:ASN:HD22	2.12	0.51
1:B:2088:TYR:HE1	1:B:2090:CYS:CB	2.12	0.50
1:B:2177:LYS:N	3:B:3017:HOH:O	2.45	0.50
1:D:4062:LEU:HB3	1:D:4067:MET:CE	2.29	0.50
1:D:4141:THR:HG22	1:D:4206:THR:HG22	1.92	0.50
1:A:1054:ASN:N	1:A:1054:ASN:HD22	2.07	0.50
1:C:3168:GLU:HA	1:C:3168:GLU:OE2	2.12	0.50
1:D:4088:TYR:HD1	1:D:4090:CYS:N	2.07	0.50
1:C:3172:ILE:HB	1:C:3186:PHE:CE2	2.47	0.50
1:B:2174:PHE:O	1:B:2181:SER:HB2	2.12	0.50
1:D:4011:ARG:NH2	1:D:4014:LEU:HD11	2.27	0.50
1:B:2034:ASN:ND2	1:B:2075:ASN:HB3	2.27	0.50
1:A:1065:GLN:O	1:A:1069:THR:HG23	2.12	0.49
1:A:1141:THR:HA	1:A:1206:THR:HA	1.94	0.49
1:D:4221:LYS:OXT	1:D:4221:LYS:HG2	2.12	0.49
1:D:4170:GLY:HA2	1:D:4217:TYR:O	2.13	0.49
1:C:3088:TYR:HD2	1:C:3090:CYS:O	1.96	0.49
1:B:2088:TYR:CD1	1:B:2093:ALA:HB3	2.47	0.49
1:D:4082:GLU:HA	1:D:4099:ILE:HG22	1.94	0.49
1:B:2090:CYS:HB3	1:B:2092:ASN:HD21	1.76	0.49
1:B:2090:CYS:HB3	1:B:2092:ASN:ND2	2.28	0.49
1:D:4044:HIS:HD2	1:D:4061:GLU:HG3	1.77	0.49
1:D:4064:ASN:C	1:D:4064:ASN:HD22	2.16	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3064:ASN:HD22	1:C:3064:ASN:C	2.15	0.49
1:B:2004:PRO:HB3	1:B:2183:TRP:CZ2	2.48	0.49
1:B:2094:GLU:OE1	1:C:3194:GLN:HG3	2.13	0.49
1:B:2111:LEU:HD21	1:B:2138:LYS:HG2	1.95	0.49
1:A:1165:SER:O	1:A:1221:LYS:HE3	2.13	0.49
1:C:3020:ASN:O	1:C:3024:LEU:HG	2.12	0.49
1:A:1051:SER:HB3	1:A:1056:ASP:HA	1.95	0.48
1:B:2172:ILE:HG23	1:B:2172:ILE:O	2.13	0.48
1:C:3040:GLN:HG3	1:C:3045:ASP:O	2.13	0.48
1:D:4056:ASP:OD1	1:D:4095:ARG:HB2	2.12	0.48
1:C:3089:LEU:N	1:C:3089:LEU:CD1	2.75	0.48
1:B:2177:LYS:HD3	1:B:2211:THR:OG1	2.12	0.48
1:A:1089:LEU:HB3	1:C:3088:TYR:OH	2.13	0.48
1:C:3052:GLY:HA3	1:C:3055:TYR:CE2	2.47	0.48
1:C:3074:LYS:HD3	1:C:3105:ASN:OD1	2.14	0.48
1:B:2017:ASN:HA	1:B:2019:GLN:NE2	2.29	0.48
1:D:4109:ASN:ND2	1:D:4138:LYS:HB2	2.28	0.48
1:C:3166:LYS:HD2	1:C:3167:TYR:CZ	2.47	0.48
1:C:3064:ASN:ND2	1:C:3067:MET:H	2.11	0.48
1:C:3141:THR:HG23	3:C:2020:HOH:O	2.12	0.48
1:B:2112:GLU:HG3	1:B:2113:ILE:HG13	1.95	0.48
1:A:1034:ASN:HD21	1:A:1075:ASN:HB3	1.71	0.48
1:D:4109:ASN:HD21	1:D:4139:MET:N	2.11	0.48
1:A:1129:LEU:HD22	1:A:1157:LYS:HE3	1.96	0.48
1:B:2093:ALA:HB1	1:B:2096:SER:OG	2.14	0.47
