



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 03:56 am GMT

PDB ID : 2IAM  
Title : Structural basis for recognition of mutant self by a tumor-specific, MHC class II-restricted TCR  
Authors : Deng, L.; Langley, R.J.; Mariuzza, R.A.  
Deposited on : 2006-09-08  
Resolution : 2.80 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](mailto: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.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

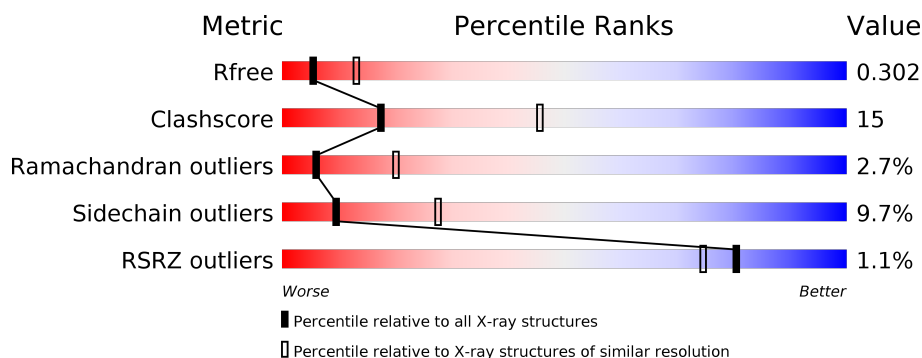
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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  $\geq 3$ , 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.

Mol	Chain	Length	Quality of chain
1	A	182	<div> <div>2%</div> <div> <div></div> <div>58%</div> <div>33%</div> <div>6%</div> <div>••</div> </div> </div>
2	B	190	<div> <div>2%</div> <div> <div></div> <div>65%</div> <div>26%</div> <div>•••</div> </div> </div>
3	P	15	<div> <div></div> <div> <div>67%</div> <div>27%</div> <div>7%</div> </div> </div>
4	C	202	<div> <div></div> <div> <div>61%</div> <div>31%</div> <div>•••</div> </div> </div>
5	D	240	<div> <div>%</div> <div> <div></div> <div>63%</div> <div>30%</div> <div>5%</div> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6551 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 HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	0	0	0
			1473	954	239	275	5			

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	182	Total	C	N	O	S	0	0	0
			1487	936	264	281	6			

- Molecule 3 is a protein called 15-mer peptide from Triosephosphate isomerase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	P	15	Total	C	N	O	0	0	0
			104	66	17	21			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	28	ILE	THR	ENGINEERED	UNP P60174

- Molecule 4 is a protein called CD4+ T cell receptor E8 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	C	198	Total	C	N	O	S	0	0	0
			1546	967	260	312	7			

- Molecule 5 is a protein called CD4+ T cell receptor E8 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	239	Total	C	N	O	S	0	0	0
			1901	1206	324	362	9			

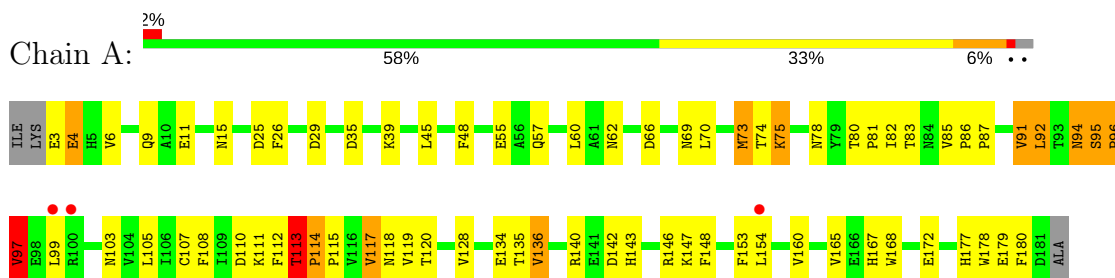
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	17	Total 17	O 17	0	0
6	B	7	Total 7	O 7	0	0
6	C	6	Total 6	O 6	0	0
6	D	9	Total 9	O 9	0	0
6	P	1	Total 1	O 1	0	0

