WORLDWIDE
wwPDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 09:07 AM GMT

PDB ID	:	2F9O
Title	:	Crystal Structure of the Recombinant Human Alpha I Tryptase Mutant D216G
Authors	:	Rohr, K.B.; Selwood, T.; Marquardt, U.; Huber, R.; Schechter, N.M.; Bode, W.; Than, M.E.
Deposited on	:	2005-12-06
Resolution	:	2.10 Å(reported)

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

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 2.10 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	Percentile Ranks	Value
Rfree		0.240
Clashscore		9
Ramachandran outliers		0.3%
Sidechain outliers		2.3%
RSRZ outliers		1.4%

Worse ◼ Better

◼ Percentile relative to all X-ray structures

◫ Percentile relative to X-ray structures of similar resolution
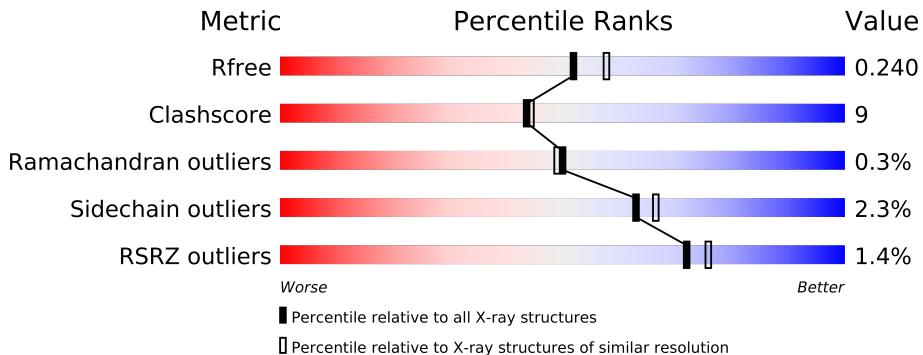
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_free	66092	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	245	
1	B	245	
1	C	245	
1	D	245	
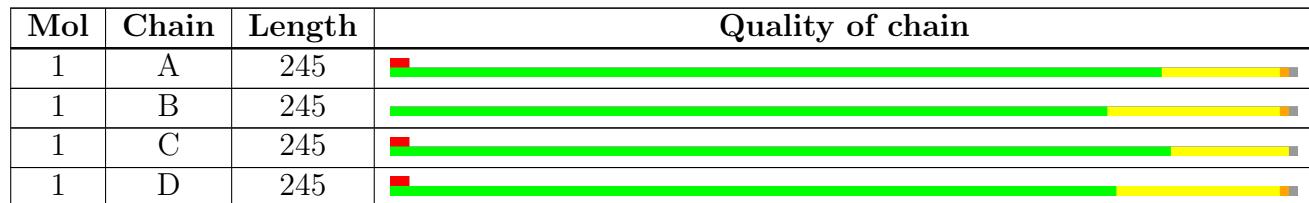
2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 8745 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Tryptase alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	242	Total	C	N	O	S	54	8	0
			1976	1264	345	353	14			
1	B	242	Total	C	N	O	S	60	8	0
			1976	1264	345	353	14			
1	C	243	Total	C	N	O	S	60	8	0
			1985	1270	347	354	14			
1	D	243	Total	C	N	O	S	57	8	0
			1985	1270	347	354	14			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	59	VAL	LEU	ENGINEERED	UNP P15157
A	216	GLY	ASP	ENGINEERED	UNP P15157
B	59	VAL	LEU	ENGINEERED	UNP P15157
B	216	GLY	ASP	ENGINEERED	UNP P15157
C	59	VAL	LEU	ENGINEERED	UNP P15157
C	216	GLY	ASP	ENGINEERED	UNP P15157
D	59	VAL	LEU	ENGINEERED	UNP P15157
D	216	GLY	ASP	ENGINEERED	UNP P15157

- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	3	Total	C	N	O	7	0
			38	22	2	14		
2	D	3	Total	C	N	O	14	0
			38	22	2	14		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	59	VAL	LEU	ENGINEERED	UNP P15157
B	216	GLY	ASP	ENGINEERED	UNP P15157
D	59	VAL	LEU	ENGINEERED	UNP P15157
D	216	GLY	ASP	ENGINEERED	UNP P15157

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	179	Total 179	O 179	0	4
3	B	194	Total 194	O 194	0	5
3	C	185	Total 185	O 185	0	3
3	D	189	Total 189	O 189	0	4

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.