1:A:1146:ASP:O	1:A:1150:ARG:HG3	2.14	0.47
1:A:1103:VAL:H	1:A:1204:ASN:ND2	2.06	0.47
1:B:2082:GLU:CA	1:B:2099:ILE:HG22	2.43	0.47
1:C:3065:GLN:HB2	3:C:2006:HOH:O	2.15	0.47
1:B:2032:HIS:CD2	1:B:2050:VAL:HG21	2.48	0.47
1:B:2131:PHE:CE1	1:B:2133:ILE:HD13	2.48	0.47
1:B:2052:GLY:HA3	1:B:2055:TYR:CE2	2.48	0.47
1:A:1213:GLN:C	1:A:1214:ILE:HD13	2.34	0.47
1:B:2176:PRO:HD3	1:B:2181:SER:HA	1.96	0.47
1:C:3031:THR:HA	1:C:3078:ILE:O	2.15	0.47
1:D:4034:ASN:ND2	1:D:4075:ASN:HB3	2.30	0.47
1:C:3025:TYR:CE2	1:C:3150:ARG:HD2	2.50	0.47
1:C:3019:GLN:N	1:C:3019:GLN:HE21	2.07	0.47
1:D:4204:ASN:O	1:D:4206:THR:HG23	2.16	0.46
1:B:2036:LYS:HE3	1:B:2075:ASN:OD1	2.16	0.46
1:D:4031:THR:HA	1:D:4078:ILE:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1166:LYS:HD2	1:A:1167:TYR:CZ	2.50	0.46
1:D:4076:VAL:HB	1:D:4104:THR:O	2.15	0.46
1:A:1005:ASP:HB3	1:A:1008:GLN:CB	2.42	0.46
1:A:1117:ILE:HB	1:A:1133:ILE:HG22	1.98	0.46
1:D:4004:PRO:HD3	1:D:4183:TRP:CE2	2.51	0.46
1:D:4133:ILE:HD13	1:D:4133:ILE:HA	1.79	0.46
1:A:1194:GLN:HG3	1:D:4094:GLU:OE2	2.16	0.46
1:D:4019:GLN:O	1:D:4022:TYR:HB3	2.16	0.46
1:B:2017:ASN:HA	1:B:2019:GLN:HE22	1.81	0.46
1:A:1053:PRO:O	1:A:1054:ASN:HB2	2.15	0.46
1:A:1196:LYS:O	1:A:1199:MET:HG3	2.15	0.46
1:B:2203:ASP:CG	1:B:2205:GLU:HG2	2.36	0.46
1:A:1053:PRO:O	3:A:2009:HOH:O	2.21	0.45
1:C:3030:VAL:HG11	1:C:3058:LEU:HD22	1.98	0.45
1:A:1092:ASN:ND2	1:A:1092:ASN:C	2.70	0.45
1:D:4036:LYS:NZ	1:D:4073:ASP:O	2.38	0.45
1:A:1094:GLU:OE1	1:D:4193:THR:HA	2.17	0.45
1:D:4088:TYR:C	1:D:4089:LEU:HD12	2.37	0.45
1:B:2176:PRO:CD	1:B:2181:SER:HA	2.47	0.45
1:C:3039:ASP:HB3	1:C:3047:ILE:HB	1.99	0.45
1:C:3064:ASN:HD22	1:C:3067:MET:H	1.63	0.45
1:A:1067:MET:HE3	1:A:1204:ASN:CB	2.45	0.45
1:C:3082:GLU:CA	1:C:3099:ILE:HG22	2.47	0.45
1:D:4152:TYR:CE1	1:D:4156:ASN:ND2	2.85	0.45
1:C:3203:ASP:OD2	1:C:3205:GLU:HB2	2.17	0.44
1:C:3033:GLU:HA	1:C:3077:ASP:OD1	2.18	0.44
1:A:1112:GLU:HG3	1:A:1113:ILE:HG13	1.98	0.44
1:A:1054:ASN:ND2	1:A:1054:ASN:N	2.65	0.44
1:C:3032:HIS:CD2	1:C:3050:VAL:HB	2.52	0.44
1:B:2030:VAL:HG11	1:B:2058:LEU:HD22	1.98	0.44
1:A:1170:GLY:HA3	1:A:1218:LEU:HD23	2.00	0.44
1:D:4067:MET:CE	1:D:4204:ASN:HB2	2.47	0.44
1:A:1069:THR:HG22	3:A:2006:HOH:O	2.17	0.44