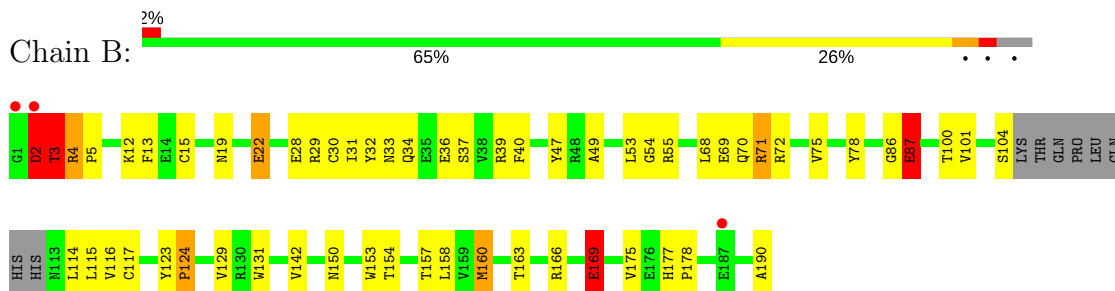
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

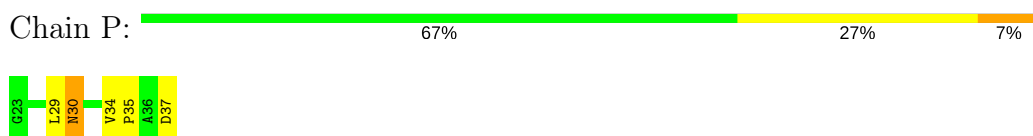
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



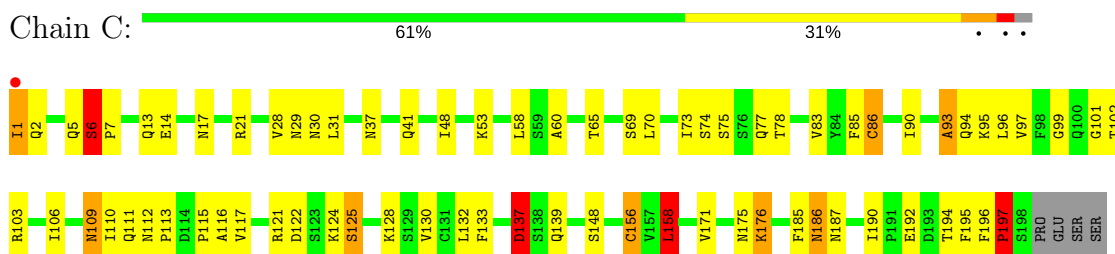
- Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain



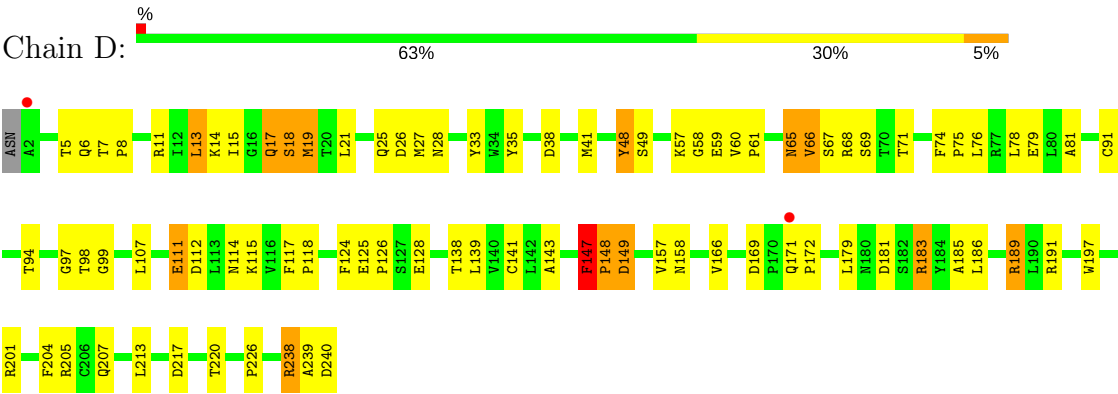
- Molecule 3: 15-mer peptide from Triosephosphate isomerase