- Molecule 1: Tryptase alpha-1

Chain A:
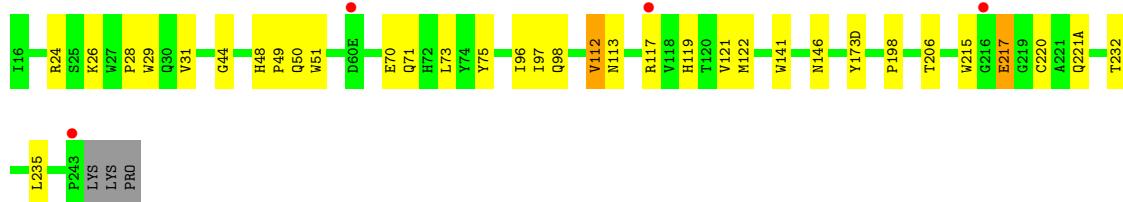
- Molecule 1: Tryptase alpha-1

Chain B:

- Molecule 1: Tryptase alpha-1

Chain C:
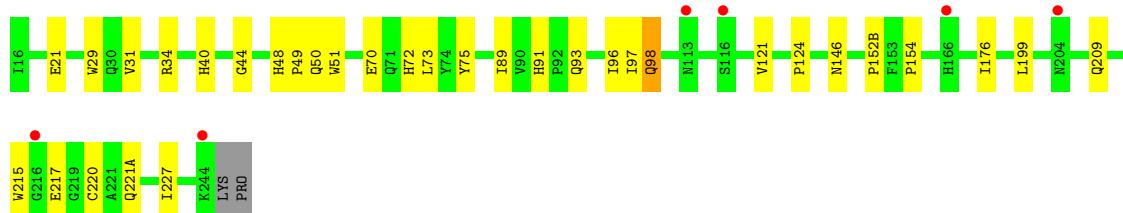
- Molecule 1: Tryptase alpha-1

Chain D:
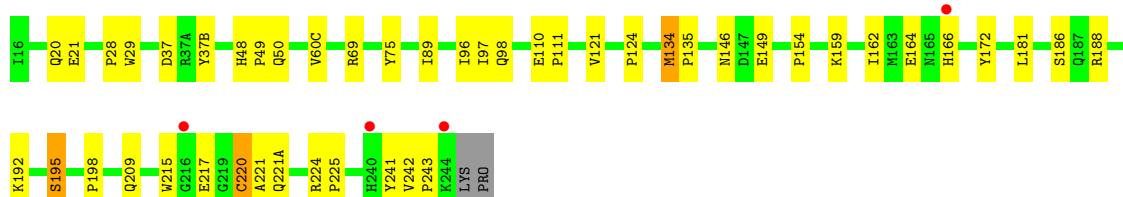
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	83.31Å 88.93Å 162.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.90 – 2.10 12.91 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.9 (12.90-2.10) 99.5 (12.91-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.91 (at 2.09Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.216 , 0.245 0.211 , 0.240	Depositor DCC
R_{free} test set	3684 reflections (5.51%)	DCC
Wilson B-factor (Å^2)	25.5	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.50 , 69.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$< |L| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Outliers	10 of 70547 reflections (0.014%)	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8745	wwPDB-VP
Average B, all atoms (Å^2)	25.0	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 43.49 % 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 1.7514e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1] Intensities estimated from amplitudes.