1:A:1206:THR:HG21	3:A:2022:HOH:O	2.18	0.44
1:D:4161:THR:O	1:D:4163:GLY:N	2.50	0.44
1:B:2019:GLN:O	1:B:2022:TYR:HB3	2.18	0.43
1:D:4079:TYR:CD2	1:D:4144:GLU:HG3	2.53	0.43
1:D:4193:THR:HG22	1:D:4196:LYS:HG2	2.00	0.43
1:A:1203:ASP:OD1	1:A:1205:GLU:N	2.45	0.43
1:B:2087:CYS:SG	1:B:2088:TYR:N	2.90	0.43
1:D:4193:THR:CG2	1:D:4196:LYS:HG2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4067:MET:HE3	1:D:4204:ASN:HB2	2.00	0.43
1:A:1089:LEU:O	1:A:1090:CYS:SG	2.77	0.43
1:A:1172:ILE:HB	1:A:1186:PHE:CE2	2.53	0.43
1:B:2067:MET:CE	1:B:2204:ASN:HB2	2.48	0.43
1:D:4030:VAL:HG23	1:D:4082:GLU:OE2	2.19	0.42
1:C:3032:HIS:NE2	1:C:3050:VAL:HB	2.34	0.42
1:A:1169:THR:HA	3:A:2026:HOH:O	2.19	0.42
1:A:1168:GLU:HA	1:A:1168:GLU:OE2	2.18	0.42
1:A:1015:VAL:HA	1:A:1190:PRO:HA	2.01	0.42
1:A:1157:LYS:O	1:A:1158:GLN:HB2	2.20	0.42
1:D:4011:ARG:HH21	1:D:4014:LEU:HD11	1.83	0.42
1:B:2180:GLU:HA	1:B:2180:GLU:OE2	2.20	0.42
1:A:1040:GLN:HG3	1:A:1045:ASP:O	2.19	0.42
1:C:3067:MET:CE	1:C:3204:ASN:HB2	2.49	0.42
1:D:4011:ARG:NE	1:D:4014:LEU:HD11	2.35	0.42
1:D:4089:LEU:H	1:D:4093:ALA:CB	2.33	0.42
1:D:4019:GLN:N	1:D:4019:GLN:HE21	2.16	0.42
1:C:3085:HIS:CE1	1:C:3086:LEU:HD13	2.55	0.42
1:A:1032:HIS:HE1	1:A:1055:TYR:OH	2.02	0.42
1:B:2062:LEU:HD12	1:B:2068:ALA:HA	2.01	0.42
1:D:4082:GLU:CA	1:D:4099:ILE:HG22	2.49	0.42
1:A:1174:PHE:CE2	1:A:1214:ILE:HD12	2.55	0.42
1:D:4079:TYR:CG	1:D:4144:GLU:HG3	2.55	0.42
1:B:2025:TYR:CE2	1:B:2150:ARG:HD2	2.55	0.42
1:D:4177:LYS:HG3	1:D:4178:ASN:ND2	2.34	0.42
1:A:1083:TYR:CD2	1:A:1198:LEU:HD12	2.55	0.42
1:C:3109:ASN:HA	1:C:3138:LYS:HD2	2.01	0.41
1:A:1213:GLN:O	1:A:1214:ILE:HD13	2.20	0.41
1:B:2004:PRO:HD3	1:B:2183:TRP:CD1	2.56	0.41
1:A:1172:ILE:HG22	1:A:1184:PHE:HB2	2.02	0.41
1:B:2193:THR:HG22	1:B:2196:LYS:HG2	2.02	0.41
1:D:4041:LEU:HB3	1:D:4045:ASP:OD2	2.21	0.41
1:B:2034:ASN:HD21	1:B:2075:ASN:HB3	1.85	0.41
1:C:3126:ILE:O	1:C:3127:GLN:C	2.57	0.41
1:D:4039:ASP:CG	1:D:4040:GLN:H	2.23	0.41
1:B:2088:TYR:C	1:B:2088:TYR:CD1	2.94	0.40
1:A:1176:PRO:HD2	1:A:1181:SER:HA	2.03	0.40
1:D:4079:TYR:CD1	1:D:4144:GLU:HG3	2.56	0.40
1:C:3070:LEU:O	1:C:3074:LYS:NZ	2.45	0.40
1:B:2031:THR:HA	1:B:2078:ILE:O	2.22	0.40