- Molecule 4: CD4+ T cell receptor E8 alpha chain



- Molecule 5: CD4+ T cell receptor E8 beta chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.39Å 270.54Å 97.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.91 – 2.80 41.91 – 2.80	Depositor EDS
% Data completeness (in resolution range)	92.2 (41.91-2.80) 92.2 (41.91-2.80)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.74 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.207 , 0.279 0.238 , 0.302	Depositor DCC
$R_{free}$ test set	1328 reflections (5.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	61.5	Xtriage
Anisotropy	0.636	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 19.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6551	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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	0.91	3/1518 (0.2%)	0.91	3/2070 (0.1%)
2	B	1.32	3/1523 (0.2%)	0.92	1/2067 (0.0%)
3	P	1.09	0/104	1.19	0/139
4	C	0.91	1/1579 (0.1%)	0.96	4/2148 (0.2%)
5	D	0.96	4/1956 (0.2%)	0.94	2/2666 (0.1%)
All	All	1.03	11/6680 (0.2%)	0.94	10/9090 (0.1%)

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	A	0	1
2	B	0	3
4	C	0	2
5	D	0	3
All	All	0	9

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	169	GLU	CD-OE2	36.50	1.65	1.25
2	B	169	GLU	CD-OE1	9.63	1.36	1.25
5	D	111	GLU	CG-CD	7.62	1.63	1.51
4	C	86	CYS	CB-SG	-7.57	1.69	1.82
2	B	190	ALA	C-O	7.11	1.36	1.23
1	A	179	GLU	CD-OE1	6.06	1.32	1.25
5	D	141	CYS	CB-SG	-5.76	1.72	1.81
5	D	111	GLU	CB-CG	5.74	1.63	1.52
5	D	26	ASP	CB-CG	5.70	1.63	1.51
1	A	179	GLU	CG-CD	5.31	1.59	1.51
1	A	179	GLU	CB-CG	5.19	1.62	1.52



All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	THR	C-N-CD	-7.39	104.34	120.60
5	D	183	ARG	NE-CZ-NH1	6.83	123.72	120.30
4	C	93	ALA	C-N-CA	-6.20	106.20	121.70
2	B	169	GLU	CG-CD-OE2	-5.57	107.16	118.30
5	D	147	PHE	C-N-CD	-5.47	108.56	120.60
4	C	156	CYS	CA-CB-SG	5.35	123.62	114.00
1	A	113	THR	C-N-CA	5.34	144.44	122.00
4	C	137	ASP	CB-CG-OD1	5.31	123.08	118.30
1	A	110	ASP	CB-CG-OD2	-5.16	113.66	118.30
4	C	158	LEU	CA-CB-CG	5.03	126.88	115.30

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	113	THR	Peptide
2	B	123	TYR	Peptide
2	B	169	GLU	Sidechain
2	B	3	THR	Peptide
4	C	1	ILE	Peptide
4	C	6	SER	Peptide
5	D	147	PHE	Peptide
5	D	18	SER	Peptide
5	D	7	THR	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	1473	0	1407	48	0
2	B	1487	0	1419	46	0
3	P	104	0	109	7	0
4	C	1546	0	1474	53	0
5	D	1901	0	1800	56	0
6	A	17	0	0	1	0
6	B	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	6	0	0	0	0
6	D	9	0	0	1	0
6	P	1	0	0	0	0
All	All	6551	0	6209	196	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 15.