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: NAG, FUC

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	0.49	0/2041	0.71	0/2795
1	B	0.52	0/2041	0.73	0/2795
1	C	0.49	0/2050	0.74	1/2806 (0.0%)
1	D	0.50	0/2050	0.72	0/2806
All	All	0.50	0/8182	0.73	1/11202 (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	C	199	LEU	N-CA-C	-5.19	97.00	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1976	0	1904	31	0
1	B	1976	0	1903	42	0
1	C	1985	0	1917	28	0
1	D	1985	0	1916	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	38	0	34	0	0
2	D	38	0	34	0	0
3	A	179	0	0	1	0
3	B	194	0	0	5	0
3	C	185	0	0	2	0
3	D	189	0	0	6	0
All	All	8745	0	7708	132	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (132) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:221(A):GLN:HG2	3:A:421:HOH:O	1.68	0.90
1:B:219[B]:GLY:HA3	3:B:1141:HOH:O	1.69	0.90
1:D:48:HIS:HD2	1:D:50:GLN:H	1.18	0.90
1:D:192:LYS:HE3	3:D:1136:HOH:O	1.77	0.85
1:B:48:HIS:HD2	1:B:50:GLN:H	1.27	0.82
1:C:21:GLU:HG3	1:C:154:PRO:HB2	1.63	0.79
1:A:48:HIS:HD2	1:A:50:GLN:H	1.31	0.77
1:C:48:HIS:HD2	1:C:50:GLN:H	1.35	0.75
1:D:217[B]:GLU:HG2	1:D:220[B]:CYS:SG	2.26	0.74
1:B:50:GLN:OE1	1:B:111:PRO:HG3	1.89	0.72
1:C:217[B]:GLU:HG3	3:C:387:HOH:O	1.89	0.72
1:B:91:HIS:HD2	1:B:93:GLN:H	1.35	0.71
1:A:75:TYR:HB2	1:B:75:TYR:CE2	2.26	0.71
1:C:75:TYR:HB2	1:D:75:TYR:CE2	2.24	0.70
1:B:98:GLN:H	1:B:98:GLN:NE2	1.89	0.70
1:B:72:HIS:HE1	3:B:1085:HOH:O	1.75	0.69
1:C:98:GLN:NE2	1:C:98:GLN:H	1.92	0.68
1:D:97:ILE:HD12	1:D:215[A]:TRP:HB3	1.77	0.65
1:A:98:GLN:HB2	1:D:96:ILE:HD13	1.78	0.65
1:D:48:HIS:CD2	1:D:50:GLN:H	2.07	0.65
1:A:49:PRO:O	1:A:112:VAL:HG13	1.97	0.65
1:B:134:MET:HE2	1:B:135:PRO:HD2	1.80	0.64
1:B:217[B]:GLU:HA	1:B:220[B]:CYS:SG	2.38	0.64
1:C:217[B]:GLU:HG2	1:C:220[B]:CYS:SG	2.39	0.63
1:A:97:ILE:HD12	1:A:215[A]:TRP:HB3	1.81	0.63
1:B:98:GLN:H	1:B:98:GLN:HE21	1.44	0.62
1:D:195:SER:HB2	3:D:1049:HOH:O	1.98	0.62
1:D:146:ASN:OD1	1:D:217[B]:GLU:OE2	2.17	0.62
1:A:96:ILE:HD13	1:D:98:GLN:HB2	1.81	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:240:HIS:HB2	3:B:1070:HOH:O	2.00	0.61
1:B:48:HIS:CD2	1:B:49:PRO:HD2	2.35	0.61
1:C:98:GLN:HE21	1:C:98:GLN:H	1.45	0.61