1:A:1004:PRO:HB3	1:A:1183:TRP:CZ2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1203:ASP:OD1	1:A:1203:ASP:C	2.60	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	219/221 (99%)	200 (91%)	18 (8%)	1 (0%)	34	60
1	B	219/221 (99%)	200 (91%)	16 (7%)	3 (1%)	14	28
1	C	219/221 (99%)	203 (93%)	11 (5%)	5 (2%)	8	14
1	D	219/221 (99%)	204 (93%)	14 (6%)	1 (0%)	34	60
All	All	876/884 (99%)	807 (92%)	59 (7%)	10 (1%)	17	36

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1091	GLU
1	C	3090	CYS
1	D	4090	CYS
1	B	2087	CYS
1	B	2091	GLU
1	C	3179	LYS
1	B	2177	LYS
1	C	3006	PRO
1	C	3004	PRO
1	C	3126	ILE

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	206/208 (99%)	196 (95%)	10 (5%)	31	57
1	B	206/208 (99%)	195 (95%)	11 (5%)	28	53
1	C	206/208 (99%)	199 (97%)	7 (3%)	44	72
1	D	206/208 (99%)	200 (97%)	6 (3%)	50	77
All	All	824/832 (99%)	790 (96%)	34 (4%)	37	66

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1014	LEU
1	A	1019	GLN
1	A	1034	ASN
1	A	1044	HIS
1	A	1057	LYS
1	A	1064	ASN
1	A	1069	THR
1	A	1088	TYR
1	A	1092	ASN
1	A	1115	LYS
1	B	2019	GLN
1	B	2034	ASN
1	B	2038	VAL
1	B	2064	ASN
1	B	2069	THR
1	B	2092	ASN
1	B	2127	GLN
1	B	2133	ILE
1	B	2165	SER
1	B	2193	THR
1	B	2220	THR
1	C	3019	GLN
1	C	3034	ASN
1	C	3064	ASN

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Mol	Chain	Res	Type
1	C	3122	SER
1	C	3193	THR
1	C	3206	THR
1	C	3207	LEU
1	D	4019	GLN
1	D	4064	ASN
1	D	4089	LEU
1	D	4092	ASN
1	D	4166	LYS
1	D	4193	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1001	GLN
1	A	1019	GLN
1	A	1032	HIS
1	A	1034	ASN
1	A	1044	HIS
1	A	1054	ASN
1	A	1064	ASN
1	A	1065	GLN
1	A	1092	ASN
1	A	1109	ASN
1	A	1127	GLN
1	A	1156	ASN
1	A	1204	ASN
1	B	2001	GLN
1	B	2019	GLN
1	B	2034	ASN
1	B	2064	ASN
1	B	2065	GLN
1	B	2092	ASN
1	B	2109	ASN
1	B	2110	HIS
1	C	3008	GLN
1	C	3019	GLN
1	C	3032	HIS
1	C	3034	ASN
1	C	3049	ASN
1	C	3064	ASN
1	C	3065	GLN

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Mol	Chain	Res	Type
1	C	3106	HIS
1	C	3109	ASN
1	C	3156	ASN
1	D	4010	HIS
1	D	4019	GLN
1	D	4034	ASN
1	D	4040	GLN
1	D	4064	ASN
1	D	4065	GLN
1	D	4109	ASN
1	D	4156	ASN
1	D	4178	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.