All (196) 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)
2:B:169:GLU:OE2	2:B:169:GLU:CD	1.65	1.31
2:B:19:ASN:HD22	2:B:22:GLU:HG2	1.11	1.16
2:B:2:ASP:O	2:B:3:THR:HB	1.49	1.11
5:D:94:THR:HG22	5:D:99:GLY:HA2	1.34	1.04
1:A:82:ILE:HD13	1:A:114:PRO:HD3	1.48	0.93
5:D:13:LEU:HD13	5:D:81:ALA:HB2	1.58	0.83
5:D:149:ASP:OD1	5:D:172:PRO:HG3	1.79	0.82
2:B:4:ARG:HB2	2:B:5:PRO:HD2	1.61	0.82
5:D:117:PHE:CD1	5:D:183:ARG:HD3	2.17	0.78
2:B:69:GLU:OE2	4:C:53:LYS:HD2	1.83	0.77
5:D:169:ASP:OD1	5:D:189:ARG:NH2	2.20	0.74
1:A:69:ASN:OD1	3:P:34:VAL:HG22	1.86	0.74
5:D:6:GLN:HE22	5:D:91:CYS:H	1.36	0.74
1:A:3:GLU:HG2	1:A:4:GLU:H	1.52	0.72
4:C:65:THR:CG2	4:C:65:THR:O	2.38	0.72
5:D:94:THR:CG2	5:D:99:GLY:HA2	2.17	0.72
2:B:19:ASN:ND2	2:B:22:GLU:HG2	1.96	0.71
1:A:94:ASN:HB3	1:A:103:ASN:OD1	1.91	0.71
4:C:117:VAL:HA	4:C:132:LEU:O	1.90	0.71
4:C:6:SER:HB3	4:C:21:ARG:HB3	1.74	0.70
2:B:2:ASP:O	2:B:3:THR:CB	2.32	0.69
5:D:38:ASP:O	5:D:41:MET:HB2	1.92	0.69
1:A:105:LEU:HG	1:A:153:PHE:CE1	2.26	0.69
1:A:15:ASN:HB2	1:A:70:LEU:HD21	1.74	0.69
5:D:6:GLN:NE2	5:D:91:CYS:H	1.90	0.68
1:A:92:LEU:HG	1:A:108:PHE:CE1	2.28	0.68
1:A:35:ASP:O	1:A:39:LYS:N	2.28	0.67
2:B:115:LEU:O	2:B:160:MET:HA	1.95	0.67
5:D:33:TYR:HD2	5:D:48:TYR:HB2	1.63	0.64
5:D:58:GLY:O	5:D:61:PRO:HD3	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:30:ASN:HD22	3:P:30:ASN:H	1.46	0.64
1:A:92:LEU:HG	1:A:108:PHE:HE1	1.62	0.64
4:C:90:ILE:HD12	4:C:95:LYS:HB2	1.80	0.64
5:D:13:LEU:HD13	5:D:81:ALA:CB	2.28	0.62
2:B:157:THR:C	2:B:158:LEU:HD12	2.20	0.62
1:A:95:SER:CB	1:A:96:PRO:HD2	2.30	0.61
4:C:29:ASN:OD1	4:C:30:ASN:N	2.30	0.61
5:D:205:ARG:NH1	5:D:207:GLN:OE1	2.28	0.61
5:D:33:TYR:CD2	5:D:48:TYR:HB2	2.36	0.61
5:D:238:ARG:HB3	5:D:238:ARG:HH11	1.66	0.60
2:B:129:VAL:HG22	2:B:175:VAL:HG13	1.82	0.60
1:A:97:VAL:HG11	1:A:178:TRP:HH2	1.66	0.60
4:C:117:VAL:O	4:C:197:PRO:HG2	2.02	0.60
1:A:113:THR:HG23	1:A:114:PRO:HD2	1.83	0.59
1:A:142:ASP:O	1:A:143:HIS:HB2	2.03	0.59
4:C:65:THR:HG22	4:C:65:THR:O	2.03	0.59
5:D:11:ARG:HG2	5:D:19:MET:CE	2.32	0.59
4:C:5:GLN:NE2	4:C:86:CYS:H	2.00	0.58
3:P:30:ASN:ND2	3:P:30:ASN:H	2.01	0.58
2:B:33:ASN:O	2:B:34:GLN:CB	2.49	0.58