1:D:164:GLU:OE1	1:D:166:HIS:HD2	1.84	0.61
1:D:97:ILE:HD12	1:D:215[A]:TRP:CB	2.30	0.61
1:B:97:ILE:HD12	1:B:215[A]:TRP:HB3	1.83	0.60
1:B:134:MET:CE	1:B:135:PRO:HD2	2.33	0.59
1:C:91:HIS:HD2	1:C:93:GLN:H	1.50	0.59
1:C:217[B]:GLU:HA	1:C:220[B]:CYS:SG	2.43	0.58
1:C:97:ILE:HD12	1:C:215[A]:TRP:HB3	1.84	0.58
1:D:221(A):GLN:HE21	1:D:224:ARG:HG3	1.70	0.57
1:B:96:ILE:HD13	1:C:98:GLN:HB2	1.85	0.57
1:A:217[B]:GLU:HA	1:A:220[B]:CYS:SG	2.45	0.57
1:A:48:HIS:CD2	1:A:50:GLN:H	2.19	0.56
1:D:146:ASN:OD1	1:D:220[B]:CYS:HB2	2.06	0.56
1:A:96:ILE:HD12	1:D:96:ILE:HD12	1.89	0.55
1:C:48:HIS:CD2	1:C:50:GLN:H	2.22	0.55
1:A:75:TYR:HB2	1:B:75:TYR:CD2	2.43	0.54
1:B:217[B]:GLU:O	1:B:217[B]:GLU:OE1	2.24	0.54
1:D:159:LYS:HE2	3:D:1100:HOH:O	2.07	0.54
1:D:50:GLN:OE1	1:D:111:PRO:HG3	2.08	0.54
1:D:134:MET:HG3	1:D:135:PRO:HD2	1.90	0.54
1:B:37:ASP:C	1:B:37(B):TYR:H	2.10	0.54
1:A:31:VAL:HG22	1:A:44:GLY:C	2.29	0.53
1:A:97:ILE:HD12	1:A:215[A]:TRP:CB	2.38	0.53
1:A:112:VAL:HG23	1:A:113:ASN:N	2.23	0.53
1:C:91:HIS:HE1	3:C:274:HOH:O	1.92	0.53
1:B:48:HIS:CD2	1:B:50:GLN:H	2.18	0.52
1:B:69:ARG:HG2	1:B:69:ARG:HH21	1.75	0.52
1:C:70:GLU:OE1	1:C:73:LEU:HA	2.09	0.52
1:D:110:GLU:HG3	3:D:1145:HOH:O	2.09	0.52
1:C:75:TYR:HB2	1:D:75:TYR:CD2	2.45	0.51
1:D:217[B]:GLU:HA	1:D:220[B]:CYS:SG	2.50	0.51
1:C:48:HIS:CD2	1:C:49:PRO:HD2	2.46	0.51
1:A:29:TRP:CG	1:A:121:VAL:HB	2.45	0.51
1:C:176:ILE:HD12	1:C:227:ILE:HD12	1.93	0.51
1:A:96:ILE:CD1	1:D:96:ILE:HD12	2.41	0.50
1:D:124:PRO:HD3	1:D:209:GLN:O	2.12	0.50
1:A:96:ILE:HD12	1:D:96:ILE:CD1	2.41	0.50
1:B:195:SER:HB2	3:B:1068:HOH:O	2.10	0.50
1:B:29:TRP:CD2	1:B:121:VAL:HB	2.46	0.50
1:D:37:ASP:C	1:D:37(B):TYR:H	2.15	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:164:GLU:OE2	1:D:166:HIS:HB2	2.12	0.48
1:A:48:HIS:CD2	1:A:49:PRO:HD2	2.48	0.48
1:A:29:TRP:CD2	1:A:121:VAL:HB	2.47	0.48
1:D:181:LEU:HD23	1:D:181:LEU:C	2.33	0.48
1:D:28:PRO:HA	1:D:69:ARG:HD2	1.96	0.48
1:B:146:ASN:OD1	1:B:220[B]:CYS:HB2	2.13	0.47
1:D:172:TYR:CE1	1:D:225:PRO:HD2	2.49	0.47
1:B:34:ARG:HD3	1:B:40:HIS:HA	1.96	0.47
1:B:96:ILE:CD1	1:C:96:ILE:CD1	2.93	0.47
1:B:97:ILE:HD12	1:B:215[A]:TRP:CB	2.44	0.47
1:A:70:GLU:OE1	1:A:73:LEU:HA	2.15	0.47
1:B:89:ILE:HD13	1:B:241:TYR:CD1	2.50	0.46
1:C:29:TRP:CG	1:C:121:VAL:HB	2.49	0.46
1:D:21:GLU:HG3	1:D:154:PRO:HB2	1.96	0.46
1:D:217[B]:GLU:HB2	3:D:1131:HOH:O	2.16	0.46
1:A:146:ASN:OD1	1:A:220[B]:CYS:HB2	2.16	0.46
1:B:134:MET:HA	1:B:134:MET:HE3	1.98	0.46
1:C:29:TRP:CD2	1:C:121:VAL:HB	2.50	0.45
1:C:31:VAL:HG22	1:C:44:GLY:C	2.37	0.45
1:D:172:TYR:HE1	1:D:225:PRO:HD2	1.82	0.45
1:B:91:HIS:CD2	1:B:93:GLN:H	2.24	0.45
1:D:186:SER:O	1:D:221[B]:ALA:HB1	2.17	0.44
1:C:146:ASN:OD1	1:C:220[B]:CYS:HB2	2.17	0.44
1:D:220[A]:CYS:O	1:D:221[A]:ALA:HB3	2.18	0.44
1:D:48:HIS:CD2	1:D:49:PRO:HD2	2.52	0.44
1:D:242:VAL:HA	1:D:243:PRO:HD3	1.92	0.43
1:D:215[B]:TRP:O	3:D:1063:HOH:O	2.21	0.43
1:A:28:PRO:HG3	1:A:119:HIS:CE1	2.53	0.43
1:A:48:HIS:HB3	1:A:51:TRP:HB2	2.00	0.43
1:B:216[B]:GLY:O	1:B:219[B]:GLY:N	2.50	0.43
1:B:164:GLU:OE2	1:B:166:HIS:HB2	2.19	0.43
1:B:84:PRO:HB2	1:B:109:GLU:CD	2.38	0.43
1:B:29:TRP:CG	1:B:121:VAL:HB	2.53	0.43
1:D:164:GLU:OE1	1:D:166:HIS:CD2	2.68	0.43
1:A:122:MET:HE2	1:A:206:THR:HG21	2.01	0.42
1:A:24:ARG:HA	1:A:71:GLN:OE1	2.19	0.42
1:B:51:TRP:CH2	1:B:107:GLU:HB2	2.54	0.42
1:A:49:PRO:O	1:A:112:VAL:CG1	2.66	0.42
1:B:185:ASN:HB2	3:B:1142:HOH:O	2.20	0.42
1:A:122:MET:CE	1:A:206:THR:HG21	2.49	0.42
1:A:232:THR:HA	1:A:235:LEU:HG	2.01	0.42
1:A:173(D):TYR:CE2	1:D:60(C):VAL:HA	2.55	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:28:PRO:HA	1:B:69:ARG:HD2	2.02	0.41
1:D:29:TRP:CD2	1:D:121:VAL:HB	2.55	0.41
1:C:51:TRP:HZ3	1:C:89:ILE:HD13	1.86	0.41
1:D:89:ILE:HD13	1:D:241:TYR:CD1	2.55	0.41
1:D:29:TRP:CG	1:D:121:VAL:HB	2.54	0.41
1:B:91:HIS:CE1	1:B:234:TYR:CE1	3.08	0.41
1:C:91:HIS:CD2	1:C:93:GLN:H	2.35	0.41
1:B:124:PRO:HD3	1:B:209:GLN:O	2.21	0.41
1:B:51:TRP:CZ3	1:B:107:GLU:HB2	2.55	0.41
1:A:96:ILE:CD1	1:D:96:ILE:CD1	2.98	0.41
1:B:73:LEU:O	1:B:74:TYR:HB2	2.20	0.41
1:C:72:HIS:HB3	1:C:152(B):PRO:O	2.21	0.41
1:C:34:ARG:HD3	1:C:40:HIS:HA	2.02	0.41
1:B:48:HIS:CD2	1:B:49:PRO:CD	3.03	0.40
1:B:181:LEU:HD23	1:B:181:LEU:C	2.42	0.40
1:C:21:GLU:CG	1:C:154:PRO:HB2	2.44	0.40
1:A:73:LEU:HG	1:A:141:TRP:CD1	2.57	0.40
1:D:162:ILE:CD1	1:D:181:LEU:HD21	2.51	0.40
1:C:124:PRO:HD3	1:C:209:GLN:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