1:A:82:ILE:HD13	1:A:114:PRO:CD	2.29	0.57
2:B:101:VAL:HA	2:B:116:VAL:O	2.05	0.57
5:D:18:SER:HB3	5:D:79:GLU:O	2.04	0.57
1:A:99:LEU:HD21	1:A:180:PHE:CE2	2.40	0.56
5:D:205:ARG:HH11	5:D:205:ARG:HG2	1.70	0.56
5:D:57:LYS:HB3	5:D:61:PRO:HG3	1.87	0.56
2:B:124:PRO:HD2	2:B:177:HIS:NE2	2.21	0.56
5:D:65:ASN:HD22	5:D:66:VAL:H	1.55	0.55
4:C:158:LEU:O	4:C:158:LEU:HD23	2.06	0.55
1:A:3:GLU:CG	1:A:4:GLU:H	2.19	0.55
5:D:15:ILE:HD12	5:D:111:GLU:HA	1.88	0.55
4:C:1:ILE:HD12	4:C:2:GLN:OE1	2.07	0.54
4:C:133:PHE:HB2	4:C:185:PHE:CE2	2.41	0.54
2:B:49:ALA:HB2	2:B:55:ARG:HA	1.87	0.54
5:D:125:GLU:OE1	5:D:238:ARG:HD2	2.07	0.54
1:A:57:GLN:N	1:A:57:GLN:OE1	2.38	0.53
5:D:169:ASP:HB2	5:D:186:LEU:HD12	1.90	0.53
2:B:78:TYR:CD2	3:P:29:LEU:HD22	2.43	0.53
1:A:85:VAL:HB	1:A:113:THR:HG22	1.91	0.53
2:B:124:PRO:CD	2:B:177:HIS:CE1	2.92	0.53
1:A:45:LEU:HD12	1:A:48:PHE:CZ	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:124:PRO:HD3	2:B:177:HIS:CE1	2.44	0.52
1:A:55:GLU:HG2	4:C:93:ALA:HB2	1.91	0.52
5:D:213:LEU:HB3	5:D:217:ASP:OD2	2.10	0.52
1:A:97:VAL:HG11	1:A:178:TRP:CH2	2.44	0.52
4:C:96:LEU:HB3	5:D:35:TYR:OH	2.09	0.52
5:D:126:PRO:HD3	5:D:139:LEU:HG	1.91	0.51
4:C:48:ILE:O	4:C:48:ILE:HG23	2.11	0.51
2:B:150:ASN:HB2	2:B:154:THR:O	2.10	0.51
4:C:158:LEU:HD11	5:D:191:ARG:HB2	1.92	0.51
5:D:118:PRO:HD3	5:D:226:PRO:HB3	1.92	0.50
1:A:111:LYS:HE2	1:A:140:ARG:HH22	1.76	0.50
4:C:5:GLN:HG3	4:C:101:GLY:H	1.76	0.50
2:B:39:ARG:O	2:B:47:TYR:HA	2.12	0.50
2:B:31:ILE:HD12	2:B:31:ILE:N	2.27	0.49
4:C:7:PRO:O	4:C:102:THR:HG23	2.13	0.49
4:C:83:VAL:HG22	4:C:103:ARG:HG3	1.94	0.49
4:C:113:PRO:HG3	4:C:137:ASP:HB3	1.95	0.49
1:A:11:GLU:OE1	1:A:66:ASP:OD2	2.30	0.49
5:D:166:VAL:HA	5:D:189:ARG:O	2.12	0.49
1:A:135:THR:O	1:A:147:LYS:HE2	2.13	0.49
1:A:142:ASP:O	1:A:143:HIS:CB	2.62	0.48
4:C:90:ILE:O	4:C:93:ALA:O	2.30	0.48
4:C:60:ALA:HA	4:C:70:LEU:O	2.14	0.48
4:C:158:LEU:C	4:C:158:LEU:HD23	2.34	0.48
1:A:25:ASP:OD1	1:A:26:PHE:N	2.47	0.47
4:C:185:PHE:C	4:C:187:ASN:H	2.16	0.47
5:D:143:ALA:O	5:D:185:ALA:HA	2.14	0.47
5:D:197:TRP:CZ2	5:D:238:ARG:HG3	2.49	0.47
2:B:19:ASN:HD22	2:B:22:GLU:CG	2.03	0.47
5:D:238:ARG:NH1	5:D:240:ASP:OD1	2.47	0.47
1:A:119:VAL:HG22	1:A:165:VAL:HG22	1.97	0.47
4:C:28:VAL:HG12	4:C:90:ILE:HA	1.95	0.47
4:C:78:THR:HA	4:C:106:ILE:HB	1.95	0.47
4:C:121:ARG:O	5:D:124:PHE:HA	2.13	0.47
4:C:122:ASP:HB2	4:C:128:LYS:HB2	1.95	0.47
5:D:138:THR:OG1	5:D:191:ARG:HG3	2.15	0.47
4:C:94:GLN:HA	4:C:94:GLN:HE21	1.80	0.46
1:A:9:GLN:O	2:B:12:LYS:HA	2.16	0.46
1:A:114:PRO:HA	1:A:115:PRO:HD2	1.54	0.46
2:B:4:ARG:HB2	2:B:5:PRO:CD	2.38	0.46
1:A:87:PRO:HB3	1:A:112:PHE:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:117:CYS:HB2	2:B:131:TRP:CZ2	2.50	0.46
2:B:33:ASN:O	2:B:34:GLN:HB2	2.15	0.46
4:C:186:ASN:N	4:C:186:ASN:OD1	2.49	0.46
1:A:73:MET:HB3	2:B:32:TYR:CD1	2.51	0.46
5:D:124:PHE:CD1	5:D:124:PHE:N	2.84	0.45
2:B:13:PHE:CE1	2:B:28:GLU:HG3	2.51	0.45
2:B:169:GLU:OE2	2:B:169:GLU:CG	2.57	0.45
4:C:111:GLN:HA	4:C:111:GLN:OE1	2.16	0.45
4:C:31:LEU:C	4:C:31:LEU:HD23	2.36	0.45
5:D:204:PHE:N	5:D:204:PHE:CD1	2.83	0.45
4:C:6:SER:CB	4:C:21:ARG:HB3	2.44	0.45
2:B:40:PHE:CE2	2:B:71:ARG:HB3	2.51	0.45
5:D:13:LEU:CD1	5:D:81:ALA:HB2	2.38	0.45
2:B:124:PRO:HD2	2:B:177:HIS:CE1	2.52	0.45
4:C:196:PHE:HA	4:C:197:PRO:HD2	1.72	0.45
1:A:82:ILE:HG12	1:A:83:THR:N	2.32	0.45
2:B:166:ARG:N	2:B:169:GLU:OE2	2.32	0.45
5:D:94:THR:HG22	5:D:98:THR:O	2.17	0.45
1:A:135:THR:CG2	1:A:148:PHE:HB2	2.46	0.44
1:A:167:HIS:ND1	1:A:168:TRP:N	2.65	0.44
4:C:5:GLN:NE2	4:C:85:PHE:HA	2.32	0.44
4:C:110:ILE:O	4:C:113:PRO:HD3	2.17	0.44
5:D:18:SER:HB2	5:D:78:LEU:O	2.17	0.44
2:B:4:ARG:CB	2:B:5:PRO:HD2	2.33	0.44
4:C:116:ALA:HB2	4:C:195:PHE:HB3	1.99	0.44
4:C:37:ASN:C	4:C:37:ASN:OD1	2.56	0.44
5:D:60:VAL:N	5:D:61:PRO:CD	2.81	0.44
5:D:205:ARG:NH1	5:D:205:ARG:HG2	2.32	0.44
2:B:29:ARG:HD3	2:B:36:GLU:OE2	2.18	0.44
5:D:157:VAL:O	5:D:158:ASN:C	2.56	0.44
1:A:80:THR:HA	1:A:81:PRO:HD3	1.70	0.43
4:C:130:VAL:HG23	5:D:124:PHE:CD2	2.53	0.43
4:C:194:THR:HB	4:C:196:PHE:CE2	2.53	0.43
1:A:6:VAL:HA	2:B:15:CYS:O	2.18	0.43
1:A:99:LEU:HG	1:A:99:LEU:H	1.66	0.43
4:C:48:ILE:HD13	4:C:53:LYS:HD3	2.00	0.43
3:P:30:ASN:HD22	3:P:30:ASN:N	2.10	0.43
5:D:13:LEU:CD2	5:D:17:GLN:HB3	2.49	0.43
2:B:124:PRO:HD3	2:B:177:HIS:HE1	1.84	0.43
4:C:185:PHE:C	4:C:187:ASN:N	2.72	0.43