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	248/245 (101%)	228 (92%)	18 (7%)	2 (1%)	27	20
1	B	248/245 (101%)	229 (92%)	17 (7%)	2 (1%)	27	20
1	C	249/245 (102%)	229 (92%)	20 (8%)	0	100	100
1	D	249/245 (102%)	232 (93%)	15 (6%)	2 (1%)	27	20
All	All	994/980 (101%)	918 (92%)	70 (7%)	6 (1%)	50	28

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	217[A]	GLU
1	A	217[B]	GLU
1	B	217[A]	GLU
1	B	217[B]	GLU
1	D	220[A]	CYS
1	D	220[B]	CYS

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	215/213 (101%)	211 (98%)	4 (2%)	69	73
1	B	215/213 (101%)	208 (97%)	7 (3%)	50	51
1	C	216/213 (101%)	214 (99%)	2 (1%)	87	91
1	D	216/213 (101%)	210 (97%)	6 (3%)	56	59
All	All	862/852 (101%)	843 (98%)	19 (2%)	63	68

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

Mol	Chain	Res	Type
1	A	26	LYS
1	A	112	VAL
1	A	117	ARG
1	A	198	PRO
1	B	20	GLN
1	B	98	GLN
1	B	110	GLU
1	B	134	MET
1	B	149	GLU
1	B	177	ARG
1	B	198	PRO
1	C	98	GLN
1	C	221(A)	GLN
1	D	20	GLN
1	D	134	MET
1	D	149	GLU
1	D	188	ARG

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Mol	Chain	Res	Type
1	D	195	SER
1	D	198	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	HIS
1	A	119	HIS
1	A	223	ASN
1	B	48	HIS
1	B	72	HIS
1	B	91	HIS
1	B	98	GLN
1	B	221(A)	GLN
1	B	240	HIS
1	C	48	HIS
1	C	91	HIS
1	C	98	GLN
1	D	30	GLN
1	D	48	HIS
1	D	166	HIS
1	D	221(A)	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

6 carbohydrates 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	NAG	B	1000	1,2	12,14,15	0.71	0	15,19,21	0.71	0
2	NAG	B	1001	2	12,14,15	0.59	0	15,19,21	0.70	0
2	FUC	B	1002	2	9,10,11	0.59	0	10,14,16	0.66	0
2	NAG	D	1000	1,2	12,14,15	0.65	0	15,19,21	0.78	0
2	NAG	D	1001	2	12,14,15	0.38	0	15,19,21	0.70	0
2	FUC	D	1002	2	9,10,11	0.54	0	10,14,16	0.30	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
2	NAG	B	1000	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1001	2	-	0/6/23/26	0/1/1/1
2	FUC	B	1002	2	-	0/0/17/20	0/1/1/1
2	NAG	D	1000	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	1001	2	-	0/6/23/26	0/1/1/1
2	FUC	D	1002	2	-	0/0/17/20	0/1/1/1

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.

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

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(Å²)	Q<0.9
1	A	242/245 (98%)	-0.06	4 (1%)	67	71	16, 24, 35, 44	14 (5%)
1	B	242/245 (98%)	-0.23	0	100	100	15, 22, 33, 41	13 (5%)
1	C	243/245 (99%)	-0.13	6 (2%)	54	59	15, 23, 36, 47	14 (5%)
1	D	243/245 (99%)	-0.12	4 (1%)	68	72	15, 23, 35, 53	13 (5%)
All	All	970/980 (98%)	-0.13	14 (1%)	72	76	15, 23, 35, 53	54 (5%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	244	LYS	3.5
1	C	204	ASN	3.4
1	C	244	LYS	2.9
1	C	113	ASN	2.8
1	D	216[A]	GLY	2.8
1	A	216[A]	GLY	2.8
1	D	166	HIS	2.7
1	C	216[A]	GLY	2.4
1	C	116	SER	2.3
1	D	240	HIS	2.3
1	A	243	PRO	2.2
1	A	117	ARG	2.2
1	A	60(E)	ASP	2.2
1	C	166	HIS	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 ⓘ

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, 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	RSR	LLDF	B-factors($Å^2$)	Q<0.9
2	NAG	B	1000	14/15	0.36	-	40,44,47,51	5
2	FUC	D	1002	10/11	0.30	-	48,49,50,50	0
2	FUC	B	1002	10/11	0.29	-	47,48,50,50	0
2	NAG	B	1001	14/15	0.39	-	51,53,54,56	2
2	NAG	D	1001	14/15	0.32	-	28,30,33,35	12
2	NAG	D	1000	14/15	0.42	-	43,45,48,50	2

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.