2:B:86:GLY:O	2:B:87:GLU:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:112:ASP:OD2	5:D:114:ASN:HB3	2.19	0.43
2:B:30:CYS:O	2:B:36:GLU:HA	2.19	0.42
5:D:67:SER:O	5:D:75:PRO:HD2	2.19	0.42
5:D:27:MET:O	5:D:28:ASN:HB2	2.19	0.42
5:D:49:SER:OG	5:D:68:ARG:NH1	2.46	0.42
5:D:21:LEU:HD12	5:D:76:LEU:HD23	2.00	0.42
1:A:95:SER:HB2	1:A:96:PRO:HD2	2.02	0.42
1:A:136:VAL:N	6:A:185:HOH:O	2.46	0.42
2:B:70:GLN:O	2:B:71:ARG:C	2.56	0.42
4:C:95:LYS:HG2	5:D:48:TYR:CE1	2.54	0.42
1:A:117:VAL:HG23	1:A:117:VAL:O	2.20	0.42
4:C:74:SER:O	4:C:75:SER:C	2.57	0.42
2:B:177:HIS:CG	2:B:178:PRO:HD2	2.55	0.41
4:C:130:VAL:CG1	4:C:171:VAL:HG12	2.50	0.41
4:C:109:ASN:HD22	4:C:109:ASN:C	2.23	0.41
2:B:114:LEU:HD11	2:B:160:MET:HB3	2.01	0.41
4:C:112:ASN:O	4:C:113:PRO:C	2.58	0.41
2:B:177:HIS:CD2	2:B:178:PRO:HD2	2.55	0.41
1:A:11:GLU:OE1	1:A:62:ASN:HB3	2.20	0.41
4:C:137:ASP:C	4:C:137:ASP:OD1	2.59	0.41
4:C:65:THR:HG23	4:C:65:THR:O	2.18	0.41
5:D:169:ASP:O	5:D:186:LEU:HD11	2.21	0.41
1:A:29:ASP:HB3	2:B:153:TRP:CE2	2.56	0.41
5:D:14:LYS:HB2	6:D:243:HOH:O	2.21	0.41
1:A:3:GLU:CG	1:A:4:GLU:N	2.84	0.41
2:B:28:GLU:HB3	2:B:40:PHE:HB3	2.03	0.41
1:A:113:THR:HG23	1:A:114:PRO:CD	2.49	0.41
1:A:73:MET:O	1:A:74:THR:C	2.57	0.41
1:A:91:VAL:HG22	1:A:107:CYS:HA	2.03	0.41
4:C:175:ASN:C	4:C:176:LYS:O	2.59	0.41
4:C:115:PRO:O	4:C:194:THR:HA	2.21	0.41
5:D:149:ASP:CG	5:D:172:PRO:HG3	2.41	0.41
3:P:34:VAL:HB	3:P:35:PRO:HD2	2.02	0.41
1:A:85:VAL:HA	1:A:86:PRO:HD3	1.91	0.41
5:D:147:PHE:CD2	5:D:148:PRO:CD	3.04	0.41
5:D:238:ARG:NH1	5:D:238:ARG:HB3	2.33	0.41
4:C:124:LYS:O	4:C:125:SER:CB	2.69	0.40
2:B:68:LEU:O	2:B:72:ARG:HG3	2.21	0.40
2:B:37:SER:O	2:B:54:GLY:HA3	2.21	0.40
5:D:238:ARG:C	5:D:240:ASP:H	2.25	0.40
1:A:75:LYS:NZ	3:P:37:ASP:OD1	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:124:PRO:HD2	2:B:177:HIS:HE2	1.85	0.40
4:C:17:ASN:HA	4:C:73:ILE:O	2.22	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	177/182 (97%)	157 (89%)	15 (8%)	5 (3%)	6	19
2	B	178/190 (94%)	161 (90%)	12 (7%)	5 (3%)	6	19
3	P	13/15 (87%)	12 (92%)	1 (8%)	0	100	100
4	C	196/202 (97%)	173 (88%)	17 (9%)	6 (3%)	5	16
5	D	237/240 (99%)	218 (92%)	13 (6%)	6 (2%)	6	22
All	All	801/829 (97%)	721 (90%)	58 (7%)	22 (3%)	6	20

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	114	PRO
2	B	2	ASP
2	B	87	GLU
2	B	169	GLU
4	C	6	SER
4	C	192	GLU
4	C	197	PRO
5	D	8	PRO
5	D	148	PRO
5	D	149	ASP
4	C	99	GLY
5	D	71	THR

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Mol	Chain	Res	Type
1	A	4	GLU
1	A	97	VAL
2	B	3	THR
2	B	124	PRO
4	C	176	LYS
1	A	96	PRO
4	C	186	ASN
5	D	239	ALA
5	D	97	GLY
1	A	136	VAL

### 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	164/166 (99%)	145 (88%)	19 (12%)	6	19
2	B	163/171 (95%)	150 (92%)	13 (8%)	14	38
3	P	10/10 (100%)	9 (90%)	1 (10%)	9	26
4	C	178/182 (98%)	162 (91%)	16 (9%)	11	32
5	D	206/207 (100%)	185 (90%)	21 (10%)	8	25
All	All	721/736 (98%)	651 (90%)	70 (10%)	9	27

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	LEU
1	A	73	MET
1	A	75	LYS
1	A	78	ASN
1	A	91	VAL
1	A	92	LEU
1	A	94	ASN
1	A	95	SER
1	A	97	VAL

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Mol	Chain	Res	Type
1	A	117	VAL
1	A	118	ASN
1	A	120	THR
1	A	128	VAL
1	A	134	GLU
1	A	146	ARG
1	A	154	LEU
1	A	160	VAL
1	A	172	GLU
1	A	177	HIS
2	B	2	ASP
2	B	3	THR
2	B	4	ARG
2	B	22	GLU
2	B	53	LEU
2	B	71	ARG
2	B	75	VAL
2	B	87	GLU
2	B	100	THR
2	B	104	SER
2	B	142	VAL
2	B	160	MET
2	B	163	THR
3	P	30	ASN
4	C	13	GLN
4	C	14	GLU
4	C	41	GLN
4	C	58	LEU
4	C	69	SER
4	C	77	GLN
4	C	97	VAL
4	C	109	ASN
4	C	125	SER
4	C	137	ASP
4	C	139	GLN
4	C	148	SER
4	C	156	CYS
4	C	158	LEU
4	C	190	ILE
4	C	197	PRO
5	D	5	THR
5	D	13	LEU

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Mol	Chain	Res	Type
5	D	17	GLN
5	D	19	MET
5	D	25	GLN
5	D	48	TYR
5	D	59	GLU
5	D	65	ASN
5	D	66	VAL
5	D	69	SER
5	D	74	PHE
5	D	107	LEU
5	D	115	LYS
5	D	128	GLU
5	D	171	GLN
5	D	179	LEU
5	D	181	ASP
5	D	189	ARG
5	D	201	ARG
5	D	220	THR
5	D	238	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	ASN
1	A	149	HIS
2	B	19	ASN
2	B	33	ASN
2	B	64	GLN
2	B	92	GLN
2	B	150	ASN
2	B	156	GLN
3	P	30	ASN
4	C	5	GLN
4	C	94	GLN
4	C	168	ASN
4	C	187	ASN
5	D	6	GLN
5	D	65	ASN
5	D	96	HIS
5	D	150	HIS
5	D	199	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](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	179/182 (98%)	-0.19	3 (1%) 70 63	53, 68, 76, 79	0
2	B	182/190 (95%)	-0.16	3 (1%) 72 65	53, 66, 72, 75	0
3	P	15/15 (100%)	-0.33	0 100 100	45, 52, 69, 76	0
4	C	198/202 (98%)	-0.39	1 (0%) 90 88	43, 60, 84, 88	0
5	D	239/240 (99%)	-0.48	2 (0%) 86 81	45, 57, 71, 83	0
All	All	813/829 (98%)	-0.32	9 (1%) 80 74	43, 64, 77, 88	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	100	ARG	5.1
2	B	1	GLY	3.0
1	A	154	LEU	2.8
4	C	1	ILE	2.6
5	D	171	GLN	2.4
2	B	187	GLU	2.3
1	A	99	LEU	2.2
5	D	2	ALA	2.0
2	B	2	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.